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Please find below and/or attached an Office communication concerning this application or proceeding.

The time period for reply, if any, is set in the attached communication.

All the aims of the present invention have been met by the embodiments as set out below.

The present inventors identified a range of specific nucleotide sequences which are involved in the molecular pathways eventually leading to programmed cell death. The present inventors were able to identify via macro array screening a range of genes involved in a pathway eventually leading to programmed cell death in the yeast *Saccharomyces cerevisiae*. As explained in Example 2, genes showing a difference of a factor 5 or more in expression as a result of *Bax*-induced cell death, were identified as differentially expressed candidate genes. Some of these genes are clearly down-regulated in a *Bax*-expressing strain, while other genes show an upregulated expression (Table 1). Example 3 describes a further experiment wherein the results of differential expression were analysed using the Pathways™ software and differentially expressed nucleic acid sequence were identified.

According to a first embodiment, the invention relates to the use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which nucleic acid sequence is selected from:

(a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

(b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more

- preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75 or 80% identical, more preferably more than 85%, or 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453 or 455;
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e); and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

Sequence similarity searches were performed using the BLAST software package version 2. Identity and similarity percentages were calculated using
5 BLOSUM62 as a scoring matrix.

As known in the art, "similarity" between two polypeptides is determined by comparing the amino acid sequence and its conserved amino acid substitutes of one polypeptide to the sequence of a second polypeptide. Moreover, also known in the art is "identity" which means the degree of sequence relatedness between two polypeptide
10 or two polynucleotide sequences as determined by the identity of the match between two strings of such sequences. Both identity and similarity can be readily calculated. While there exist a number of methods to measure identity and similarity between two polynucleotide or polypeptide sequences, the terms "identity" and "similarity" are well known to skilled artisans (Carillo and Lipton, 1988). Methods commonly employed to
15 determine identity or similarity between two sequences include, but are not limited to, those disclosed in "Guide to Hige Computers (Bishop, 1994) and Carillo and Lipton (1988). Preferred methods to determine identity are designed to give the largest match between the two sequences tested. Methods to determine identity and similarity are codified in computer programs. Preferred computer program methods to determine
20 identity and similarity between two sequences include, but are not limited to, GCG program package (Devereux *et al.*, 1984), BLASTP, BLASTN and FASTA (Altschul *et al.*, 1990).

The nucleic acid sequences to be used according to this aspect of the invention from *Saccharomyces cerevisiae* are defined in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15,
25 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207,
30 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 457, 459, 461, 463, 465, 467, 469, 471 and 473 .

The invention also relates to nucleic acid sequences from *Candida albicans*, as represented by the SEQ ID NOs 285, 287, 289, 291, 293, 295, 297, 299, 301, 303,
35 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371,

373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481, and 483.

The expression "a pathway eventually leading to programmed cell death" refers
5 to a sequence of steps ultimately leading to cell death and which can be triggered at various steps in this pathway by various agents, such as Bax, Bak, CED4, hydrogen peroxide, diamide and farnesol.

The yeast or fungi according to the invention may be, but are not restricted to, pathogenic yeast or fungi. As such, yeast or fungi may cause infections in healthy
10 individuals as well as in immunocompromised patients.

The expression "treating diseases associated with yeast and fungi", not only refers to diseases or infections caused by said organisms but also refers to allergic reactions caused by said organisms, such as the so-called "professional diseases" in, for instance, bakery and brewery and that are caused by yeast or fungi which are
15 commonly known as "non-pathogenic".

The invention further relates to the use of nucleic acid sequence homologues of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125,
20 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295,
25 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465,
30 467, 469, 471, 473, 475, 477, 479, 481 or 483 but isolated from other yeast and fungi strains which are also involved in a pathway eventually leading to programmed cell death.

According to the invention, these sequences and their homologues in other yeast and fungi as well as the polypeptides which they encode represent novel
35 molecular targets which can be incorporated into an assay to selectively identify compounds capable of inhibiting or activating expression of such polypeptides.

Furthermore, the invention also relates to the potential use of said sequences in alleviating diseases or conditions associated with yeast or fungi infections, such as diseases caused by *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis* spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*, and *Sporothrix schenckii*.

According to another embodiment, the invention also relates to a nucleic acid sequence encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi selected from:

- (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90% or 95% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;

- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NO 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 475, 477, 479, 481 or 483; and,
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e), and
- (g) the complement of any of the nucleic acid sequences as specified in a) to f).

According to a more specific embodiment, these nucleic acid sequences are derived from *Saccharomyces cerevisiae*, *Candida albicans* or *Aspergillus fumigatus*.

A nucleic acid sequence according to the invention may comprise an mRNA sequence or alternatively a DNA sequence and preferably a cDNA sequence. A nucleic acid sequence according to the invention may also comprise any modified nucleotide known in the art.

The present invention further relates to a nucleic acid molecule capable of selectively hybridising to at least one of the nucleic acid molecules according to the invention, or the complement thereof.

The term "selectively hybridising" or "specifically hybridising" means hybridising under conditions wherein sequences can be detected which are homologues of the sequences of the invention, but which are for instance derived from heterologous cells or organisms, and wherein said sequences do not hybridize with known sequences. In a preferred embodiment, mammalian homologues can be detected. It is well known to the person skilled in the art which methods for hybridisation can be used and which conditions are necessary for selectively or specifically hybridising. Preferably, hybridization under high stringency conditions can be applied (Sambrook et al., 1989).

As such, the present invention also relates to the use of the nucleic acid sequences of the invention for detecting homologues in heterologous organisms including but not limited to mammalian organisms.

The term "nucleic acid sequence" also includes the complementary sequence
5 to any single stranded sequence given, or the antisense version thereof.

The invention also relates to mRNA, DNA or cDNA versions of the nucleic acid molecules of the invention.

The present invention more particularly relates to an antisense molecule comprising a nucleic acid sequence capable of hybridizing to any of the above defined
10 nucleic acid sequences.

Polynucleotides according to the invention may be inserted into vectors in an antisense orientation in order to provide for the production of antisense RNA. Antisense RNA or other antisense nucleic acids may also be produced by synthetic means.

The present invention also advantageously provides nucleic acid sequences of
15 at least approximately 10 contiguous nucleotides of a nucleic acid according to the invention and preferably from 10 to 50 nucleotides. These sequences may, advantageously be used as probes or primers to initiate replication, or the like. Such nucleic acid sequences may be produced according to techniques well known in the art, such as by recombinant or synthetic means. The probes will hybridise specifically
20 with any of the nucleic acid molecules of the invention. The primers will specifically amplify any of the nucleic acid molecules of the invention.

The probes or primers according to the invention may also be used in diagnostic kits or the like for detecting the presence of a nucleic acid according to the invention. These tests generally comprise contacting the probe with the sample under
25 hybridising conditions and detecting the presence of any duplex or triplex formation between the probe and any nucleic acid in the sample.

According to the present invention these probes may be anchored to a solid support. Preferably, they are present on an array so that multiple probes can simultaneously hybridize to a single biological sample. The probes can be spotted onto
30 the array or synthesized *in situ* on the array. (Lockhart *et al.*, 1996). A single array can contain more than 100, 500 or even 1,000 different probes in discrete locations. Such arrays can be used to screen for compounds interacting with said probes.

Advantageously, the nucleic acid sequences, according to the invention may be produced using recombinant or synthetic means, such as for example using PCR
35 cloning mechanisms which generally involve making a pair of primers, which may be from approximately 10 to 50 nucleotides to a region of the gene which is desired to be

cloned, bringing the primers into contact with mRNA, cDNA, or genomic DNA from the yeast or fungal cell, performing a polymerase chain reaction under conditions which bring about amplification of the desired region, isolating the amplified region or fragment and recovering the amplified DNA. Generally, such techniques as defined
5 herein are well known in the art, such as described in Sambrook *et al.* (1989). These techniques can be used to clone homologues of the nucleic acid sequences of the invention in other organisms.

The nucleic acids or oligonucleotides according to the invention may carry a revealing label. Suitable labels include radioisotopes such as ^{32}P , ^{33}P or ^{35}S , enzyme
10 labels or other protein labels such as biotin or fluorescent markers. Such labels may be added to the nucleic acids or oligonucleotides of the invention and may be detected using techniques known in the art.

According to another embodiment of the invention, the nucleic acid sequences according to the invention as defined above may, advantageously, be included in a
15 suitable expression vector which may be transformed, transfected or infected into a host cell. In such an expression vector the nucleic acid is operably linked to a control sequence, such as a suitable inducible promotor, or the like, to ensure expression of the proteins according to the invention in a suitable host cell. The expression vector may also comprise a reporter molecule. The expression vector may advantageously be
20 a plasmid, cosmid, virus or other suitable vector which is known to those skilled in the art. The expression vector and the host cell defined herein also form part of the present invention. Preferably the host cell is a lower eukaryotic cell such as a yeast cell or a fungal cell. Yeast and fungal cells are particularly advantageous because they provide the necessary post-translational modifications to the expressed proteins of the
25 invention, similar to those of the natural proteins from which they are derived. These modifications confer optimal conformation of said proteins, which when isolated may advantageously be used in kits, methods or the like.

The invention further relates to any nucleic acid as defined above for use as a medicament.

30 Nucleotide sequences according to the invention are particularly advantageous for providing selective therapeutic targets for treating yeast or fungi-associated infections. For example, an antisense nucleic acid capable of binding to the nucleic acid sequences according to the invention may be used to selectively inhibit expression of the corresponding polypeptides, leading to impaired growth or death of yeast and
35 fungi with reductions of associated illnesses or diseases.

According to another embodiment, the invention also relates to the use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2,
5 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48,
50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92,
94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126,
128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158,
160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190,
10 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222,
224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254,
256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286,
288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318,
320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350,
15 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382,
384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414,
416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446,
448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478,
480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of
20 said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar,
preferably more than 75% or 80% similar, more preferably more than 85%, 90% or
95% similar and most preferably more than 97% similar to any of the amino acid
sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28,
25 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72,
74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112,
114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144,
146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176,
178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208,
30 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240,
242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272,
274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304,
306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336,
338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368,
35 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400,
402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

- (c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 75% or 80% identical, more preferably more than 85%, 90% or 95% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),
for the preparation of a medicament for treating diseases associated with yeast or fungi.

The term "functional fragment" of a protein means a truncated version of the original protein or polypeptide referred to. The truncated protein sequence can vary widely in length; the minimum size being a sequence of sufficient size to provide a sequence with at least a comparable function and/or activity of the original sequence referred to, while the maximum size is not critical. In some applications, the maximum size usually is not substantially greater than that required to provide the desired activity and/or function(s) of the original sequence. A functional fragment can also relate to a subunit with similar function as said protein. Typically, the truncated amino acid sequence will range from about 5 to about 60 amino acids in length. More typically, however, the sequence will be a maximum of about 50 amino acids in length, preferably a maximum of about 60 amino acids. It is usually desirable to select sequences of at least about 10, 12 or 15 amino acids.

Functional fragments include those comprising an epitope which is specific or unique for the proteins according to the invention. Epitopes may be determined using, for example, peptide scanning techniques as described in Geysen *et al.* (1996). Preferred functional fragments have a length of at least, for example, 5, 10, 25, 50, 75,
5 100, 125, 150, 175 or 200 amino acids.

The polypeptides to be used according to this aspect of the invention from *Saccharomyces cerevisiae*, are represented by SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106,
10 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276,
15 278, 280, 282, 284, 458, 460, 462, 464, 466, 468, 470, 472 and 474 . Also according to the invention is the use of the polypeptides from *Candida albicans* as represented by the SEQ ID NOs 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378,
20 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 476, 478, 480, 482 and 484.

The polypeptide or protein according to the invention may also include variants of any of the polypeptides of the invention as specified above having conservative
25 amino acid changes.

The nucleic acid molecules or the polypeptides of the invention may be provided in a pharmaceutically acceptable carrier, diluent or excipient therefor.

The present invention also relates to a vaccine for immunizing a mammal against infections caused by yeast and fungi comprising at least one (recombinant)
30 nucleic acid molecule or at least one (recombinant) polypeptide of the invention in a pharmaceutically acceptable carrier.

Pharmaceutically acceptable carriers include any carrier that does not itself induce the production of antibodies harmful to the individual receiving the composition. Suitable carriers are typically large, slowly metabolizing macromolecules such as
35 proteins, polysaccharides, polylactic acids, polyglycolic acids, polymeric amino acids,

amino acid copolymers; and inactive virus particles. Such carriers are well known to those of ordinary skill in the art.

A "vaccine" is an immunogenic composition capable of eliciting protection against infections caused by yeast or fungi, whether partial or complete. A vaccine may
5 also be useful for treatment of an individual, in which case it is called a therapeutic vaccine.

Said vaccine compositions may include prophylactic as well as therapeutic vaccine compositions.

The term "therapeutic" refers to a composition capable of treating infections
10 caused by yeast or fungi.

Some of the pathways leading to apoptosis are conserved between mammalian cells and yeast or fungi. Therefore, targets which are part of such a conserved pathway may be used to stimulate or inhibit the apoptosis in mammalian cells. E.g. stimulation of apoptosis is desirable in the treatment of tumor cells/tissues.

15 According to another embodiment, the present invention provides a method of identifying compounds which selectively inhibit, induce or interfere with the expression/production of the polypeptides encoded by the nucleotide sequences of the invention, or compounds which selectively inhibit, activate or interfere with the functionality of polypeptides expressed from the nucleotide sequences according to the
20 invention, or which selectively inhibit, induce or interfere with the metabolic pathways in which these polypeptides are involved. Compounds may carry agonistic or antagonistic properties. The compounds to be screened may be of extracellular, intracellular, biologic or chemical origin.

Such a screening method may comprise the following steps (a) contacting a
25 compound to be tested with cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound, (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated cells is indicative of selective action of said
30 compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively
35 monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

The term "cells" as used above relates to any type of cells such as, but not limited to bacterial, yeast, fungal, plant or human cells:

Compounds found using this approach may additionally be tested on their efficiency in killing or inhibiting the growth of wild type cells in order to confirm their utility as medicament for treating wild type pathogenic strains/tumor cells.

According to the invention, the term "mutation" includes point mutations, deletions, insertions, duplications or any modification in the nucleic acid encoding said polypeptide, or at a different location in the genome of said cells, influencing the expression of said nucleic acid or polypeptide. In case point mutations occur, the number of nucleotides will be identical compared to the original sequence; only a change in nucleotide sequence can be observed. This stands in contrast with the other listed mutations where the number of the nucleotides will be different from the number observed in the wild type sequence and consequently will also reflect in a change of the nucleotide sequence.

Changes in morphologic and/or functional properties of cell components which can be monitored include for example morphological and molecular changes such as abnormal cell morphology, nuclear fragmentation, DNA breakage or changes in the expression of certain enzymes such as caspases, as well as monitoring changes in membrane potential or activity of mitochondria and release of cytochrome c from mitochondria. All these changes can be monitored on the whole cell which is contacted to the compound to be tested.

The invention also relates to a method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound, (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein

differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway, (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

Alternative methods for identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said compounds are involved, may comprise the use of any other method known in the art resulting in gene activation, gene inactivation, gene modulation or gene silencing.

The invention also relates to a method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene and (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested. This enables to analyse the influence of the compound onto all/most aspects of transcriptional activation. Alternatively additional tests can routinely be performed to test the influence of the compound onto mRNA stability, translation and protein stability. All these aspects influence the concentration of corresponding proteins and consequently influence the effect of these on the metabolism of the cell.

The invention further relates to a method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2, (b) detecting the complex formed between the compound to be tested and said polypeptide, (c) alternatively, examining the diminution/increase of complex formation between said polypeptide and a receptor/binding partner, caused by the addition of the compound being tested, (c) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

Detection of the complex formation can be performed using several approaches. First, binding of a compound onto a polypeptide can be studied using classical binding tests: one of the binding partners, compound or polypeptide is labeled and interaction of both is measured. Most of these tests comprise following steps:

incubating both binding partners in conditions where binding is allowed, separation of free label from bound label present in the complex formed between both partners, and measuring the number of labeled complexes formed. Separation of free and bound label can be performed via filtration, centrifugation or other means as known by the person skilled in the art. Other techniques allow visualisation of complex formation without the need of such a separating step. For example, test systems using SPA (scintillation proximity assay) beads are based on the principle that radioactive ^3H can only be measured when present in scintillation fluid. SPA beads contain scintillation fluid and can be coated with one of the binding partners. When this bead is approached and binds the other binding partner which is radioactively labeled, a signal will be detected allowing the complex to be visualised. Binding of the radioactive compound onto the scintillation bead is needed in order to result in a detectable signal; non-bound radioactive partners that stay free into the solution will not result in a detectable signal.

The protein or peptide fragments according to the invention employed in such a method may be for example in solution or coated on suspended beads as described above. Alternatively, these can be affixed to a solid support, borne on a cell or phage surface or located intracellularly.

When protein or peptide fragments are coated on solid supports, they can be tested for their binding affinity for large numbers of compounds. These can be used in different kinds of high throughput screenings in order to identify compounds having suitable binding affinity to the polypeptides according to the invention. Platform technologies or technologies based on SPR (see below) can be applied.

One may measure for example, the formation of complexes between the proteins of the invention and the compound being tested. Alternatively, one may examine the diminution or increase of complex formation between the protein according to the invention and a receptor/binding partner caused by the compound being tested.

Proteins which interact with the polypeptide of the invention may be identified by investigating protein-protein interactions using the two-hybrid vector system first proposed by Chien *et al.* (1991).

This technique is based on functional reconstitution *in vivo* of a transcription factor which activates a reporter gene. More particularly the technique comprises providing an appropriate host cell with a DNA construct comprising a reporter gene under the control of a promoter regulated by a transcription factor having a DNA binding domain and an activating domain, expressing in the host cell a first hybrid DNA sequence encoding a first fusion of a fragment or all of a nucleic acid sequence

according to the invention and either said DNA binding domain or said activating domain of the transcription factor, expressing in the host at least one second hybrid DNA sequence, such as a library or the like, encoding putative binding proteins to be investigated together with the DNA binding or activating domain of the transcription factor which is not incorporated in the first fusion; detecting any binding of the proteins to be investigated with a protein according to the invention by detecting for the presence of any reporter gene product in the host cell; optionally isolating second hybrid DNA sequences encoding the binding protein.

An example of such a technique utilizes the GAL4 protein in yeast. GAL4 is a transcriptional activator of galactose metabolism in yeast and has a separate domain for binding to activators upstream of the galactose metabolising genes as well as a protein-binding domain. Nucleotide vectors may be constructed, one of which comprises the nucleotide residues encoding the DNA binding domain of GAL4. These binding domain residues may be fused to a known protein encoding sequence, such as for example the nucleic acids according to the invention. The other vector comprises the residues encoding the protein-binding domain of GAL4. These residues are fused to residues encoding a test protein. Any interaction between polypeptides encoded by the nucleic acid according to the invention and the protein to be tested leads to transcriptional activation of a reporter molecule in a GAL-4 transcription deficient yeast cell into which the vectors have been transformed. Preferably, a reporter molecule such as β -galactosidase is activated upon restoration of transcription of the yeast galactose metabolism genes. Alternatively, other reporter proteins can be used such as EGFP (enhanced green fluorescent protein), or hEGFP. This latter has a decreased lifetime enabling the system to screen for compounds improving the interaction of studied binding partners.

The two-hybrid approach was first developed for yeast, and is an ideal screening system when looking for compounds active in killing yeast or fungi. Indeed, proteins expressed in this system will most probably carry the correct modifications as found in the pathogenic yeast strains. In addition, compounds active in this test system allow to screen and select compounds which are able to enter the cell, this selection is not possible when using *in vitro* test systems. When compounds are needed to target mammalian cells, modification of the studied proteins can be different, changing the structure of corresponding proteins. Moreover working with yeast might block certain compounds to enter the cell, which are normally able to traverse the mammalian cell membrane. Consequently, working with mammalian two-hybrid system for this purpose

will give already an immediate selection of the compounds that may enter mammalian cells.

Alternative *in vitro* methods can be used to investigate protein - protein interactions. Protein interaction analysis *in vitro* can shed light on their role in the intact
5 cell by providing valuable information on specificity, affinity, and structure-function relation ship. Significant process in this respect has become with the advent, in the last few years, of commercially available biosensor technology. This allows to study macromolecular interactions in real-time, providing a wealth of high-quality data that can be used for kinetic analysis, affinity measurements, competition studies, etc. A
10 major advantage of biosensor analysis is that there is no requirement for labeling one of the interacting components and then separating bound from free molecules- a fact that simplifies experimental procedures and provides more accurate measurements. The principle of surface plasmon resonance (SPR) is based on the detection of a change of the refractive index of the medium when a compound or protein binds to an
15 immobilised partner molecule. For the SPR technology, one needs to load one of the interacting partners to the chip surface, followed by the superfusion of the second binding partner or more molecules. The second partner can be available as purified product, but alternatively a complex suspension containing this partner can also be used. Interaction of two or more compounds can be analysed, alternatively,
20 compounds can be identified interfering or increasing this binding affinity towards each other.

SPR is not restricted to protein-protein interactions; any macromolecule with a suitable size will change the refractive index of the medium in contact with the biosensor surface and therefore give a signal. Studies have been done with protein-
25 DNA interactions, as well as protein-lipid interactions. Moreover intact viruses, abd even cells, can also be injected over the biosensor surface, in order to analyse their binding to receptors, lectins, and so on.

Alternatively, NMR is also an excellent tool for a detailed study of protein-protein or DNA-protein interactions. Isotope edited or isotope filtered experiments
30 whereby one compound is isotopically labeled with ^{15}N or ^{13}C are an ideal way to study these complexes. This method does not allow high throughput analysis of compounds interfering or enhancing molecular interactions. Nevertheless, medium or low throughput systems can be used to confirm results obtained by the high throughput assays or in cases where none of the binding partners are labeled. Other techniques
35 which can be used to study interactions are: overlay, ligand blotting, band-shift, co-

immuno-precipitation, size exclusion chromatography and microcalorimetry (In. "Protein trageting Protocols" Ed. Clegg R.A. Humana Press, Totowa, New Yersey).

Compounds modulating pathways leading to apoptosis may change the activity of the polypeptide of the invention. Therefore screening tests may be setup looking for
5 altered protein activity of the polypeptide of the invention. Based on the amino acid sequence a possible function of the polypeptide might be envisaged; activities can be confirmed and corresponding activity test can be started.

Alternatively additional tests can be performed to test the influence of the compound onto protein stability, post-translational modification, precursor processing
10 and protein translocation. All these aspects influence the concentration and/or activity of corresponding proteins and consequently influence the effect of these onto the metabolism of the cell. Also here, medium or low throughput systems can be used to confirm results obtained by the high throughout assays.

In cases compounds need to be found to target tumor cells, screening assays
15 will have to be used focused on the stimulation of the apoptotic pathway. This invention therefore also relates to in vitro and in vivo model systems comprising tumor tissue or cells expressing the polypeptides according to the invention which can be used to screen for therapeutic agents. In vivo modelsystems allow to test for compound efficacy but also the toxicity of these compounds can be tested. The compounds
20 identified using any of the methods described in the invention not only include compounds which exert their effect in promoting cell death of yeast and fungi, but also include compounds which prevent or delay cell death. The latter compounds can be used to prevent or delay apoptosis of endogenic yeast or fungi in humans and other mammals which may be caused by pathogens or toxic environmental components.

25 According to a preferred aspect of the invention, the yeast or fungi according to any of the methods described, are chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.

The invention also relates to a compound identified using any of the methods of the invention.

30 Compounds identifiable or identified using a method according to the invention, may advantageously be used as a medicament. The invention also relates to a method for treating diseases associated with yeast or fungi comprising admixing a compound obtainable by a method of the invention with a suitable pharmaceutically acceptable carrier.

35 The compounds of the invention can be used for the preparation of a medicament to treat diseases or conditions associated with yeast and fungi infections,

for instance *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp.,
Fusarium spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp.,
Epidermophyton floccosum, *Blastomyces dermatitidis*, *Coccidioides immitis*,
Histoplasma capsulatum, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
5 and *Sporothrix schenckii* infections.

These compounds may also advantageously be included in a pharmaceutical composition together with a pharmaceutically acceptable carrier, diluent or excipient therefor.

10 A medicament according to the invention not only relates to fungistatic compounds for treating humans or mammals but also relates to fungicides for treating plants.

The invention also relates to genetically modified yeast or fungi in which modification results in the overexpression or underexpression of at least one of the nucleic acids or polypeptides of the invention, which overexpression or
15 underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungi. These genetically modified organisms may have a positive effect on the endogenic flora of humans and other mammals. The genetically modified yeast or fungi can be included in a pharmaceutical composition or can be used for the preparation of a medicament for prophylactic or therapeutic use.

20 Also according to the invention is the use of a compound obtainable by a method of the invention for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.

According to another embodiment, the invention also relates to an isolated protein which is involved in a pathway for programmed cell death of yeast or fungi
25 selected from:

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394,
30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482, or 484 or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 75% or 80% similar, more preferably more than 85%, 90 or
35 95% similar and most preferably more than 90% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,

306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452
5 454, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 75% or 80% identical, more preferably more than 85%, 90%
or 95% identical and most preferably more than 97% identical to any of the amino
acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302,
10 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342,
344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376,
380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416,
418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450,
452, 454, 476, 478, 480, 482, or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c).

According to the invention, the polypeptides as defined above may be used as
a medicament.

Also encompassed within the present invention are antibodies, monoclonal or
polyclonal, capable of specifically binding to one or more epitopes of the proteins of the
20 invention. The term "specific binding" implies that there is substantially no cross-
reaction of the antibody with other proteins.

The antibodies according to the invention may be produced according to
techniques which are known to those skilled in the art. Monoclonal antibodies may be
prepared using conventional hybridoma technology as described by Kohler and
25 Milstein (1979). Polyclonal antibodies may also be prepared using conventional
technology well known to those skilled in the art, and which comprises inoculating a
host animal, such as a mouse, with a protein or epitope according to the invention and
recovering the immune serum. The present invention also includes fragments of whole
antibodies which maintain their binding activity, such as for example, Fv, F(ab') and
30 F(ab')₂ fragments as well as single chain antibodies.

Antibodies according to the invention may also be used in a method of
detecting the presence of a polypeptide according to the invention, which method
comprises reacting the antibody with a sample and identifying any protein bound to
said antibody. A kit may also be provided for performing said method which comprises
35 an antibody according to the invention and means for reacting the antibody with said
sample.

The antibodies according to the invention may be used as a medicament or may be comprised in a pharmaceutical composition. According to a more specific embodiment, the antibodies may be used in the preparation of a medicament for treating diseases associated with yeast and fungi such as, but not restricted to,
5 *Candida albicans*, *Aspergillus* spp., *Fusarium* spp., *Botritis*, spp., *Cladosporium* spp.

The invention also relates to a method of preventing infection with yeast or fungi, comprising administering a composition containing at least one polypeptide of the invention to a mammal in effective amount to stimulate the production of protective antibody or protective T-cell response.

10 According to another embodiment, the invention relates to a genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids of the invention or a human homologue thereof or at least one of the polypeptides of the invention or a human homologue thereof, which overexpression or underexpression of said nucleic
15 acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

Human homologues according to the invention can be obtained by selective hybridisation of the yeast and candida nucleic acid molecules of the invention against human genome or cDNA libraries according to methods well known in the art
20 (Sambrook et al., 1989). Human polypeptide homologues are obtained from the corresponding human nucleic acid homologous nucleotide sequences.

The invention also relates to a method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences of the invention or a human homologue thereof and/or at least one of the polypeptides
25 of the invention or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism as described in the invention.

The invention further relates to the compounds identifiable according to the above-described method and its use as a medicament.

The invention further relates to a method for preparing a pharmaceutical
30 composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

The expression "proliferative disorders" or "proliferative diseases" refers to an abnormality within a patient or animal such as cancer. Normal cells start to proliferate
35 due to a change in the coding or non-coding sequence of the DNA resulting in a swollen or distended tissue. Mutation may arise without obvious cause. An abnormal

benign or malignant mass of tissue is formed that is not inflammatory. Cells of pre-existent tissue start to divide unexpectedly and resulting cell mass possesses no physiologic function.

The expression "apoptosis" or "apoptosis-related diseases" includes diseases
5 such as autoimmunity diseases, ischemia, diseases related with viral infections or neurodegenerations.

The invention also relates to the use of compounds obtainable by the above described methods for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain disorders.

10 According to another embodiment, the invention relates to the use of a nucleic acid molecule or a polypeptide described in the invention or human homologues thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

The invention also relates to a pharmaceutical composition for use as a
15 medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule of the invention or a human homologue thereof or a polypeptide of the invention or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.

The invention also relates to a vaccine for immunizing mammals against
20 proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule of the invention or a human homologue thereof or at least one polypeptide of the invention or a human analogue thereof in a pharmaceutically acceptable carrier.

The invention also relates to the use of an antibody of the invention capable of
25 binding to at least one of the polypeptides of the invention or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

According to yet another embodiment, the invention relates to an expression vector comprising a human homologue of a nucleic acid sequence of the invention.
30 Said expression vector may comprise an inducible promoter and may further comprise a sequence encoding a reporter molecule.

The invention also relates to a host cell transformed, transfected or infected with any of the above described vectors.

According to another embodiment the invention relates to a nucleic acid
35 molecule comprising a human homologue of at least one of the nucleic acid sequences described in the invention.

The invention also relates to an antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to a nucleic acid molecule which is a human analogue of the invention.

5 The invention also relates to a polypeptide encoded by the nucleic acid molecule comprising said human homologues of the nucleic acids described in the invention.

10 The invention, now being generally described, may be more clearly understood by reference to the following examples, which are included merely for purposes of illustration of certain aspects and embodiments of the present invention and are not intended to limit the invention. The contents of all references referred to in this text are hereby incorporated by reference.

FIGURE AND TABLE LEGENDS

- Figure 1.** *Saccharomyces cerevisiae* sequences based on information obtained from the Saccharomyces Genome Database (SGD) (SEQ ID Nos 1 to 284)
- Figure 2.** *Candida albicans* sequences (SEQ ID Nos 285 to 456).
- 5 **Figure 3.** Yeast genome macroarray containing a total of 6144 gene ORFs spotted on 2 nylon membrane filters. The filters are cut in the upper right corner for orientation and the DNA is on the labelled side of the filter. Each filter contains 2 fields and each field is divided into 8 grids, organised in 24 rows and 8 columns.
- 10 The spots represent the genome wide expression profile without (A) and with (B) *Bax* modulated expression (Example 2).
- Figure 4.** Results from a second experiment analogous and analysed as described in the examples section (Example 3).
- 15 **Table 1.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed more than fivefold in a first experiment (see Example 2). The factor by which the transcript level was affected, is expressed as the Qt value. A Qt value higher than 1 indicates upregulation while a Qt value lower than 1 indicates a downregulation. For instance, a Qt of 0.5 indicates a two-fold lower transcript level of a particular mRNA due to *Bax* expression in *S. cerevisiae*. Upregulation or downregulation of a specific mRNA is stated when Qt had a value of at least five or at most 0,21, respectively.
- 20
- 25 **Table 2.** Genes modulated by *Bax* expression in *S. cerevisiae*. This list includes all the genes for which mRNA levels changed significantly in a second experiment (see Example 3). In this experiment, the Qt values were calculated using the Pathways Software (Research Genetics).

EXAMPLES

Example 1. Differential gene expression analysis upon Bax-induced cell death

Materials and media

Bacterial strain *Escherichia coli* MC1061 (Casadaban and Cohen, 1980) was
5 used for the construction and the amplification of plasmids. Yeast strains were grown
under normal conditions on standard media (Sherman *et al.*, 1979). The
Saccharomyces cerevisiae strain INVSc1 (Invitrogen®) was transformed by means of
the lithium acetate method (Schiestl and Gietz, 1989) with YlpUTyL or YlpUTyLMuBax,
after linearisation in the Ty δ element (Zhu, 1986).

10

Cloning of mouse BAX cDNA

Mouse *Bax* cDNA, encoding the mouse Bax- α protein, was cloned by Pfu DNA
polymerase (Stratagene®) chain reaction amplification (PCR) from an EL4/13.18
thymoma cDNA library (BCCM™/LMBP-LIB15) by making use of the primers:

15

5'-ATGGACGGGTCCGGGAGCAG-3' and

5'-TCAGCCCATCTTCTTCCAGATGGTGAG-3'.

The resulting PCR product was cloned in a *HincII*-openend pUC19 according to
standard procedures (Sambrook J. *et al.*, 1989).

20 **Plasmid constructions**

The 2 μ ori and the *URA3* marker gene were removed from pUT332 (Gatignol *et al.*, 1990) by successive digestions with *Clal* and *BglII*. A *BamHI-HindIII* GAL1 promoter fragment was ligated into the *BglII-HindIII*-opened plasmid. A *XbaI-FspI* FLP terminator fragment was inserted into this *XbaI-HindIII*(blunted)-opened plasmid so that
25 the plasmid YlpUT was obtained. Insertion of a blunted *EcoRI-BsaAI* Ty δ element in
the *KpnI-AatII*-opened and blunted YlpUT resulted in the plasmid YlpUTy. Subsequent
insertion of the *LEU2* marker gene, as a blunted *BsaAI-BsrGI* fragment, in the *BamHI*-
openend and blunted YlpUTy resulted in the plasmid YlpUTyL.

30 Mouse *Bax* cDNA was excised from pUC19 by digestion with *XbaI* and *HindIII*
and subcloned into the *XbaI-HindIII*-opened plasmid YlpUTyL, obtaining the final
expression plasmid YlpUTyLMuBax.

The plasmid YlpUTyLMuBax has been deposited in the BCCM™/LMBP culture
collection as p5CTyGALmBax with accession number 3871 under restricted use.

GeneFilters

The Yeast GeneFilters™ were purchased from Research Genetics Inc. (Huntsville, AL, USA).

5 The Yeast GeneFilters™ are hybridization ready nylon membranes containing a total of 6144 gene ORFs (Open Reading Frames) individually amplified by PCR and spotted on 2 nylon membrane filters (Filter I and II). The filters are cut in the upper right corner and the DNA is on the labeled side of the filter.

10 Filter I contains 3072 ORFs organized into two fields (fields 1 and 2). Each field contains 1536 ORFs divided into 8 grids (A, B, C, D, E, F, G and H). The grids are organized in 24 rows and 8 columns.

Filter II contains 3072 ORFs organized in two fields (field 3 and 4). Fields 3 and 4 are organized in the same way as fields 1 and 2.

The Yeast ORF target

15 The yeast filters consist of over 6000 PCR products corresponding to 6144 yeast ORFs derived from the SGD. The PCR reactions used ORF specific primer pairs designed to amplify the entire open reading frame. The primers were generated from unique sequences containing the start codon ATG and termination codon (kindly provided by M. Cherry at Stanford Genome Center). Thus the PCR product contains
20 the complete open reading frame including the start and stop codons. These products were purified and resuspended at 50 nanograms per microliter in a colored solution to allow the printing to be monitored. A robotic device was used to spot approximately 1/10 of a microliter of the denatured PCR product solution on a positively charged nylon membrane. The DNA was then UV cross-linked to the membrane.

25

Results**Induction of Bax-expression in yeast cells**

30 *S. cerevisiae* cells (strain INVSc1) were transformed with the expression plasmid YIpUTyLMuBax or the parental plasmid YIpUTyL as a negative control. Alternative yeast strains (such as W303-1A (Thomas and Rothstein, 1989)) with equivalent properties are known in the art and can also be used.

The Ty δ element of both plasmids allowed a stable multi-copy integration in the genome of the yeast cell. Southern analysis of the cells containing YIpUTyLMuBax
35 revealed the integration of 5 GAL1-controlled Bax-cassettes near Ty elements.

The yeast cells containing YipUTyLMuBax and the yeast cells containing YipUTyL were grown overnight in 10 ml minimal glucose-containing medium. The precultures were then further diluted to an OD₆₀₀ of 0,2 in 100 ml minimal glucose-containing medium and grown until an OD₆₀₀ of 1 was reached. Subsequently, the yeast cells containing YipUTyL were washed and a dilution thereof was transferred into 100 ml galactose-containing medium and incubated for 15 hours. After this additional period the cultures reached an OD₆₀₀ of 1. The yeast cells containing YipUTyLMuBax were also washed and transferred into 100 ml galactose-containing medium and incubated for 15 hours.

RNA isolation

Total RNA was isolated using RNApure™ Reagent (Genhunter Corporation Nashville, TN, USA) according to the GenHunter protocol. 1.5 10⁹ cells were concentrated in a microcentrifuge tube and 1ml RNApure™ Reagent was added together with 1 g of glass pearls. The yeast cells were broken by thorough mixing during five 2-minutes periods, and placed on ice in-between to avoid RNA digestion. Chloroform (150 µl) was added to the lysate and centrifuged for 10 min at 4°C and at 15000 rpm. The supernatant was transferred to a new tube and the RNA was precipitated with an equal volume of isopropanol. After 10 min incubation on ice, the RNA was pelleted by centrifugation and the pellet was washed with 70% ice-cold ethanol. The dried RNA pellet was resuspended in 50 µl RNase free dH₂O.

First strand cDNA synthesis in the presence of α -³³P dCTP

Probes with high specific activity were prepared by first strand cDNA synthesis using total RNA isolated from INVSc1 YipUTyLMuBax or INVSc1 YipUTyL yeast cells and incorporation of α -³³P dCTP as follows: 2 µl (1 µg/ml) of Oligo dT was added to 20 µg of total RNA in a maximal volume of 8 µl RNase-free dH₂O and incubated at 70°C for 10 min. After cooling down on ice for 1 min, the following components were added:

- 6 µl 5x concentrated First Strand Buffer (GIBCO-BRL)
- 1 µl 0,1 M DTT
- 1 µl RNase Block (40 units/µl) (Stratagene)
- 1,5 µl 20 mM dXTP-solution (X = A, G and T) (Pharmacia)
- 1,5 µl SuperScript™ Reverse Transcriptase (200 units/µl) (GIBCO-BRL)
- 10 µl α -³³P dCTP (10mCi/ml, 3000 Ci/mmol) (Amersham)

and incubated for 2 h at 37°C during which first strand cDNA synthesis took place.

Unincorporated label was separated from the probe on a Sephadex G-50 column (Pharmacia). The radioactivity incorporated in the probe was measured by liquid scintillation. The specific activity of the probes was 3 or 5 10^8 cpm/ μ g for both the INVSc1YIpUTyL and the INVSc1YIpUTyLMuBax probe.

Additionally, the length of first strand cDNA probes was controlled on an alkaline 2% agarose gel using standard electrophoresis techniques, and resulted in the detection, via stimulated phosphorescence autoradiography, of the bulk of the fragments around 500 bp.

Hybridisation with the *S. cerevisiae* Yeast GeneFilters™ and signal detection

The Yeast GeneFilters™ were successively hybridised with the α - 32 P dCTP labelled cDNA probes using the MicroHyb™ solution provided by the manufacturer (Research Genetics Inc., Huntsville, AL, USA). This solution was applied as well in the prehybridisation step as during hybridisation. The MicroHyb solution contains formamide to allow hybridisation to occur at lower temperatures.

The hybridisation experiment was performed essentially as follows: during prehybridisation, the Yeast GeneFilters™ were placed in a hybridisation flask (35x250 mm) filled with 5 or 10 ml MicroHyb™ solution (42°C) containing 5 μ l polydA (0,5 or 1 μ g/ml) and incubated for 24 hours at 42°C whilst rotating (10 rpm). After disposal of the prehybridisation solution, the denatured (3 min at 100°C) cDNA was added in 5 ml prewarmed MicroHyb solution and again incubated overnight at 42°C whilst rotating. Following two wash steps of 20 min in wash buffer (2x SSC, 1% SDS) at 50°C, a third wash step was performed in a second wash buffer (0,5x SSC, 1% SDS) for an additional 15 min at room temperature. The Yeast GeneFilters™ were placed in a PhosphorImager™ cassette with storage phosphorscreen. After 4 days of development the screen was developed and scanned using the PhosphorImager™ 455 SI from Molecular Dynamics. The results of these can be seen in Figure 3.

In-between the hybridisation experiments, the filters were stripped off by incubation in 500 ml of a 0,5% SDS solution (prewarmed to near boiling temperature) during at least 1 hour at room temperature.

Example 2. Quantification of Hybridisation Signals

Quantification of the hybridisation signals was done using the ImageQuant™ 4.1 software tool from Molecular Dynamics (Sunnyvale, CA). The quantification was performed per grid of the Yeast GeneFilters™, and by drawing a roster of 24 columns and 8 rows onto each grid of each filter. As such, each rectangle of the roster corresponds to a spot on the Yeast GeneFilters™. Subsequently, from each grid a volume-report (quantification) was drawn up and the data were transferred to a Microsoft™ Excel sheet. Also for each grid a correction factor was calculated. Signals neighboring big and dark spots were separately quantified. For each grid, a background level was calculated.

10

Statistical processing of quantification results

The statistical processing of the results was accomplished in Microsoft™ Excel. For each grid, the following statistical functions were separately defined:

1. The frequency of occurrence of the values in a precisely defined intensity range(data range), established between 1000 and 61000, split up in intervals of 5000.
2. The frequency in terms of percentage.
3. The cumulated frequency in terms of percentage.

These numeric values were used for the graphical display of the cumulated frequency in terms of percentage.

20

Subsequently, the results of the two experiments (hybridization with cDNA from YlpUTyL containing INVSc1 cells and hybridization with cDNA from YlpUTyLMuBax containing INVSc1 cells) were integrated by determination of a second range of statistical functions:

1. The average of the values of the two experiments for each spot on the filter.
2. The standard deviation on this average. This is a measure for the distribution of the values around this average.
3. The standard deviation in terms of percentage.

The quotient of the values of the second experiment (Bax expression) against the values from the first experiment (control) was determined. This immediately gave the factor by which the expression of a specific gene is changed upon Bax induction.

In order to process all these data and to be able to discriminate between differences in gene expression, a gene showing a standard deviation in terms of percentage of at least 90% and a difference of a factor 5 in expression as a result of Bax induction, was identified as a differentially expressed candidate gene. (Table 1).

Requantification of these candidates confirmed their selection.

When the expression pattern of all 6144 genes is compared in the two experiments, it could be concluded that the expression profile of 142 genes (this is 2,3 %) has been changed with at least of factor 5. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 1. The sequences of these genes and the amino acid sequences which they encode are shown in Figure 1.

Example 3 . Quantification of Hybridisation Signals using the Pathways™ software

Quantification of the hybridisation signals was done using the Pathways™ Software (Research Genetics) and these signals were normalised against all data points. Comparison of these normalised data revealed differentially expressed candidate genes. Visual inspection of the hybridisation spots confirmed their selection. An overview of these genes as well as the factors with which they are up- or down-regulated is shown in Table 2.

Surprisingly, using this Software package for analysing the results in this example and when compared to the results of example 2, some additional genes were found which expression are up-or down-regulated upon *Bax* expression in *S. cerevisiae*.

The sequences of up- and down regulated genes and the corresponding amino acid sequences from Examples 2 and 3 are shown in Figure 1.

Example 4 Search for homologues in *Candida albicans*

Sequence similarity searches against public and commercial sequence databases were performed with the BLAST software package (Altschul *et al.*, 1990) version 2. Both the original nucleotide sequence and the six-frame conceptual translations were used as query sequences. The used public databases were the EMBL nucleotide sequence database (Stoesser *et al.*, 1998), the SWISS-PROT protein sequence database and its supplement TrEMBL (Bairoch and Apweiler, 1998), and the ALCES *Candida albicans* sequence database (Stanford University, University of Minesota). The commercial sequence database used was the PathoSeq™ microbial genomic database (Incyte Pharmaceuticals Inc., Palo Alto, CA, USA).

Sequence similarity searches were performed using the BLAST software package version 2. The identity between 2 sequences was calculated as percentage identical residues, the similarity percentage between two sequences was calculated using BLOSUM62 as a scoring matrix.

Example 5 . Screening for compounds modulating expression of polypeptides involved in induction of cell death of *C. albicans*

The method proposed is based on observations (Sandbaken *et al.*, 1990; 5 Hinnebusch and Liebman 1991; Ribogene PCT WO 95/11969, 1995) suggesting that underexpression or overexpression of any component of a process (e.g. translation) could lead to altered sensitivity to an inhibitor of a relevant step in that process. Such an inhibitor should be more potent against a cell limited by a deficiency in the macromolecule catalyzing that step and/or less potent macromolecule, as compared to 10 the wild type (WT) cell.

Mutant yeast strains, for example, have shown that some steps of translation are sensitive to the stoichiometry of macromolecules involved. (Sandbaken *et al.*, 1990). Such strains are more sensitive to compounds which specifically perturb translation (by acting on a component that participates in translation) but are equally 15 sensitive to compounds with other mechanisms of action.

This method thus not only provides a means to identify whether a test compound perturbs a certain process but also an indication of the site at which it exerts its effect. The component which is present in altered form or amount in a cell whose growth is affected by a test compound is potentially the site of action of the test 20 compound.

The assay to be set up involves measurement of growth or death rate of an isogenic strain which has been modified only in a certain specific allele, relative to a wild type (WT) *Candida albicans* strain, in the presence of R-compounds. Strains can be ones in which the expression of a specific protein is impaired upon induction of anti- 25 sense or strains which carry disruptions in an essential gene. An *in silico* approach to find novel genes in *Candida albicans* will be performed. A number of essential genes identified in this way will be disrupted (in one allele) and the resulting strains can be used for comparative growth and/or death rate screening.

30 **Example 6. Assay for High Throughput screening for drugs**

35 $35\ \mu\text{l}$ minimal medium (S medium + 2% galactose + 2% maltose) is transferred in a transparent flat-bottomed 96 well plate (MW96) using an automated pipetting system (Multidrop, Labsystems). A 96-channel pipettor (Hydra, Robbins Scientific) transfers $2.5\ \mu\text{l}$ of R-compound at $10^{-3}\ \text{M}$ in DMSO from a stock plate into the assay plate.

- The selected *Candida albicans* strains (mutant and parent (CAI-4) strain) are stored as glycerol stocks (15%) at -70°C . The strains are streaked out on selective plates (SD medium) and incubated for two days at 30°C . For the parent strain, CAI-4, the medium is always supplemented with $20\text{ }\mu\text{g/ml}$ uridine. A single colony is scooped
- 5 up and resuspended in 1 ml minimal medium (S medium + 2% galactose + 2% maltose). Cells are incubated at 30°C for 8 hours while shaking at 250 rpm. A 10 ml culture is inoculated at 250.000 cells/ml. Cultures are incubated at 30°C for 24 hours while shaking at 250 rpm. Cells are counted in Coulter counter and the final culture (S medium + 2% galactose + 2% maltose) is inoculated at 20.000 to 50.000 cells/ml.
- 10 Cultures are grown at 30°C while shaking at 250 rpm until a final OD_{600} of 0.24 (+/- 0.04) is reached.

200 μl of this yeast suspension is added to all wells of MW96 plates containing R-compounds in a 450 μl total volume. MW96 plates are incubated (static) at 30°C for 48 hours.

- 15 Optical densities are measured after 48 hours.

Test growth is expressed as a percentage of positive control growth for both mutant (x) and wild type (y) strains. The ratio (x/y) of these derived variables is calculated.

Table 1.

ORF	Qt	Sequence ID Number
YAR061W	7.80	SEQ ID NO 1
YAR073W	11.19	SEQ ID NO 3
YBL048W	5.07	SEQ ID NO 5
YBL051C	5.22	SEQ ID NO 7
YBL066C	6.04	SEQ ID NO 9
YBL078C	6.94	SEQ ID NO 11
YBR072W	26.56	SEQ ID NO 13
YBR073W	5.46	SEQ ID NO 15
YBR086C	7.14	SEQ ID NO 17
YBR093C	11.05	SEQ ID NO 19
YBR181C	0.15	SEQ ID NO 21
YCL007C	20.99	SEQ ID NO 23
YCL016C	23767.57	SEQ ID NO 25
YCR052W	10.51	SEQ ID NO 27
YCR064C	14.91	SEQ ID NO 29
YCR073WA	5.92	SEQ ID NO 31
YDL010W	5.31	SEQ ID NO 33
YDL036C	5.34	SEQ ID NO 35
YDL083C	0.16	SEQ ID NO 37
YDL125C	6.80	SEQ ID NO 39
YDL133CA	0.21	SEQ ID NO 41
YDL136W	0.20	SEQ ID NO 43
YDL167C	6.37	SEQ ID NO 45
YDL184C	0.21	SEQ ID NO 47
YDL191W	0.17	SEQ ID NO 49
YDR103W	6.26	SEQ ID NO 51
YDR238C	5.75	SEQ ID NO 53
YDR259C	9.68	SEQ ID NO 55
YDR294C	8.38	SEQ ID NO 57
YDR430C	5.66	SEQ ID NO 59
YDR438W	6.47	SEQ ID NO 61
YDR450W	0.16	SEQ ID NO 63
YDR471W	0.11	SEQ ID NO 65
YDR486C	5.27	SEQ ID NO 67
YDR499W	6.14	SEQ ID NO 69
YDR507C	6.34	SEQ ID NO 71
YDR515W	5.42	SEQ ID NO 73
YDR518W	6.15	SEQ ID NO 75
YDR519W	5.57	SEQ ID NO 77
YER102W	0.19	SEQ ID NO 79
YER153C	5.63	SEQ ID NO 83
YFL014W	41.08	SEQ ID NO 85
YFL015C	5.62	SEQ ID NO 87
YFR022W	9.44	SEQ ID NO 89
YGL011C	6.14	SEQ ID NO 91
YGL031C	0.11	SEQ ID NO 93
YGL032C	0.14	SEQ ID NO 95
YGL043W	10.74	SEQ ID NO 97
YGL102C	0.15	SEQ ID NO 99
YGL103W	0.17	SEQ ID NO 101
YGL130W	8.35	SEQ ID NO 103

YGL147C	0.08	SEQ ID NO 105
YGL213C	6.02	SEQ ID NO 107
YGL235W	6.23	SEQ ID NO 109
YGL260W	6.61	SEQ ID NO 111
YGR085C	0.16	SEQ ID NO 113
YGR118W	0.17	SEQ ID NO 115
YGR142W	8.91	SEQ ID NO 117
YGR236C	12.72	SEQ ID NO 119
YGR277C	6.27	SEQ ID NO 121
YGR284C	5.95	SEQ ID NO 123
YGR285C	5.84	SEQ ID NO 125
YHR010W	0.20	SEQ ID NO 127
YHR021C	0.16	SEQ ID NO 129
YHR141C	0.10	SEQ ID NO 131
YHR217C	7.6	SEQ ID NO 133
YIL112W	11.15	SEQ ID NO 135
YIL115C	7.67	SEQ ID NO 137
YIL148W	0.13	SEQ ID NO 139
YIL150C	6.83	SEQ ID NO 141
YIL167W	6.66	SEQ ID NO 143
YJL034W	11.61	SEQ ID NO 145
YJL035C	14.48	SEQ ID NO 147
YJL070C	5.29	SEQ ID NO 149
YJL078C	5.16	SEQ ID NO 151
YJL179W	0.19	SEQ ID NO 153
YJL180C	0.14	SEQ ID NO 155
YJL181W	0.21	SEQ ID NO 157
YJL187C	0.17	SEQ ID NO 159
YJL188C	0.1	SEQ ID NO 161
YJL189W	0.08	SEQ ID NO 163
YJL190C	0.09	SEQ ID NO 165
YJL197W	0.13	SEQ ID NO 167
YJL198W	0.2	SEQ ID NO 169
YJR049C	0.17	SEQ ID NO 171
YKR094C	0.14	SEQ ID NO 173
YLR040C	10.13	SEQ ID NO 175
YLR048W	8.55	SEQ ID NO 177
YLR088W	6.09	SEQ ID NO 179
YLR159W	0.18	SEQ ID NO 181
YLR167W	0.06	SEQ ID NO 183
YLR232W	7.4	SEQ ID NO 185
YLR233C	7.63	SEQ ID NO 187
YLR234W	5.68	SEQ ID NO 189
YLR238W	6.74	SEQ ID NO 191
YLR241W	6.48	SEQ ID NO 193
YLR321C	12.17	SEQ ID NO 195
YLR322W	5.54	SEQ ID NO 197
YLR325C	0.06	SEQ ID NO 199
YLR344W	0.12	SEQ ID NO 201
YLR367W	0.19	SEQ ID NO 203
YLR393W	7.05	SEQ ID NO 205
YLR423C	8.61	SEQ ID NO 207
YML026C	0.11	SEQ ID NO 209
YML063W	0.16	SEQ ID NO 211

YML128C	5.1	SEQ ID NO 213
YML130C	5.41	SEQ ID NO 215
YMR022W	6.45	SEQ ID NO 217
YMR118C	5.13	SEQ ID NO 219
YMR143W	0.08	SEQ ID NO 221
YMR174C	6.75	SEQ ID NO 223
YMR191W	9.56	SEQ ID NO 225
YMR230W	0.13	SEQ ID NO 227
YNL054W	5.19	SEQ ID NO 229
YNL067W	0.12	SEQ ID NO 231
YNL075W	0.16	SEQ ID NO 233
YNL096C	0.14	SEQ ID NO 235
YNL162W	0.07	SEQ ID NO 237
YNL178W	0.11	SEQ ID NO 239
YNL182C	0.18	SEQ ID NO 241
YNL190W	0.07	SEQ ID NO 243
YNL208W	5.87	SEQ ID NO 245
YNL210W	0.02	SEQ ID NO 247
YOL031C	5.32	SEQ ID NO 249
YOL048C	14.34	SEQ ID NO 251
YOR010C	7.27	SEQ ID NO 253
YOR019W	5.19	SEQ ID NO 255
YOR027W	6.03	SEQ ID NO 257
YOR031W	5.35	SEQ ID NO 259
YOR096W	0.12	SEQ ID NO 261
YOR248W	0.18	SEQ ID NO 263
YOR293W	0.11	SEQ ID NO 265
YOR312C	0.12	SEQ ID NO 267
YOR369C	0.21	SEQ ID NO 269
YPL047W	5.09	SEQ ID NO 271
YPL090C	0.1	SEQ ID NO 273
YPL137C	10.41	SEQ ID NO 275
YPL159C	5.61	SEQ ID NO 277
YPL175W	5.95	SEQ ID NO 279
YPL180W	7.68	SEQ ID NO 281
YPL218W	6.26	SEQ ID NO 283
YPR102C	0.17	SEQ ID NO 285

Table 2.

ORF	Qt	Sequence ID Number
YGR236C	7.25	SEQ ID NO 119
YDR442W	0.049	SEQ ID NO 459
YGR182C	0.602	SEQ ID NO 467
YGR106C	0.478	SEQ ID NO 465
YKR040C	2.23	SEQ ID NO 471
YJL188C	0.075	SEQ ID NO 161
YOR096W	0.067	SEQ ID NO 261
YOR293W	0.107	SEQ ID NO 265
YDR450W	0.056	SEQ ID NO 63
YML026C	0.051	SEQ ID NO 209
YHR021C	0.114	SEQ ID NO 129
YLR167W	0.033	SEQ ID NO 183
YGL147C	0.061	SEQ ID NO 105
YGR085C	0.107	SEQ ID NO 463
YOR312C	0.083	SEQ ID NO 267
YOL127W	0.101	SEQ ID NO 473
YHR010W	0.077	SEQ ID NO 127
YDR471W	0.046	SEQ ID NO 65
YDL191W	0.128	SEQ ID NO 49
YDL136W	0.125	SEQ ID NO 43
YLR325C	0.061	SEQ ID NO 199
YJL189W	0.07	SEQ ID NO 163
YIL148W	0.145	SEQ ID NO 139
YHR141C	0.069	SEQ ID NO 131
YBL003C	0.119	SEQ ID NO 457
YDR529C	0.352	SEQ ID NO 461
YGR183C	0.781	SEQ ID NO 469

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CLAIMS

1. Use of a nucleic acid molecule encoding a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi and which
 - 5 nucleic acid sequence is selected from:
 - (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
 - (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300,

- 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- 5
- (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;
- 10
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- 20
- 25
- (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261,
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- 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483;
- (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 1, 3, 5, 7, 9, 11, 13, 15, 17, 19, 21, 23, 25, 27, 29, 31, 33, 35, 37, 39, 41, 43, 45, 47, 49, 51, 53, 55, 57, 59, 61, 63, 65, 67, 69, 71, 73, 75, 77, 79, 81, 83, 85, 87, 89, 91, 93, 95, 97, 99, 101, 103, 105, 107, 109, 111, 113, 115, 117, 119, 121, 123, 125, 127, 129, 131, 133, 135, 137, 139, 141, 143, 145, 147, 149, 151, 153, 155, 157, 159, 161, 163, 165, 167, 169, 171, 173, 175, 177, 179, 181, 183, 185, 187, 189, 191, 193, 195, 197, 199, 201, 203, 205, 207, 209, 211, 213, 215, 217, 219, 221, 223, 225, 227, 229, 231, 233, 235, 237, 239, 241, 243, 245, 247, 249, 251, 253, 255, 257, 259, 261, 263, 265, 267, 269, 271, 273, 275, 277, 279, 281, 283, 285, 287, 289, 291, 293, 295, 297, 299, 301, 303, 305, 307, 309, 311, 313, 315, 317, 319, 321, 323, 325, 327, 329, 331, 333, 335, 337, 339, 341, 343, 345, 347, 349, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 377, 379, 381, 383, 385, 387, 389, 391, 393, 395, 397, 399, 401, 403, 405, 407, 409, 411, 413, 415, 417, 419, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 455, 457, 459, 461, 463, 465, 467, 469, 471, 473, 475, 477, 479, 481 or 483; and
- (f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),
- (g) the complement of any of the nucleic acid sequences as specified in a) to f), for the preparation of a medicament for treating diseases associated with yeast or fungi.

2. Use of a polypeptide which is involved in a pathway eventually leading to programmed cell death of yeast or fungi, said polypeptide being selected from :

- (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;
- (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432,

434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484;

(c) a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 32, 34, 36, 38, 40, 42, 44, 46, 48, 50, 52, 54, 56, 58, 60, 62, 64, 66, 68, 70, 72, 74, 76, 78, 80, 82, 84, 86, 88, 90, 92, 94, 96, 98, 100, 102, 104, 106, 108, 110, 112, 114, 116, 118, 120, 122, 124, 126, 128, 130, 132, 134, 136, 138, 140, 142, 144, 146, 148, 150, 152, 154, 156, 158, 160, 162, 164, 166, 168, 170, 172, 174, 176, 178, 180, 182, 184, 186, 188, 190, 192, 194, 196, 198, 200, 202, 204, 206, 208, 210, 212, 214, 216, 218, 220, 222, 224, 226, 228, 230, 232, 234, 236, 238, 240, 242, 244, 246, 248, 250, 252, 254, 256, 258, 260, 262, 264, 266, 268, 270, 272, 274, 276, 278, 280, 282, 284, 286, 288, 290, 292, 294, 296, 298, 300, 302, 304, 306, 308, 310, 312, 314, 316, 318, 320, 322, 324, 326, 328, 330, 332, 334, 336, 338, 340, 342, 344, 346, 348, 350, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 378, 380, 382, 384, 386, 388, 390, 392, 394, 396, 398, 400, 402, 404, 406, 408, 410, 412, 414, 416, 418, 420, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 456, 458, 460, 462, 464, 466, 468, 470, 472, 474, 476, 478, 480, 482, or 484; and,

(d) a functional fragment of any of said proteins as defined in a) to c),

for the preparation of a medicament for treating diseases associated with yeast or fungi.

25

3. A pharmaceutical or fungicidal composition comprising a nucleic acid molecule as defined in claim 1 or a polypeptide as defined in claim 2 together with a pharmaceutically acceptable carrier diluent or excipient therefor.

30

4. A vaccine for immunizing a mammal against yeast or fungal infections comprising at least one nucleic acid molecule as defined in claim 1 or at least one polypeptide as defined in claim 2 in a pharmaceutically acceptable carrier.

35

5. A genetically modified yeast or fungus in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or the polypeptides as defined in claim 2, which overexpression or

underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified yeast or fungus.

5 6. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast or fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 10 (a) contacting a compound to be tested with yeast or fungal cells having a mutation which results in overexpression or underexpression of at least one of the polypeptides as defined in claim 2, in addition to contacting wild type cells with said compound,
- 15 (b) monitoring the growth, death rate or activity of said mutated cells compared to said wild type cells; wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 20 (c) alternatively monitoring the growth, death rate or activity of said mutated cells compared to mutated cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast or fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- (d) alternatively monitoring changes in morphologic and/or functional properties of components in said mutated cells caused by the addition of the compound to be tested.

25 7. A method of identifying compounds which selectively modulate expression or functionality of polypeptides involved in a pathway eventually leading to programmed cell death of yeast and fungi or in metabolic pathways in which said polypeptides are involved, which method comprises:

- 30 (a) contacting a compound to be tested with yeast or fungal cells transformed, transfected or infected with an expression vector comprising an antisense sequence of at least one of the nucleic acid sequences as defined in claim 1, which expression results in underexpression of said polypeptide, in addition to contacting one or more wild type cells with said compound,
- 35 (b) monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to said wild type cells; wherein differential growth or activity of said transformed, transfected or infected yeast or fungal cells is

indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,

- 5 (c) alternatively monitoring the growth, death rate or activity of said transformed, transfected or infected cells compared to transformed, transfected or infected cells which were not contacted with the compound to be tested, wherein differential growth or activity of said mutated yeast of fungi cells is indicative of selective action of said compound on a polypeptide in the same or a parallel pathway,
- 10 (d) alternatively monitoring changes in morphologic and/or functional properties of components in said transformed, transfected or infected cells caused by the addition of the compound to be tested.

8. A method of identifying compounds which bind to or modulate the properties of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi, which method comprises:

15

- (a) contacting a compound to be tested with at least one of the polypeptides as defined in claim 2,
- (b) detecting the complex formed between the compound to be tested and said polypeptide,
- 20 (c) alternatively, examining the diminution of complex formation between said polypeptide and a binding partner, caused by the addition of the compound being tested.
- (d) alternatively, examining the alteration in the functional activity of the polypeptide, caused by the addition of the compound being tested.

25

9. A method of identifying compounds which selectively modulate expression of polypeptides which are involved in a pathway eventually leading to programmed cell death of yeast or fungi which method comprises:

- (a) contacting host cells transformed, transfected or infected with an expression vector comprising a promoter sequence of a nucleic acid molecule as defined in claim 1 joined in frame with a reporter gene,
- 30 (b) monitoring increased or decreased expression of said reporter gene caused by the addition of the compound being tested.

10. A method according to any of claims 6 to 9 wherein said yeast or fungus is chosen from *Saccharomyces cerevisiae*, *Schizosaccharomyces pombe*, *Candida albicans*, or *Aspergillus fumigatus*.
- 5 11. A compound identifiable according to the method of any of claims 6 to 9.
12. A compound according to claim 11 for use as a medicament.
- 10 13. A method for preparing a pharmaceutical composition for treating diseases associated with yeast or fungi comprising admixing a compound according to claim 12 with a suitable pharmaceutically acceptable carrier.
14. Use of a compound according to claim 11 or 12 for the preparation of a medicament for treating diseases associated with yeast and fungi.
- 15 15. Use of a compound according to claim 11 or 12 or a genetically modified organism as defined in claim 5 for the preparation of a medicament for modifying the endogenic flora of humans and other mammals.
- 20 16. Use of a compound according to claim 12 where the yeast or fungus is chosen from *Candida* spp., *Aspergillus* spp., *Microsporum* spp., *Trichophyton* spp., *Fusarium* spp., *Zygomycetes* spp., *Botritis*, spp., *Cladosporium* spp., *Malassezia* spp., *Epidermophyton floccosum*, *Blastomyces dermatitidis*, *Coccidioides immitis*, *Histoplasma capsulatum*, *Paracoccidioides brasiliensis*, *Cryptococcus neoformans*,
25 and *Sporothrix schenckii*.
17. A nucleic acid sequence encoding a polypeptide which is involved in a pathway for programmed cell death of yeast or fungi selected from:
- 30 (a) a nucleic acid encoding a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
35 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,

454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

- 5 (b) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 10 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 15 (c) a nucleic acid molecule encoding a protein having an amino acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 20 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484;
- 25 (d) a nucleic acid molecule comprising a sequence as represented in any of SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483;
- 30 (e) a nucleic acid sequence which is more than 70% identical, preferably more than 80% identical, more preferably more than 90% identical and most preferably more than 97% identical to any of the nucleic acid sequences shown in SEQ ID NOs 285, 287, 289, 291, 295, 297, 299, 301, 303, 305, 307, 309, 311, 315, 317, 319, 321, 323, 325, 327, 329, 331, 337, 341, 343, 345, 347, 351, 353, 355, 357, 359, 361, 363, 365, 367, 369, 371, 373, 375, 379, 381, 383, 385, 387, 389, 391, 393, 397, 401, 403, 405, 407, 409, 411, 415, 417, 421, 423, 425, 427, 429, 431, 35 433, 435, 437, 439, 441, 443, 445, 447, 449, 451, 453, 475, 477, 479, 481 or 483; and,

(f) a nucleic acid sequence encoding a functional fragment of any of the nucleic acid sequences as specified in a) to e),

(g) the complement of any of the nucleic acid sequences as specified in a) to e).

5 18. A nucleic acid according to claim 16 characterized in that it is derived from *Candida albicans*.

 19. A nucleic acid molecule capable of selectively hybridizing to a nucleic acid sequence as defined in claim 1 or the complement thereof.

10

 20. A nucleic acid sequence according to any of claim 17 to 19 which is mRNA

 21. A nucleic acid sequence according to any of claims 17 to 19 which is
15 DNA.

 22. A nucleic acid sequence according to any of claims 17 to 19 which is cDNA.

20 23. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridizing to the nucleic acid sequences according to any of claims 17 to 22.

 24. An isolated protein which is involved in a pathway for programmed cell
25 death of yeast or fungi selected from:

 (a) a protein having an amino acid sequence as represented in any of SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384, 386, 388, 390, 392, 394, 30 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476, 478, 480, 482 or 484, or encoding a functional equivalent, derivative or bioprecursor of said protein;

 (b) a protein having an amino acid sequence which is more than 70% similar, preferably more than 80% similar, more preferably more than 90% similar and
35 most preferably more than 97% similar to any of the amino acid sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304, 306, 308,

310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344, 346, 348,
352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380, 382, 384,
386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418, 422, 424,
426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452, 454, 476,
5 478, 480, 482 or 484;

(c) a protein having an amino acid sequence which is more than 70% identical,
preferably more than 80% identical, more preferably more than 90% identical
and most preferably more than 97% identical to any of the amino acid
sequences shown in SEQ ID NOs 286, 288, 290, 292, 296, 298, 300, 302, 304,
10 306, 308, 310, 312, 316, 318, 320, 322, 324, 326, 328, 330, 332, 338, 342, 344,
346, 348, 352, 354, 356, 358, 360, 362, 364, 366, 368, 370, 372, 374, 376, 380,
382, 384, 386, 388, 390, 392, 394, 398, 402, 404, 406, 408, 410, 412, 416, 418,
422, 424, 426, 428, 430, 432, 434, 436, 438, 440, 442, 444, 446, 448, 450, 452,
454, 476, 478, 480, 482 or 484; and,

15 (d) a functional fragment of any of said proteins as defined in a) to c)

25. An expression vector comprising a nucleic acid sequence according to
any of claims 17 to 23 .

20 26. An expression vector according to claim 25 which comprises an
inducible promoter.

27. An expression vector according to claim 25 or 26 which comprises a
sequence encoding a reporter molecule.

25 28. A host cell transformed, transfected or infected with the vector of any of
claims 25 to 27.

29. A nucleic acid molecule according to any of claims 17 to 23 for use as a
30 medicament.

30. A polypeptide according to claim 24 for use as a medicament.

31. An antibody capable of specifically binding to a polypeptide according to
35 claim 24.

32. An antibody according to claim 31 for use as a medicament.

33. A pharmaceutical composition comprising an antibody according to claim 31 or 32.

5

34. Use of an antibody according to claim 31 or 32, or an antibody capable of binding to at least one of the polypeptides as defined in claim 2, for the preparation of a medicament for treating diseases associated with yeast and fungi.

10

35. Use of an antibody according to claim 34 where the fungus is *Candida albicans*.

15

36. A nucleic acid probe which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively hybridises with any of said nucleic acid molecules.

20

37. A nucleic acid primer which comprises a fragment of at least 15 contiguous nucleotides of a nucleic acid molecule as defined in claim 17 and which selectively amplifies any of said nucleic acid molecules.

25

38. A genetically modified mammalian cell or non-human organism in which modification results in the overexpression or underexpression of at least one of the nucleic acids as defined in claim 1 or a human homologue thereof or at least one of the polypeptides as defined in claim 2 or a human homologue thereof, which overexpression or underexpression of said nucleic acid or polypeptide prevents or delays apoptosis of said genetically modified mammalian cell or in said genetically modified non-human organism.

30

39. A method for identifying compounds for stimulating or inhibiting apoptosis comprising the use of at least one of the nucleic acid sequences as defined in claim 1 or a human homologue thereof and/or at least one of the polypeptides as defined in claim 2 or a human homologue thereof and/or a genetically modified mammalian cell or non-human organism according to claim 38.

35

40. A compound identifiable according to the method of claim 39.

41. A compound according to claim 40 for use as a medicament.

42. A method for preparing a pharmaceutical composition for treating proliferative disorders or for preventing apoptosis in certain diseases comprising
5 admixing a compound according to claim 40 or 41 with a suitable pharmaceutically acceptable carrier.

43. Use of a compound according to claim 40 or 41 for the preparation of a medicament for treating proliferative disorders or for preventing apoptosis in certain
10 disorders.

44. Use of a nucleic acid molecule selected from any of the nucleic acid molecules as defined in claim 1 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
15

45. Use of a polypeptide selected from any of the polypeptides as defined in claim 2 or a human homologue thereof for treating proliferative disorders or for the prevention of apoptosis in certain diseases.

46. A pharmaceutical composition for use as a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases comprising a nucleic acid molecule as defined in claim 1 or a human homologue thereof or a polypeptide as defined in claim 2 or a human homologue thereof together with a pharmaceutically acceptable carrier diluent or excipient therefor.
20

47. A vaccine for immunizing mammals against proliferative disorders or for preventing apoptosis in certain diseases comprising least one nucleic acid molecule as defined in claim 1 or a human homologue thereof or at least one polypeptide as defined in claim 2 or a human analogue thereof in a pharmaceutically acceptable carrier.
25

48. Use of an antibody according to claim 31 or 32 or an antibody capable of binding to at least one of the polypeptides as defined in claim 2 or a human homologue thereof for the preparation of a medicament for treating proliferative disorders or for the prevention of apoptosis in certain diseases.
30

35

55

49. An expression vector comprising a human homologue of a nucleic acid sequence as defined in claim 1.

50. An expression vector according to claim 49 which comprises an inducible promoter.

5

51. An expression vector according to claim 49 or 50 which comprises a sequence encoding a reporter molecule.

52. A host cell transformed, transfected or infected with the vector of any of claims 49 to 51.

10

53. A nucleic acid molecule comprising a human homologue of at least one of the nucleic acid sequences as defined in claim 1.

15

54. An antisense molecule comprising a nucleic acid sequence capable of selectively hybridising to the nucleic acid molecule of claim 53.

55. A polypeptide encoded by a nucleic acid molecule according to claim 53.

20

FIG. 1:

YAR061W, 704 bp, CDS: 501-704 (SEQ ID NO 1)

AAAATTTGGCACTTCAGAGCTTATCGTATCTTCTCCCGGAGTTCCTCAAGACTTATACTT
CAGCCCGTTTAGGAATGCATAAAAGCAAATAGGATTCGTTACAACCTGCTGCAGGACTCTT
TAGGACTGCATCAAGGTAAGCCTCGCTGCACCTAAACGCAAAATGTGGTTGTAACCTTTT
TAATTTTTTTCTTGAACCTGTTGAGTCGTAATAAATCGTTTCTGGGAAGTGGAAGGTAAT
AATGTAATGGAATCGGCGTTACTCGCATGTGCAGATATCAGCGACAAAAGTGTGTAGG
GACGTTTCGATACCAAATTTCTAAATACAGCGCAGGAACATCACTACGCTAAACAAAT
CGTAGCGCATACATCTGATCGAAAAAGACAGTTCCCAAAACAATGACATATGAAGAGAC
CAGCATCAAAATTTTCATCATTAACAGCATGGCTAAAAGTTATTGTTTAATATACCCATA
CCTGATTGACGAACCAAGAAATGCCTTATCACTATTTATTTTTTGGCACTCTTCACCTACC
TGGCCACGTCCAATGTTGTTTCAGGAAGTACACAAGCATGCCTGCCAGTGGGCCCCGAGGA
AAAATGGGATGAATGTCAACTTTTATAAATACTCATTACTGGATTCAACAACGTATTCCT
ACCCGCAATATATGACTTCTGGATATGCCTCGAATTGGAATTAG

YAR061W, 67 aa (SEQ ID NO 2)

MPYHYLFLALFTYLATSNVVSQACLPVGPRKNGMNVNFYKYSLLDSTTYSYPQYMTS
GYASNWN

YAR073W, 1712 bp, CDS: 501-1712 (SEQ ID NO 3)

AGTGGCTCATGATCTGTAAATGATCGGTTGACCGCAGTATTATATAATAACATCCGTATA
AGTACATATACTACCATGTCTGTTCTCTACATTGCTTTTTTATTCAAGATTATTGGTTTTTC
CTAACCGCCGCGCCGCGCAGGTACCCCGCGCATCTCTTCTCTCGAAGAAAGCGGAAAAA
ACAAAAAAGTATAAATAGTGGAGTCTTTTCCCATTTAACAATTTAGAAAAAATTCG
AATGGAAATTTCTTGCCGAACATTTAACCGGAGACCTTGGCGGCTTTTTCTCAGTTTCG
TGGGCTAGTACATTTTACCTAGTATGCTGGGAACCTTTTTTCCGTATTCTATTCTATTCC
TTGCCTTACTTTTCTTATCATTTTTTTATATAACCAATTTCAAAAATACTTTTTTAAGTGC
ATAGACGCATTTTGTATTATTACAAATTAAGAATCAAATATAATATGTGCAATTAATAA
CTCCACAAGTAGCGAAAGCAATGGCCGCCATTAGAGACTACAAGACCGCACTAGATCTTA
CCAAGAGCCTACCAAGACCGGATGGTTTGTGTCAGTGCAGGAAGTATGGACTCCAAGATCA
GAGGTGGGTTGGCTTATAACGATTTTTTAATCTTACCAGGTTTAGTCGATTTTGCCTCCT
CTGAAGTTAGCCTACAGACCAAGCTAACCAGGAATATTACTTTAAACATTCCATTAGTAT
CCTCTCCAATGGACACTGTGACGGAATCTGAAATGGCCACTTTTATGGCTCTGTTGGATG
GTATCGGTTTCATTACCATTAAGTACTCCAGAGGACCAAGCTGACATGGTCAGAAGAG
TCAAGAACTATGAAAATGGGTTTATTAACAACCTTATAGTGATTTCTCCAACCTACGACCG
TTGGTGAAGCTAAGAGCATGAAGGAAAAGTATGGATTTGCAGGCTTCCCTGTCACGGCAG
ATGGAAAGAGAAATGCAAAGTTGGTGGGTGCCATCACCTCTCGTGATATACAATTCGTTG
AGGACAACCTCTTTACTCGTTTCAGGATGTGATGACCAAAAACCTGTTACCGGCGCACAAG
GTATCACATTATCAGAAGGTAACGAAATCTAAAGAAAATCAAAAAGGGTAGGCTACTGG
TTGTTGATGAAAAGGGTAACTTAGTTTCTATGCTTTCCCGAACTGATTTAATGAAAATC
AGAAGTACCCATTAGCGTCCAAATCTGCCAACCAAGCAACTGTTATGGGGTGCTTCTA
TTGGGACTATGGACGCTGATAAAGAAAGACTAAGATTATTGGTAAAGCTGGCTTGGATG
TCGTCATATTGGATTCTCTCAAGGTAAGTCTATTTTCCAATTGAACATGATCAAATGGA
TTAAAGAACTTTCCAGATTTGGAAATCATTTGCTGGTAACGTTGTCACCAAGGAACAAG
CTGCCAATTTGATTGCTGCCGGTGCGGACGGTTTGAGAATTGGTATGGGAAGTGGCTCTA
TTTGTATTACCCAAAAAGTTATGGCTTGTGGTAGGCCACAAGGTACAGCCGCTACAACG
TGTGTGAATTTGCTAACCAATTCGGTGTTCATGTATGGCTGATGGTGGTGTTCAAAAAC
ATTGGTCATATTATTACCAAGCTTTGGCTCTTGGTTCTTCTACTGTTATGATGGGTGGT
ATGTTGGCCGGTACTACCGAATCACCAGGTGA

YAR073W, 403 aa (SEQ ID NO 4)

MAAIRDYKTALDLTKSLPRPDGLSVQELMDSKIRGGGLAYNDFLILPGLVDFASSEVSLQT
KLTRNITLNIPLVSSPMDTVTESEMAFMALLDGIGFIHNNCTPEDQADMVRRVKNYENG
FINNPVIVISPTTTVGEAKSMKEYGFAGFPVTADGKRNAKLVGAITSRDIQFVEDNSLLV
QDVMTKNPVTGAQGITLSEGNEILKKIKKGRLLVDEKGNLVSMLSRTDLMKNQKYPLAS
KSANTKQLLWGASIGTMDADKERLRLLVKAGLDVVILDSSQGNSIFQLNMIKWIKETFPD
LEIIAGNVVTKEQAANLIAAGADGLRIGMGTSICITQKVMACGRPQGTAVYNVCEFANQ
FGVPCMADGGVQKHWSYYYQSFGSWFFYCYDGYVGRYYRITR

YBL048W, 812 bp, CDS: 501-812 (SEQ ID NO 5)

GGGAGAAGCTTATCTTACTGTAGAAGAAAATGGGATTGCGTTACTCCATATATATTGAAA
ATCCGTTATCTTCCCCATCATCATCGTATAAATCAATAAACGACCCGTTATTCCACTCTC
AGCATCGATCGCAAAAAAACGTGAGCTTCATCACCTACGGTTGTAGACATTGCAAGACAC
ATCTTTCCAGTTCCTTCCAGATTATTTCTAGAGATTATAGGGGTAGGACCGGAAGTCTT
ATTTAATGAACAAAGTTGTTAATGTCGTTGAAGGAAAGGTCGAGCAACGAAGAATGTTGA
CTGGCGACTACTTAGTCTGTGATATTCTTTGTCATTGGTGCAAGAGGAACGTAGGTTGGA
AATACTTGCAGAGCAGCAATGATGATCAGCAGTATAAGGAAGGAAAGTTTATCTTAGAGC
TGAAAAACATTTGTAAATGTACTTGATGTCTTCCTTTGTCTGCTATCTAGCACCTCTCGT
CTTTTAGTGCTTTTGTAGCGTATGATTCTTTTAAAGAATCTGGTCTTTCTTCCTTCTATTT
TGATTGGGTATATTTCTATTCGTGTTTCATTACTGGTCTGGGTTAATTGGGTTTGGTTT
GGTCCAGTTGTTTTCAAGTAGCCTTTATTTTTTCATTGTGGTATTTTATCTTATCGATTT
ATACTTTTTTTTATTCAAAGAAAATTAAACAGATAATCTCTTATGAGCCTAGCTACTTTG
TTTTTTCTTACAGGGCCATTGACTTATGCCCTGAACGAGTCTTACTTTACTTTTTTTGTA
TTTTCAATAATGTCGTGTTTCCCATGTTGTAA

YBL048W, 103 aa (SEQ ID NO 6)

MILFKNLVFLPSILIGYISIRVSLLVWVNWVLWSSCFQVAFIFSLWYFILSIYTFYFSK
KIKQIISYEPSYFVFSYRAIDLCPERVLLYFFCIFNNVFPML

YBL051C, 2507 bp, CDS: 501-2507 (SEQ ID NO 7)

GGGAAATATCAATTCCCGTATTTCAATGTTAGTAATTTGCCTTCGTAAATTACGGAATCA
CATAGCTTTCATTTTGTTCCTTTGATATATTTCCCTACTACATACTCTTTTCAATAACTC
TACAGGGTCTGACATTTTAACTTTCAGGTTAATGATGGTGTCTTACTATATTCTCGAG
TCGTACAGAAGTTAGTTCAGATAAACTGCTTCGGTGCTGCCCACTTCTTATCATTACTTC
AACTTTACCTTCCCTATACCTGTGTGTCCTTATTAATTCAAGTTAATCCGAGGTAATAGA
TTAGGGTAACCTTCAATGATGTACGAAACACGGATGCTGCAACTTTGCGATTTTTTCCT
GGAAAAGAATAACAATTAAAGGCAGCCTTTCAGCTGAGATTACCAGCAGGTCTTTGGAGA
TTAGCGCAAGAAGAAGTGTGATATAGTACTCATAGAGGCAGGCTACAGACTAGGGAAAGC
GTGTTCAACAACAATAAGAAATGGAGACCAGTTCTTTTGAGAATGCTCCTCCTGCAGCCA
TCAATGATGCTCAGGATAATAATATAAATACGGAGACTAATGACCAGGAAACAATCAGC
AATCTATCGAAACTAGAGATGCAATTGACAAAGAAAACGGTGTGCAACGGAAACTGGTG
AGAACTCTGCAAAAAATGCCGAACAAAACGTTTCTTCTACAAATTTGAATAATGCCCCCA
CCAATGGTGCTTTGGACGATGATGTTATCCCAAATGCTATTGTTATTAAAAACATTCCGT
TTGCTATTAAAAAAGAGCAATTGTTAGACATTATTGAAGAAATGGATCTTCCCCTTCCTT
ATGCCCTTCAATTACCACTTTGATAACGGTATTTTCAGAGGACTAGCCTTTGCGAATTTCA
CCACTCCTGAAGAACTACTCAAGTGATAACTTCTTTGAATGGAAAGGAAATCAGCGGGA
GGAAATTGAAAGTGGAATATAAAAAAATGCTTCCCCAAGCTGAAAGAGAAAGAATCGAGA
GGGAGAAGAGAGAGAAAGAGGACAATTAGAAGAACAACACAGATCGTCATCTAATCTTT
CTTTGGATTCTTTATCTAAATGAGTGGAAGCGGAAACAATAACTTCTAACAATCAAT
TATTCTCGACTCTAATGAACGGCATTAATGCTAATAGCATGATGAACAGTCCAATGAATA
ATACCATTAACAATAACAGTTCTAATAACAACAATAGTGGTAACATCATTCTGAACCAAC
CTTCACTTTCTGCCCAACATACTTCTTCATCGTTGTACCAACAAACGTTAATAATCAAG
CCCAGATGTCCACTGAGAGATTTTATGCGCCTTTACCATCAACTTCCACTTTGCCTCTCC
CACCCCAACAACCTGGACTTCAATGACCCTGACACTTTGGAAATTTATTCCCAATTATTGT
TATTTAAGGATAGAGAAAAGTATTATTACGAGTTGGCTTATCCCATGGGTATATCCGCTT
CCCACAAGAGAATTATCAATGTTTTGTGCTCGTACTTAGGGCTAGTAGAAGTATATGATC
CAAGATTTATTATTATCAGAAGAAAGATTCTGGATCATGCTAATTTACAATCTCATTTGC
AACAACAAGGTCAAATGACATCTGCTCATCCTTTGCAGCCAAACTCCACTGGCGGCTCCA
TGAATAGGTCACAATCTTATACAAGTTTGTTACAGGCCCATGCAGCAGCTGCAGCGAATA
GTATTAGCAATCAGGCCGTTAACAATTCTTCCAACAGCAATACTATTAACAGTAATAACG
GTAACGGTAACAATGTCATCTAATAACAATAGCGCCAGCTCAACACCAAAAATTTCTT
CACAGGGACAATTCTCCATGCAACCAACACTAACCTCACCTAAAATGAACATACACCATA
GTTCTCAATACAATTCCGCAGACCAACCGCAACAACCTCAACCACAAACACAGCAAAATG
TTCAGTCAGCTGCGCAACAACAACAATCTTTTTTAAGACAACAAGCTACTTTAACACCAT
CCTCAAGAATTCCATCCGGTTATTCTGCCAACCATTATCAAATCAATTCCGTTAATCCCT
TACTGAGAAATTCTCAAATTTACCTCCAAATTCACAAATCCCAATCAACAGCCAAACCC

TATCCCAAGCGCAACCACCAGCACAGTCCCAAACCTCAACAACGGGTACCAGTGGCATAACC
AAAATGCTTCATTGTCTTCCCAGCAGTTGTACAACCTTAACGGCCCATCTTCAGCAAACCT
CACAGTCCCAACTGCTTCCACAGCACACAAATGGCTCAGTACATTCTAATTTCTCATATC
AGTCTTATCACGATGAGTCCATGTTGTCCGCACACAATTTGAATAGTGCCGACTTGATCT
ATAAATCTTTGAGTCACTCTGGACTAGATGATGGCTTGGAACAGGGCTTGAATCGTTCTT
TAAGCGGACTGGATTTACAAAACCAAAACAAGAAGAATCTATGGTAA

YBL051C, 668 aa (SEQ ID NO 8)

METSSFENAPPAINDAQDNNINTETNDQETNQOSIETRDAIDKENGVOETETGENSAKNA
EQNVSSSTNLNNAPTNGALDDDDVIPNAIVIKNIPFAIKKEQLLDIEEMDLPLPYAFNYHF
DNGIFRGLAFANFTTPEETTQVITSLNGKEISGRKLKVEYKMLPQAERERIEREKREKR
GQLEEQHRSSSNLSLDSLSKMSGSGNNNTSNNQLFSTLMNGINANSMMNSPMNNTINNNS
SNNNNSGNIILNQPSLSAQHTSSSLYQTNVNNQAQMSTERFYAPLPSTSTLPLPPQQLDF
NDPDTLEIYSQLLLFKDREKYYYELAYPMGISASHKRIINVLC SYLGLVEVYDPRFIIIR
RKILDHANLQSHLQQQGQMTSAHPLOPNSTGGSMNRSQSYTSLQLAHAAAAANSISNQAV
NNSNSNTINSNNGNGNVIINNNSASSTPKISSQGQFSMQPTLTSPKMNIHSSQYNSA
DQPQQPQPQTQQNVQSAQQQQSFLRQQATLTSPSRIPSGYSANHYQINSVNPLLRSQI
SPFNSQIPINSQTL SQAQPPAQSQQTQQRVPVAYQNASLSSQQLYNLNGPSSANSQSQLLP
QHTNGSVHSNFSYQSYHDESMLSAHNLSADLIYKSLSHSGLDDGLEQGLNRSLSGLDLQ
NQNKKNLW

YBL066C, 3674 bp, CDS: 501-3674 (SEQ ID NO 9)

ATCCCAAGAAGAAGATTAGACTGATTTTTACCTACCCTTCCACCGTCGGAAGAAACACTT
CTGAAGTGTTAAGGGTAATCGACGCCTTGCAATTGACTGACAAGGAGGGCGTAGTAACCTC
CAATTAATTGGCAGCCAGCTGACGATGTCATTATTCCTCCCTCTGTCTCCAATGATGAGG
CGAAGGCTAAATTTGGTCAATTTAATGAAATTAAACCTATTTAAGATTCACCAAGTCGA
AATAAGCTTTGAAATAAACGACTTTACTATATACAGGTATATGAAGTATCTCTAACTAAA
ACTTTTATCTATCTTTTATTCTTATTATATCTCATCTCGTACGAAGGGCCGCTCATTGGA
TCATTTTTCTTTACATACCGTAAAGGAATGGCGTTAAAAATATATATGAAAATGCATG
TAATAAACTCTCTGCAGAAACCTTAATGTCAAAGGTCCCGTATACAGATTATATTGGCTC
TGCGTATACGCATTCTCGTCATGGTGAAGGATAATCGAGATTCTGACCAAGACCAAGATT
TTAGTTCTGCTCACATGAAAAGACAACCGGAGCAGCAACAGTTGCAACAGCACCAGTTCC
CAAGTAAGAAACAACGAATATCTCACCATGATGACAGTCATCAAATCAACCATAGACCAG
TTACCTCATGTACACATTGTAGACAGCACAAAATCAAATGCGATGCTAGTCAAAATTTCC
CTCATCCTTGCTCCAGATGCGAAAAAATTGGTCTCCACTGTGAAATCAATCCTCAATTCA
GGCCTAAGAAGGGCTCACAGTTGCAACTACTGAGACAAGATGTGGATGAAATCAAATCTA
AACTCGATACTCTTCTGGCCAATGACAGCGTTTTCGTTTCATCTTTTACAACAGATTCCCA
TGGGCAATAGCCTTTTGAATAAGCTCAATCTGCATCCAACCTCCAACCTCCGGGTACTATTA
TCCCTAACCAGATTCTTCTCCTTCCCTCAGGTTCTCCAACCTTCTTCCGCGGCTCAACGAG
ATTCTAAGGTTTTCAGTTCAAACCTTATTTGTCCAGGGAACCCCAACTCTTACAAGCAAATC
AGGGCAGCAATACGAATAAATTTAAAGCAAATAATGAAGCATCTTCTCACATGACGTTGC
GCGCATCTTCTTTAGCGCAAGATTTCGAAAGGCTTGGTTGCAACAGAGCCAAATAAGCTGC
CCCCGCTGCTAAATGACTCAGCATTGCCTAATAATTCAAAGAATCTTTACCTCCTGCTT
TGCAAATGGCTTTTTATAAGAACAACCTCTGCAGGTAACACTCCGAACGGCCCTTCTCTC
CAATTCAAAAAACATATTCCCCTCATACTACGTCGACCACCGTTACAACGACAACAAATC
AACCACCATTTCAGCAACAAGCCACGTAGCAACAAATAACAATGCAGATAGGACGAAGA
CGCCGGTAGTAGCCACCACCACGACTATGCCATTATTGCCCTTCGCCGCATGCAAATGTAG
ATGAGTTTGTACTGGGCGATATTAGTATTTCCATTGAAAAAGCGAATAGATTACACCATA
TTTTCGTGACTAGGTATCTGCCGTATTTTCTTATTATGTATTCCAATAACGCCACCGAAT
TATACTCCCAATCTCAGTTGCTTTTCTGGACCGTGATGTTGACGGCATGTCTGTCTGATC
CTGAACCGACGATGTATTGCAAGCTAAGCTCTTTGATCAAGCAACTTGCCATAGAGACCT
GCTGGATAAGAACACCTAGATCCACACATATTTGCAAGCTTTGTTAATATTGTGCATTT
GGCCTTTGCCTAACCAGAAAGTCTTAGATGATTGTTCTTACCGTTTGTAGGATTAGCAA
AGTCACTGTCTTATCAATTAGGTTTGCACAGAGGTGAATTCATTTCTGAATTCACAAGAA
CTCAAACATCAATGCCAAATGCAGAAAAGTGGAGAACTAGGACTTGGCTGGGAATATTTT
TTGCCGAACCTTTGTTGGGCGAGTATCCTTGGTTTGGCCACCAACTTCACAGACAGACTATT
TATTAGAAAAGCCTTATCCTGTGGTGACGAAGAATCAGAAGAAGATAACAATGACAGTA
TTGACAATAACAACAATGATAAAAGGAACAAGAAAGACGAGCCGCACGTTGAAAGTAAAT
ACAAACTACCGGGCAGTTTTAGAAAGATTGCTCAGCCTGGCGAATTTCCAAGCAAATTTGT
CTCATATCATTGGTTCTTCCACTTCCAGTCCTGATGGTTTATTGGAACCAAGTATCGTG

CTGAGACACTGTCCATCTTGGGAAAAGAGTTAGATTTATTAGCAAAAACCTTTAAATTTCC
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CATTCCTACCCGAAACACCTCCTACCGATCAAATTCATATGTCACAGAGGCCTATCTAA
CAGCTACTAAAATTGTCACTCTATTGAATAATCTTTTAGAAACACACCAATTAATTGAAC
TGCCTATTTATATTAGACAAGCTGCTACATTTTCTGCACTGATTCTCTTTAAATTGCAGT
TGACTCCTTTACTTCCTGACAAATATTTTGATTGAGCAAGGCAATCCGTGGTCACTATCC
ATAGACTTTATAGAAATCAGTTAACTGCGTGGGCCACTAGTGTTGAGAATGATATTTCTGA
GAACTGCAAGTATGTTAGAAAACTGAACTTCGTACTGATCATGCATCCAGAAGTTTTTG
TGGAAGAAGACGGTATTTATTTCTAGGATGAGATCACATTTAACAGGGTCTCTATTCTATG
ATTTGGTTTGGTGTGTTACAGAGGCGAGAAGAAGGGAAATGGATCCCGAATATAACAAGC
AAGCCTTAGAGAAAGCCGCTAAGAAAAGAAAATTTTCTCAAATGGTATCTACAATGGCA
CTTCGTCTACGGGTGGCATAACGGACAGAAAACCTATATCCATTGCCACTATATAACCATA
TCTCCAGAGATGACTTTGAACTGTAACAAAAACAACCAAGTGGAACCACTGTTACCA
CTTTAGTTCCTACTAAGAATGCCTTAAAGCAGGCAGAAAAGCTAGCCAAGACAAATAACG
GAGATTCTGACGGTTCTATAATGGAGATTAACGGGATACCTCTTCCATGCTCGGGGAAA
CAGGCAGCGTAAAATTTCAAAGTTTATTCGCTAATACCTCGAATAGTAACGATTATAATA
ATAATAGGACGTTATTGGATGCGTCTAATGACATATCAATTCCTCTAATTCATTTATC
CAGTGGCTTCTGTCCCCGCTTCGAATAACAATCCACAAAGTACTAAGGTAGACTATTATA
GTAACGGACCTAGTGTAATTCCTGATCTCTCCATGAAAAGATCAGTAAGCACTCCCGTTA
ATCATTTCCTGCGTCCGTTCCAGGGTTAAGGAACCAACCCCGTTGGCAACTTATCTAATA
ATGTTACATTGGGAATAGACCACCCTATTCCAAGGGAGCACAGTAATTTACAAAATGTCA
CCATGAATTATAAATCAATTCAGCAACGCCAACGCGATTGGAAGATCACAAAGTAGTA
TGTCCTCATTCACGTACACCTTTGTTTCGGTCAATATATGACAGTTGGATTCCGCGTCCGA
CCCCGGTCCTCTAA

YBL066C, 1057 aa (SEQ ID NO 10)

MVKDNRDSDDQDFSSAHMKRQPEQQQLQHQFPSKKQRI SHHDDSHQINHRPVTSC₁THC
RQHKIKCDASQNFPHPCSRCEKIGLHCEINPQFRPKKGSQQLQLLRQDVDEIKSKLD₂TLA
NDSV₃FVHLLQQIPMGNSLLNKLNLHPTPTPGTII₄PNPDSSPSSGSPTSSAAQRDSK₅VSQ
TYLSREPQLLQANQGSNTNKFKANNEASSHMTLRASSLAQDSKGLVATEPNKLPPL₆LND
ALPNNSKESLPPALQMAFYKNNSAGNTPNGPFSPIQK₇TYSPHTTSTTVTTT₈TNQP₉PPFAAT
SHVATNNNADRTKTPVVATTTT₁₀TMPLLPSPHANVDEFVLGD₁₁ISISIEKANRLHHIFVTRYL
PYFPIMYSNNATELYSQS₁₂QLLFWTVMLTAC₁₃LS₁₄DPEPTMYCKLSS₁₅LIKQLAIETC₁₆WIRTPR
STHISQALLILCIWPLPNQKVLDDC₁₇SYRFVGLAKSLSYQLGLHRGEFI₁₈SEFTRTQT₁₉SMPN
AEKWRTRTWLGIFFAELCWASILGLPPTSQTDYLLEKALSCGDEE₂₀SEEDN₂₁NSIDNN₂₂NND
KR₂₃NKDEPHVESKYKLPGSFRLLSLANFQAKLSHIIG₂₄SSTSSPDGLLEPKYRAETLSIL
GKELDLLAKTLNFQSDDTVNIYFLYVKLTVCCFAFLPETPPTDQIPYVTEAYLTATKIVT
LLNNLLETHQLIELPIYIRQAATFSALILFKLQLTPLL₂₅PKYFDSARQSVVTI₂₆HRLYRNQ
LTAWATSVENDISRTASMLEKLNFLVIMHPEVFVEEDGII₂₇SRMRSHLTGSLFYDLVWC₂₈VH
EARREMDPEYNKQALEKA₂₉AKKRKFSSNGIYNGTSS₃₀TGGITDRKLYPLPLYNHI₃₁SRDDFE
TVTKTTPSGTTVTTLVPTKNALKQAEKLAKTNNGDS₃₂SGSIMEINGIPLSMLGETGSVKFQ
SLFANTSNSNDYNNNR₃₃TLLDASNDISIPNSIYPVASVPASNNNPQSTKVDYYSNGPSVI
PDL₃₄SMKRSVSTPVNHFPASVPGLRNHPVGNLSNNVTLGIDHPIPREHSNLQNV₃₅TMN₃₆YNNQ
FSNANAIGRSQSSMSHSRTPLFRSIYDSWIPRPTPV₃₇L

YBL078C, 854 bp, CDS: 501-854 (SEQ ID NO 11)

TAGTGGAGTACGAATTAGTTAAAGATACTATCGACTTTGAAGCCATTGTCAAAGAACATT
TTGATATGTTAAGCAAGACCTGTAGATCCGACATTGCCAAATATGACGGCTCAAAGACAG
ACCCAATTGGTGATGAAGAACAATCTATTAATGACACCATTTTCAAATTTAAAGTGTTCA
AATTATGAAAACAACCTCATATAAATACGTACAAATTTTCTCTACTCGAAGTGATATAGA
TGTATATGTGTAAGTTTACGTTTAAAGTTAGAGTCATGTAATGCTAACTGTCTCCACCGAT
AATGTTGTATAATACCCGTGAAATCATAGCACATGATATATCATCACCCGGAGGCCGTT
ATTTTCGGCGGCGGCAAAAATATTTGGTATAATTATGGAAATACAAAAGGGGAACCATT
AAAGGTTGAGGAGGGGATTGATAAGAGAATCTAATAATTGTAAAGTTGAGAAAATCATAA
TAAAAATAATTACTAGAGACATGAAGTCTACATTTAAGTCTGAATATCCATTTGAAAAAA
GGAAGCGGAGTCGGAGAGGATTGCTGACAGGTTCAAGAATAGGATACCTGTGATTTCG
AAAAAGCTGAAAAGTCAGATATTCAGAGATTGATAAGCGTAAATATCTAGTTCCTGCTG
ACCTTACCGTAGGGCAATTTGTTTATGTTATAAGAAAGAGAATTATGCTACCCCTGAGA
AGGCCATCTTCATTTTGTCAATGATACTTTGCCACCTACTGCGGCGTTGATGTCTGCCA
TATATCAAGAACACAAGGATAAGGACGGGTTTTTGTATGTCACTTACTCAGGAGAAAATA

CATTTGGCAGGTAG

YBL078C, 117 aa (SEQ ID NO 12)

MKSTFKSEYPFEKRKAESERIADRFKNRIPVICEKAEKSDIPEIDKRKYLVPADLTVGQF
VYVIRKRIMLPPEKAIFIFVNDTLPPTAALMSAIYQEHKDKDGLYVTYSGENTFGR

YBR072W, 1145 bp, CDS: 501-1145 (SEQ ID NO 13)

GCAGCAGCAACTCCGTGTGTACCCCTAACTCCGTGTGTACCCCTAAAGAACCTTGCCCTGT
CAAGGTGCATTGTTGGATCGGAATAGTAACCGTCTTTACATGAACATCCACAACCAACGA
AAGTGCTTTTTCAAGCATTGCTTGATTTCTAGAAAGATCGATGGTTATTCCCTCCCCCTT
ATGCGTCCAAAAATATAGGGTGCTCGTAACAGTAAGGTATTGCGACTTAGCGTGCTCGCA
ACACAAAATTAAGTAATATGCGAGTTTATAGATGTCTTGCGGATCTATGCACGTTCTTGA
GTGGTATTTTCATAACAACGGTTCTTTTTTACCCTTATTCTTAAACATATAAATAGGACCT
CCATTAGTTAGAGATCTGTTTTTAATCCATTACCTTTTATTCTACTCTCTTATACTAAT
AAAACCACCGATAAAGATATATCAGATCTCTATTAACAGGTATCCAAAAAAGCAAACA
AACAACTAAACAAATTAACATGTCAATTAACAGTCCATTTTTTGTATTTCTTTGACAACA
TCAACAACGAAGTTGATGCCTTTAACAGATTGCTGGGTGAAGGCGGCTTAAGAGGCTACG
CACCAAGACGTCAGTTAGCAAACACACCCGCAAAGGATTCTACTGGCAAGGAAGTTGCTA
GACCAAATAACTATGCTGGCGCTCTTTATGATCCCAGAGATGAAACCTTAGATGATTGGT
TCGACAATGACTTGTCCCTGTTCCCATCTGGTTTCGGTTTCCCTAGAAGTGTCGCAGTTC
CAGTTGATATTTTGGACCATGACAACAACACTACGAGTTGAAAGTCGTGGTTCCCTGGTGTCA
AAAGCAAGAAGGACATTGATATTGAGTACCATCAAACAAGAACCAAATTTTGGTTTCTG
GTGAAATTCCATCTACCTTGAATGAAGAGAGTAAAGACAAGGTCAAGGTCAAGGAGAGCA
GCTCTGGTAAGTTCAAGAGAGTCATCACTTTGCCAGACTACCCAGGTGTGGATGCAGACA
ACATTAAAGCAGACTACGCAAATGGTGTTTTGACATTAACAGTTCCAAAATTGAAGCCTC
AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAA

YBR072W, 214 aa (SEQ ID NO 14)

MSFNSPFFDFFDNINNEVDFAFNRLLEGGLRGYAPRRQLANTPAKDSTGKEVARPNNYAG
ALYDPRDETLDDWFDNDLSLFP SGFGFPRSVAVPVDILDHDNNYELKVVPVGVKSKKDID
IEYHQKNQILVSGEIPSTLNEESKDKVKVKESSGKFKRVITLPDYPGVDADNIKADYA
NGVLTLTVPKLPQKDGKNHVKKIEVSSQESWGN

YBR073W, 3377 bp, CDS: 501-3377 (SEQ ID NO 15)

AGAAGGATGGTAAGAACCACGTCAAGAAGATTGAGGTTTCTTCTCAAGAATCGTGGGGTA
ACTAAAGTGACCTGGCTCTATAGTGTGTCCCTCTCGCGAGGACCATTGTTGCTTGCATA
TGGCTTGAAACATATGTCATCACATCTGAGCGATTTTACCTCTTAGAATTAGTTTAGATA
TATATGAGTTGATGAATAAATAGTTATAAAAACTTGCTTTGGCTTCGATATATGACCGTT
ATTTTTGACTAAGTTTAAACGAAGGAATCTAACCTCGTTCTTGTAATTACCAAAATCTTC
AACAACGCGCTGTTGGAGGTATCTCTATGGATGTGGCTTGAAATATGGATGTCTTGCCCTA
CTTCTACTTCTGGGAAAGGCATTTTTTACTCGATCGCGTTAATATATGCATCAAGAAAATA
AAAAATAAAACGCGAAGAGCTAAAAAAGAAACCTACTATAAATAACCGATTAG
AATCGAGTTTTTGTATTGAAATGGCGGTAATAAGCGTTAAACCTCGACGAAGAGAGAAGA
TCCTACAGGAGGTAAAAACAGCTCGGTATATCAAACGGTATTTGATTCCGGTACTACTC
AAATGCAGATACCGAAATATGAGAACAAGCCATTCAAGCCTCCAAGAAGGGTTGGATCAA
ATAAGTACACAACTCAAACCAACCGCCACTGCAGTCACAACAGCCCCCTATATCTAAAG
CCAAAGTTACTGTCAACTTGAAAAGAAGCATTTCCGGCGGGACCTACTTTAAATCTTGCCA
AGAAGCCGAATAATCTGTCTCAAATGAAAACACTAGATATTTTACTATCATGTACAGGA
AGCCTACTACCAAAAAGCACAAAGACTTGGAGTGGTGATGGCTACGCTACCTTAAAGCCA
GTAGCGATAAGTTATGCTTTTATAACGAAGCAGGGAAATTTCTTGGGTCAAGTATGCTAC
CAAGTGATTGAGATTCTCTCTTCGAAACTCTTTTCAAAGCAGGCTCCAATGAAGTACAAT
TGGATTACGAATTGAAGGAAAATGCAGAAATACGTAGCGCCAAAGAAGCCTTATCACAAA
ACATGGGAAATCCCAGCCCACCGACCACAAGCACAACAGAAACAGTGCCTTCTACGAAGA
ATGACGGTGGCAAATACCAAATGCCTCTGTCTCAGCTGTTTTCACTAAACACTGTGAAAA
GATTCAAATCAGTAACAAAGCAAACAAATGAACACATGACCACAGTACCTAAAACCAGTC
AAAATTCCAAAGCCAAAAAATATTATCCAGTATTTGATGTCAACAAAATCGATAATCCTA
TAGTAATGAACAAAATGCAGCCGCTGAAGTTGACGTAATTGTTGATCCATTACTGGGCA
AATTCTTGGCGCCCTCATCAGAGGGAAGGGGTGAAGTTCATGTATGATTGCTTAATGGGCT
TGGCAAGACCAACTATTGAAAATCCGGATATCGATTGTACTACTAAAAGTTTAGTGTTAG

AAAATGACTCAGATATTAGTGGATGCCTTTTGGCTGATGATATGGGTTTAGGTAAAACAC
TAATGAGTATAACTTTGATTTGGACATTAATTAGGCAAACCTCCTTTTGCATCAAAAAGTTT
CATGTTTCGCAATCAGGCATACCATTAAGTGGACTTTGTAAGAAGATTTTAGTCGTTTGTG
CCGTTACTTTAATAGGAAATTGGAAAAGAGAATTGGAAAATGGTTAAATTTGTCAAGAA
TAGGTGTTTTGACATTAAGCTCAAGGAATTCTCCTGATATGGATAAAATGGCTGTCAGAA
ATTTTTTAAAAGTGCAACGAACCTTATCAAGTCTTGATTATTGGCTACGAAAAACTCTTGA
GTGTTTCTGAAGAATTAGAGAAAAATAAACATTTGATTGACATGCTGGTGTGTGACGAAG
GCCATCGACTAAAAAACGGGGCTTCTAAAATTTTAAATACGCTGAAGAGTTTAGACATAA
GAAGGAAGCTTTTGCTTACGGGAACCTCTATACAAAATGATCTTAATGAGTTTTTCACTA
TTATAGATTTTCATAAACCCAGGAATCCTTGGAAGCTTCGCTTCTTTCAAAGAAGATTCA
TTATCCCTATAACTAGAGCCAGAGACACTGCAAACAGATACAACGAAGAATTGTTGGAAA
AGGGGGAAGAAAGGTCAAAGAGATGATAGAAATTACGAAAAGATTTATTTTGAGACGAA
CAAATGCGATTTTAGAAAAGTACCTTCCTCCAAAGACGGATATAATTTTATTCTGTAAAC
CATACAGCCAACAGATATTGGCATTCAAAGATATTTTGCAGGGCGCACGTTTAGATTTTG
GACAATTGACGTTTCACTTCTTCGCTAGGACTAATAACATTACTGAAAAAGGTTTGTAACT
CTCCTGGATTGGTTGGCTCAGATCCCTATTACAAATCACATATAAAGGATACCCAATCTC
AGGACAGCTATAGTCGTTCTTTGAACTCTGGTAAGTTAAAGGTATTAATGACATTACTAG
AAGGTATTAGGAAGGGTACCAAGGAGAAGGTCGTCGTAGTGTCTAACTACACTCAAACAT
TGGATATAATTGAAAATTTGATGAATATGGCTGGGATGTCACATTGCAGACTCGACGGTT
CCATACCTGCTAAACAAAGGGACTCTATCGTCACATCTTTCAATCGGAATCCAGCCATAT
TTGGATTCTTGTGTTGAGTGCAAAATCGGGAGGTGTAGGATTGAATCTAGTCGGTCGTTCCG
GACTTATTTTATTTGATAATGATTGGAATCCTTCAGTAGATTTGCAAGCGATGTCACGAA
TTCATAGAGATGGTCAAAAAAGCCGTGCTTCATATATAGACTTGTCCAACTGGGTGTA
TCGATGAGAAAATATTGCAAAGGCAATTAATGAAGAACAGTTTGAGCCAAAAATTTCTAG
GTGACTCGGAGATGAGAAATAAAGAATCTTCTAATGATGATCTTTTCAATAAAGAGGACT
TGAAGGACCTGTTTCTGTCCATACAGATACCAAGAGTAACACACATGACTTAATTTGTT
CTTGCGATGGTTTAGGTGAGGAAATTGAATATCCTGAAACAAATCAACAGCAGAACACCG
TAGAGCTGAGAAAGCGTAGCACTACGACATGGACAAGTGCCTGGATTTACAAAAGAAAA
TGAATGAAGCAGCCACCAACGATGATGCCAAAAAGTCACAATACATTAGGCAATGTCTCG
TTCATTATAAGCATATCGATCCAGCAAGACAAGATGAATTATTTGATGAGGTTATCACAG
ATTTCGTTACCGAATTGAAAGATAGTATTACCTTTGCGTTTGTAAGCCCGCGGAGATAT
GTCTCAGAGAACAATGA

YBR073W, 958 aa (SEQ ID NO 16)

MAVISVKPRRREKILQEVKNSSVYQTVFDSGTTQMQUIPKYENKPFKPPRRVGSNKYTQLK
PTATAVTTAPISKAKVTNLRKRSISAGPTLNLAKKPNNLSSNENTRYFTIMYRKPTTKKH
KTWSGDGYATLKASSDKLCFYNEAGKFLGSSMLPSDSLSLFTLKFAGSNEVQLDYELKE
NAEIRSAKEALSQNMGNPSPPTTSTTETVPSTKNDGGKYQMPLSQLFSLNTVKRFKSVTK
QTNEHMTTVPKTSQNSKAKKYYPVFDVNKIDNPIVMNKNAAAEVDVIVDPLLKFLRPHQ
REGVKFMYDCLMGLARPTIENPDIDCTTKSLVLENDSDISGCLLADDMGLGKTLMSITLI
WTLIRQTPFASKVSCSQSGIPLTGLCKKILVVCPTLIGNWKREFGKWLNLNRIGVLTLS
SRNSPDMDKMAVRNFKVQRTYQVLIIGYEKLLSVSEELEKNKHLIDMLVCDEGHRLKNG
ASKILNTLKSLEDIRRKLTLTGTPIQNDLNEFFTIIIDFINPGILGSFASFRRFIIPITRA
RDTANRYNEELLEKEEERSKEMIEITKRFILRRTNAILEKYLPPKTDIILFCKPYSQOIL
AFKDILQGARLDFGQLTFSSSLGLITLLKKVCNSPGLVGSDPYKSHIKDTQSQDSYSRS
LNSGKLKVLMTLLEGIRKGTKEKVVVVSNTYTQTLDIENLMNMAGMSHCRLDGSIPAKQR
DSIVTSFNRPNAIFGFLLSAKSGGVGLNLVGRSRLILFDNDWNPSVDLQAMSRIHRDGQK
KPCFIYRLVTTGCIDEKILQRQLMKNSLSQKFLGDSEMRNKESNDDLNFNKEDLKDLFSV
HTDTKSNTHDLICSCDGLGEEIEYPETNQOQNTVELRKRSTTTWTSALDLQKKMNEAATN
DDAKKSQYIRQCLVHYKHIDPARQDELDFDEVITDSFTELKDSITFAFVKPGEICLREQ

YBR086C, 3341 bp, CDS: 501-3341 (SEQ ID NO 17)

AGATCCTAAACAGCACGAAGCATATTATTGCGCATAATTTGTTCTTGTAGGATCTTTTC
TTGACATTTTTTTTCACTCTGCGAGAACTTCTCTTTTTTTTCTCTCTGTTGTTTTCAAACAAAAAGAT
CAAACAAGGGCACTTTTTTTTATCTTTTTTTTTTCTCTGTTGTTTTCAAACAAAAAGAT
TCCACCACTACATCAGTGTGAAAGACTGTAAAAGCTTTCTGATAAATAAGCACTTTCCAT
ATTTTTCACTGAAAAATAGTTTTCTTTTTTGACGCTATTATTGACTTCATTAAGAAATAT
CCCTTTTTTCCCGTTGCAATTATTTCTATAAGGGAAGCTGGAAATAGGGGGCTGGAAAA
GATATTTGAACAGTCGCTCCAATAACCGTTCTCACCATCATTAACATTTTTGAAGGTGAA
TACTGTTTCGGTCGATTTATGGCTAATTTGTCAAATACATTTGAAAAAGATTAAACAAG

CACAAGCGGTTGAGCATACTATGTGCGCAGACAATTACATCTCTAGATCCGAATTGTGTTA
TTGTATTCAATAAAACTTCGAGTGCAAACGAGAAGAGTTTGAATGTCGAATTCAAACGTT
TGAATATACATTCTATTATCGAACCTGGCCATGATCTGCAAACAAGCTATGCGTTTATTA
GAATCCATCAGGATAATGCGAAACCGCTTTTTTTCATTTTTTGCAGAATCTGGACTTCATTG
AATCCATCATACCATATCATGATACTGAATTGTCCGATGATTTGCATAAACTGATTTCTA
TCAGCAAATCAAAAATACTGGAGGCTCCAAAACAGTATGAGTTGTACAACCTATCGAATT
TGACCAATAATCCCAAACAATCCTTATATTTTGCATTCTTACAGAACTATATAAAATGGT
TGATTCCCTTCTCCTTTTTTGGATTATCAATTAGATTTTTATCTAATTTTACGTATGAAT
TCAATTCCACATACTCGCTGTTCCGATCCTATGGACATTGTCATTTACAGCCTTTTGGC
TTTATAAATATGAACCATTTTGGTCTGATAGACTGAGTAAATACTCATCATTTTCTACCA
TTGAGTTTCTTCAAGATAAACAGAAAGCCCAAAAAAAGCTAGTTCCGTTATCATGTTGA
AGAAATGTTGTTTTATTCTGTGGCTTTGTTGTTTGGCGCAATATTACTATCATTCAGC
TATATTGTTTTGCGTTGGAAATTTCTACAAGCAAATTTATAACGGCCCAATGATTTCCA
TCTTGTCTTTTTTGCCTACTATACTTATTTGCACGTTTACTCCGGTTTTAACTGTGATTT
ACAACAAATATTTTCGTAGAACCAATGACAAAGTGGGAAAATCATAGCAGTGTGTGAATG
CAAAGAAATCTAAAGAAGCTAAGAAGCTTTGTTATTATTTTTCTATCCAGTTACGTTCCCC
TATTAATTACACTATTTCTTTATCTGCCAATGGGGCATTGTTGACCGCAGAAATAAGAA
CTAAGGTTTTCAATGCCTTTTCAATATTGGCCCGTTTACCTACCCATGATTCAGATTTTA
TTATTGATACAAAGCGCTATGAAGATCAATTTTTCTACTTTATTGTTATCAACCAACTGA
TTCAATTTAGCATGGAAAACCTTTGTTCCAAGCCTTGTTAGCATTGCTCAGCAGAAAATTA
ATGGACCAAATCCTAAGCTTTGTCAAAGCTGAGAGTGAAATCGGTAAAGCTCAACTCAGCT
CATCAGATATGAAAATTTGGTCAAAGGTTAAGTCGTACCAAACAGACCCCTGGGGAGCAA
CATTTGATTTGGACGCCAAGCTTCAAAAAGCTTCTTCTACAATTCGGGTATCTTGTATGT
TTTCTACAATTTGGCCACTAGCTCCATTTATCTGTTTGATAGTCAATTTGATTGTTTACC
AAGTCGATTTGAGGAAAGCTGTGCTTTATAGTAAACCTGAGTATTTTCCATTTCCAATCT
ACGATAAGCCATCCTCTGTGTCTAATACCCAAAAACTGACGGTTGGTCTATGGAACCTCTG
TCTTAGTTATGTTCTCCATCTTAGGTTGTGTTATCACTGCTACTTTGACCTATATGTACC
AGAGCTGTAATATACCAGGTGTGCGCGCTCATACTTCCATCCATACGAATAAAGCTTGGT
ACCTAGCAAATCCAATAAACCACCTCGTGGATAAATATTGTACTATATGCTGTTTTTATTG
AGCATGTTAGTGTGCTATTTTCTTCTTTTCTCTAGTATTTTGAAATCTTCCCATGATG
ACGTTGCAAATGGCATTGTGCCAAAGCATGTAGTTAACGTGCAAACCCACCAAAACAAG
AAGTCTTTGAAAAAATTCCTTCCCCTGAATTTAATTGCAATAACGAAAAAGAACTAGTTC
AAAGAAAAGGGTCTGCGAATGAGAAGTTGCACCAAGAACTCGGTGAGAAACAGCCTGCCT
CTTCTGCCAATGGATATGAGGCACATGCTGCCACTCATGCCAACAATGATCCGTCTTCTT
TATCCTCAGCCTCCTCGCCTTCATTATCTTCTTCTTCTTCTAGCAGCAAAACCGGTGTAG
TCAAAGCTGTTGATAACGATACAGCCGGATCTGCTGGTAAAAGCCATTGGCCACAGAAA
GTACTGAAAAAAGAAATCTTTGGTGAAGGTGCCTACCGTTGGCTCATATGGTGTGCGG
GCGCCACTTTACCAGAAACAATTCACATCTAAAAATTACTACTTAAGGTTTGATGAGG
ACGGTAAATCCATTAGGGATGCGAAATCCAGTGCAGAATCTTCCAACGCCACCAATAACA
ACACCTTAGGCACGGAAAGTAAGCTTTTGGCAGATGGTGACGCCGTTGATGCACTAAGTA
GAAAAATTGATCAAATACCCAAAATTGCTGTTACTGGTGGCGAAAATAACGAAAATACCC
AGGCCAAAGACGATGCTGCCACTAAGACTCCACTCATTAAAGATGCAAATATTAAGCCTG
TTGTCAACGCAGCTGTTAACGATAACCAATCGAAGGTTTCAGTGGCTACTGAACAAACAA
AAAAGACTGAAGTAAGCACGAAAAATGGCCCATCAAGATCTATTTCCACGAAGGAACTA
AGGATTCTGCGAGACCATCTAATAACAATACTACTACTACTACTACTACAGATGCTACTC
AGCCCCACCATCATCATCACCACCACCGCCATCGTGATGCTGGAGTGAAGAATGTCACGA
ACAATTCTAAGACAACCGAATCCTCTTCTCTTCTCATCGGCGGCAAAGGAAAAACCAAAAC
ATAAAAAGGGGCTATTGCATAAGCTGAAAAAGAAGCTTTAA

YBR086C, 946 aa (SEQ ID NO 18)

MSQTITSLDPNCVIVFNKTSSANEKSLNVEFKRLNIHSIIEPGHDLQTSYAFIRIHQDNA
KPLFSFLQNLDFIESIIPYHDTLSDDLHKLISISKSKILEAPKQYELYNLSNLTNNPKQ
SLYFAFLQNYIKWLIPFSFFGLSIRFLSNFTYEFNSTYSLFAILWTLSTAFWLYKYEPF
WSDRLSKYSSFSTIEFLQDKQKAQKKASSVIMLKKCCFIPVALLFGAILLSFQLYCFAL
IFYKQIYNGPMISILSFLPTILICTFTPVLTVIYNKYFVEPMTKWENHSSVNAKKSKEA
KNFVIIIFLSSYVPLLITLFLYLPMGHLLTAEIRTKVFNAFSILARLPTHDSDFIIDTKRY
EDQFFYFIVINQLIQFSMENFVPSLVSIAQQKINGPNPNFVKAESEIGKAQLSSSDMKIW
SKVKSQYQDPWGATFDLDANFKKLLQFGYLVMFSTIWPLAPFICLIVNLIVYQVDLRKA
VLYSKPEYFPPIYDKPSSVSNTQKLTVGLWNSVLVMSILGCVITATLTMYQSCNIPG
VGAHTSIHTNKAWYLANPINHSWINIVLYAVFIEHVSVAIFFLFSSILKSSHDDVANGIV

PKHVNVQNPQEVFEKIPSPFNSNNEKELVQRKGSANEKLHQELGEKQPASSANGYE
AHAATHANNDPSSLSSASSPSLSSSSSSSSKTVGVKAVDNDTAGSAGKKPLATESTTEKRNS
LVKVPTVGSYGVAGATLPETIPTSKNYLRFDEDEGKSIRDAKSSAESSNATNNNTLGTES
KLLPDGDAVDALSRKIDQIPKIAVTGGENNENTQAKDDAATKTPLIKDANIKPVVNAAVN
DNQSKVSVATEQTKKTEVSTKNGPSRSISTKETKDSARPSNNNTTTTTTTTDTATQPHHHHH
HHRHRDAGVKNVTNNSKTTESSSSSSAAKEKPKHKKGLLHKLKKKL

YBR093C, 1904 bp, CDS: 501-1904 (SEQ ID NO 19)

ACGTATTTGGAAGTCATCTTATGTGCGCTGCTTTAATGTTTTCTCATGTAAGCGGACGTC
GTCTATAAACTTCAAACGAAGGTAAAGGTTTCATAGCGCTTTTTCTTTGTCTGCACAAAG
AAATATATATTAATAATTAGCACGTTTTTCGCATAGAACGCAACTGCACAATGCCAAAAAAG
TAAAAGTGATTAAAAGAGTTAATTGAATAGGCAATCTCTAAATGAATCGATACAACCTTG
GCACTCACACGTGGGACTAGCACAGACTAAATTTATGATTCTGGTCCCTGTTTTTCGAAGA
GATCGCACATGCCAAATTATCAAATTTGGTCACCTTACTTGGCAAGGCATATACCCATTTG
GGATAAGGGTAAACATCTTTGAATTGTGCGAAATGAAACGTATATAAGCGCTGATGTTTTG
CTAAGTCGAGGTTAGTATGGCTTCATCTCTCATGAGAATAAGAACAACAACAAATAGAGC
AAGCAAATTCGAGATTACCAATGTTTAAATCTGTTGTTTATTCAATTTTAGCCGCTTCTT
TGGCCAATGCAGGTACCATTCCTTAGGCAAACTAGCCGATGTCGACAAGATTGGTACCC
AAAAAGATATCTTCCCATTTTTTGGGTGGTGCCGGACCATACTACTCTTCCCTGGCGACT
ATGGTATTTCTCGTGATTGTGCTGAAGGTTGTGAAATGAAGCAACTGCAAATGGTTGGTA
GACATGGTGAAAGATACCTACTGTGCTGCTGCTAAGACTATCAAGAGTACATGGTATA
AGTTGAGCAATTACACTCGTCAATTCAACGGCTCATTTGTCATTCTTGAACGATGATTACG
AGTTTTTTCATCCGTGATGACGATGATTGGAATGGAACCACTTTTGCCAACTCGGACG
ATGTTTTGAACCCATACACTGGTGAAATGAACGCCAAGAGACATGCTCGTGACTTCTTGG
CTCAATACGGTTACATGGTCAAAACCAACAGTTTCGCCGTTTTTACCTCTAATTCTA
AGAGATGTCATGACACTGCTCAATATTTTATTGATGGTTTAGGTGACCAATTCAACATCA
CCTTGCAGACTGTGCTGAAAGCTGAATCCGCTGGTGCCAACACTTTGAGTGCTTGTAACCT
CATGTCCTGCTTGGGACTACGATGCCAATGATGACATTGTAAATGAATACGACACAACCT
ACTTGGATGACATTGCCAAGAGATTGAACAAGGAAAACAAGGGTTTGAACCTTGACCTCAA
CTGACGCTAGTACTTTATTCTCGTGGTGTGCTTTGAAGTGAACGCTAAAGGTTACAGTG
ATGTCTGTGATATTTTACCAAGGATGAATTAGTCCATTACTCCTACTACCAAGACTTGC
ACACTTATTACCATGAGGGTCCAGGTTACGACATTATCAAGTCTGTCGGTTCCAACCTTGT
TCAATGCCTCAGTCAAATTATTAAAGCAAAGTGAGATTCAAGACCAAAAGGTTTGGTTGA
GTTTTTACCCACGATACCGATATCCTAACTTTTTTGACCACCGCTGGTATAATTGACGACA
AAAACAACCTTAACCTGCCGAATACGTTCCATTTCATGGGCAACACTTTCCACAGATCCTGGT
ACGTTCCCTCAAGGTGCTCGTGTCTACACCGAAAAATTCGAATGTTCTAACGACACCTACG
TCAGATACGTCATTAAACGATGCTGTTGTTCCAATTGAAACCTGTTCCACTGGTCCAGGGT
TCTCTTGTGAAATCAATGACTTCTACGACTATGCTGAAAAGAGAGTAGCCGGTACTGACT
TCCTAAAGGTCTGTAACGTCAGCAGCGTCAGTAACCTCTACTGAATTGACCTTCTACTGGG
ACTGGAACACTACTCATTACAACGCCAGTCTATTGAGACAATAG

YBR093C, 467 aa (SEQ ID NO 20)

MFKSVVYSILAASLANAGTIPLGKLADVQKIGTQKDIFPFLGGAGPYYSFPGDYGISRDL
PEGCEMKQLQMVGRHGERYPVSLAKTIKSTWYKLSNYTRQFNGSLSLNDDYEFFIRDD
DDLEMETTFANSDDVLNPHYTGEMNAKRHARDFLAQGYMVENQTSFAVFTSNSKRCHDTA
QYFIDGLGDQFNITLQTVSEAESAGANTLSACNSCPAWDYDANDDIVNEYDTTYLDDIAK
RLNKENKGLNLTSTDASTLFSWCAFEVNAKGYSVDCDIFTKDELVHYSYYQDLHTYYHEG
PGYDIKSVGSNLFNASVKLLKQSEIQDQKVWLSFTHDITDILNFLTLAGIIDDKNLTAE
YVPFMGNTFHRWYVPQGARVYTEKFQCSNDTYVRYVINDAVVPIETCSTGPGFSCEIND
FYDYAEKRVAGTDFLKVCNVSSVSNSTELTFYWDWNTTHYNASLLRQ

YBR181C, 1563 bp, exon1: 501-506, intron1: 507-858, exon2:
859-1563 (SEQ ID NO 21)

TAACCTCTCAACATAATTATGTAAAAAATTATCTCATTAAGCCAGATAGCAAATATATCA
CATATTGCATTGATTAATTTGAGAAAAATATACATGTATCTTTTCAGTTAATTTTATTAA
AAATAAATTATTTCTTACTTTTTTTTTCTACAGTTTGCACCATTAACCTCTTTCTTGCA
TCCATACATCTTTGAACTCCATACATCTTATTTTTTTTGTGCTGTTTTTTTTTCAGTGTCTCGG
GCATACAGGCCGCTTATCTTCATGCGCGCCCATCATCCTAGGAACTCTTTCCGGTATGGG
CCAAGGGCAGGCGAAAATCCTATGTGCGTGGAGCTGATACAATCTCGGCTGGCTTGGTTT
GTAGGGCACGGTCAATGAATGCCTGATGGGAGAAAAATTCATCTTTATGAAAAGTGATCT

TAATTTGAATAGTGTGCCCTTCAAAACATTTGGAAGTCATTAATTGAAACTATCCAGTGT
GAATAGACGACTGAGCCATCATGAAGGTATGTAATATCACCCAAATCCTTAGAATTCTAA
TGAATCAGCACGCGCTAACCGGCTGTTTCTGACTGTTTGATAAACGTATACCCACAAATT
AGTGCACTATAATAAAAATTCTCAAGAACACGTTGTTTAAACGAGATAATTCCTCTAA
TATACACGTACCGACACTTAGGAAAATATCTCGCTAAGTTCAAATTAAGGAATGAAAAAG
GAATTTACGAAAAGGGTTTAGAAATATCAATGAAAATAAGAAAAACCTGTAACGGAAGAA
AGGACAGCAGGGATTTCGTTGGAATTTGTCGATATTGGCTTCGGACAACCTTACTAACAAA
TGGTATTATTTATAACAGTTGAACATTTCTTACCCAGTCAACGGGTCTCAAAGACCTTC
GAAATTGATGATGAACACCGTATTTCGTGTTTTCTTCGACAAGAGAATCGGTCAAGAAGTC
GATGGTGAAGCCGTTGGTGATGAATTCAAGGGCTACGTCTTCAAGATCTCTGGTGGTAAC
GACAAACAAGGTTTCCCAATGAAGCAAGGTGTTTTGTTGCCAACTAGAATCAAGTTGTTG
TTGACCAAGAACGTTTCTTGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCC
GTCAGAGGTGCCATTGTTGGTCCAGATTTGGCTGTCTTGGCTTTGGTCATTGTCAAGAAG
GGTGAACAAGAATTGGAAGGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAG
AGAGCTAACAACATCAGAAAGTTCTTCGGTTTGTCCAAGGAAGATGACGTTCGTGATTTTC
GTCATCAGAAGAGAAGTCACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAA
AGATTGGTTACTCCTCAAAGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTCAGA
AACGCTCAAGCTCAAAGAGAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTG
TCTGAAAGAAAGGCTGAAAAGGCCGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCT
TAA

YBR181C, 236 aa (SEQ ID NO 22)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEV DGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAIVGPD LAVLALVIVKKGEQE
LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQRKRHQ RALKVRNAQAQREAAEYAQLLAKRLSERKA EKA EIRKRRASSLKA

YCL007C, 893 bp, CDS: 501-893 (SEQ ID NO 23)

ATTACTTTAAATTGTTTGTCTATTCCAACATAATCATTAGCAGCACATGTCGAGCAACAG
ATAAACACAGCAGCGGCACGGTGAACCACATAAGTGTATGTGCACACGCGTGTTTGTGC
AGTGTATTACCAACTTGCGCATGCAAGGATATCACACTCCTGTTTCTGCCTCATGTCTTT
TAAAACGCTTCCACGGGACATGGGTTCTAATTATGGAGAAGATCAAGCTTTGAAATGGCC
CGTTTACACATTTTGATACAACCGTAGACGGCGTCTCGTTTCAAAGACCGTGTGGTTGTC
TATCAGTATATACTCATTTGTGTTTTTCAAAAATCTCTGGGTTGTTTAGATGCCACTATA
TTTCTATTCTGATTTATTTTATGTATACTTATTTTGCTTATTTTCTTATACTCAGGAA
ACGTCACTTGGCTTGATATACTCGACGCTTTATTCTGCAAATTCAGGTCTCAAATCTGAA
CGGCGTGGAGCCACCAAGGGATGGAGCTGGCAAAGGAACGTAATGGCCACATCAAAAAC
ATCATGGCCAATGTCAAATCACTGTACTTCTCAAACACTGTACGACAAAACAAAACAA
ACAAACTCTTGTTAGTAAAAAAGAAAGGGAAACTAGTAATATGGAGACACATCGTAAAAA
AAATGTTGCACATACGCTTGGTTGTTCTTTGGAGCCATTATCCAGAACAGCACGGACATG
GACTAACCACATATGAATACACCAACAACAGTATAGCTAAATTGGACGCGCAGAGAGTTA
GTAGAAGAAGAAGGAAGAAAAGGGAAGCGGAGAGAAGAGATTATGACACATACAAACTAC
TCATTACTCTTTGTTCTTTATTATTCGTTGGACCTTTGTTTCTTAAAGTATAG

YCL007C, 130 aa (SEQ ID NO 24)

MELAKERNGPHQKHGQCQNHCTSPNTVRQNKTNKLLLVKKKGKLV IWRHIVKKMLHIRL
VVLWSHYPEQHGHGTNHYEYTNNSIAKLDAQRVSRRRRKREAE RRDYDTYKLLITLCSL
LFVGPLFLKV

YCL016C, 1430 bp, CDS: 501-1430 (SEQ ID NO 25)

ACATGACCTAATTTATAGCTTAGGGTTCTTTTTTGTCAATTCTATGCGTATGACAAAGA
GCACCACGATGGTGATCGAAATCTCTAGGAGTAGCATACCACAGCGATATTATTTAGTAG
TAGGCGGTTTATTATCTTTGTCCCTTTATACTGTTGTGTTTCTTGCTTATTGCTTCAGTA
GGCAGCGTATAGTATAACCAGAAAAAAGTGAAAAATAAACTAAAAAAGCACTATGAGATG
AACGGTAAAAATCCACCAGAGATTGCTCACTAATAATCCTGTACCATGTCCATCAACCT
ACATTCGCGACCCGAGTATGATCCATCTTATAAGCTGATCCAGTTGACACCAGAGTTACT
GGATATAATACAGGATCCGGTTCAAATCACCAGTTAAGGTTTAAGTCATTGGACAAAGA
CAAGTCTGAAGTTGTACTGTGTTTCGCACGACAAGACTTGGGTGCTGCAAGCAGCGCAAAC
ATTCAAACACAGTTCTACTAATGAGAGAATTTGTTCTGTAACAACCTATTACTTTTCGACG
AAACGCTCTTGTTTGGACTGTCCAAGCCGTACATGGACGTCGTGGGATTCGCCAAGACTG

AATCAGAATTTGAGACCAGAGAGACACATGGCGAATTGAACTTGAATTCAGTACCAATAT
ACAACGGAGAAGTGGATTTCTCCGACAAAATCATGAAGAGGTCATCTACAAAGGTTATCG
GGACCCTGGAAGAAGTACTTGTGAGAACTCACCATGTTCTGCGCTAGAAGGTATATCAAAT
GGCATAAGATTGGTGGATCTGTGAAAGACGGTGTGTTGTGTATTCTTTCACAAGACTTCC
TTTTCAAAGCACTGCATGTACTACTGATGAGCGCAATGGCAGAATCACTCGATCTACAGC
ATCTGAATGTTGAGGATACACATCACGCTGTGGGGAAGGACATTGAGGACGAGTTCATC
CATACACAAGAGAAATCATTTGAAACAGTGCTGAATAAATTTGCTGTTCAAGAGCAAGAGG
CTGAAAACAATACGTGGCGCTTGAGAATACCGTTTATAGCTCAGTGGTACGGGATTCAAG
CGCTAAGGAAATATGTTTCTGGAATAAGCATGCCAATTGATGAGTTCCTCATCAAGTGGA
AGTCCCTTTTCCACCTTTCTTCCCATGTGACATTGACATTGACATGCTGCGAGGCTATC
ATTTCAAGCCTACCGATAAGACTGTCCAGTATATAGCGAAAAGCACACTACCAATGGACC
CCAAAGAACGGTTTAAAGTCCTGTTTAGGCTACAGTCACAGTGGGACTTGGAGGATATCA
AGCCTCTAATTGAAGAACTAAATTCAAGAGGTATGAAAATAGACAGTTTCATCATGAAGT
ATGCCCGCCGTAAAAGACTGGGCAAAAAGACCGTGGTTCACGAGCAGGTAG

YCL016C, 309 aa (SEQ ID NO 26)

MREFVPEQPITFDETLFLGLSKPYMDVVGFAKTESEFETRETHGELNLSVPIYNGELDF
SDKIMKRSSTKVIGTLEELLENTPCSALEGISKWHKIGGSVKDGVLCILSQDFLFKALHV
LLMSAMAESLDLQHLNVEDTHHAVGKDIEDEFNPYTREIIETVLNKFVQEQEAENNTWR
LRIPFIAQWYGIQALRKVSGISMPIDEFLIKWKSFPFPFPCDIDIDMLRGYHFKPTDK
TVQYIAKSTLPMDPKERFKVLFRLQSQWLEDIKPLIEELNSRGMKIDSFIMKYARRKRL
GKKTVVTSR

YCR052W, 1952 bp, CDS: 501-1952 (SEQ ID NO 27)

GTCATCGACAGCAAATTGCTGGAAGAGTTCAAGGACAACGTGAGATACACCTTGGAAT
GACCCTGAGGAAGGAGCCGATGAGGCCACTCTGCAACGCAGGAGGCAGTTGGAACAGATC
ATTACGGGAGACAACGCTGAGGAGGAGTTGGAAGGTACATCCGTGCTATGGTCAGAGAG
CAGATGCTGGGCCAGGGCTCCATGGCGGGTTCGGGGACGAACCAGATTCCAAGAGAAGA
AAATAACGACCCAGCACAAAGGCTCTTACAGCTTGCTAAAAGAAATTGAACGCGACGCTA
CATGAACACTTCTTTCTTCTTACATAGTCTTTTCCCTTATGTATCTTTTCTGTACATTAA
TAGACGTTCTTACAAGGTAAATTTTACC CGCTTTTAAATAGAATGAAAAAACGTTGT
AGAGTGAAAGAAAAGCAACAAATATACAGTTCACAAGGCAGCTTCGTATAGTAATACAGC
ACGAAAAACAGCTCATAGAAATGGTAACACAGACCAATCCGGTCCCTGTTACATATCCAA
CGGATGCTTATATCCCCACGTATCTGCCCCGATGATAAGGTCTCCAATCTGGCAGATTGA
AAAAATTGATAGAAATGGATTCCAGACTAGATTTGTATCTGACAAGAAGGAGGCTGGATA
CGTCCATCAATTTACCTACAAACACCAAGACCAAGGACCATCCCCCAATAAAGAGATGC
TGAGGATTTACGTCTACAACACTACGGAAAGCAGCCCTCGCAGCGATTCTGGCACCCAG
CGGACTCAGGCAAGACTACATGGACACTGAGAATAGAAGGTAAGCTTCTGCACGAGTCCG
CAAACGGAAAGCACCCATTTAGTGAGTTTTTGGAAAGGTGTCGCGGTGACTTTAAAAGAC
TGAAACCGCTGGGCATGGGCAAGAAGAGGAAACGCGATTTCGTCATTGAGCCTTCTTTGA
ATCTGCAACAACCCGAATACAATGATCAAGATAGCACCATGGGCGATAACGACAACGGCG
AGGATGAGGACAGTGCAGAGGCAGAATCCAGGGAGGAAATTGTAGACGCACTGGAATGGA
ACTACGATGAAAACAACGTTGTGGAGTTTGATGGTATCGACATCAAGAGGCAAGGCAAGG
ATAATTTGCGATGCAGTATAACCATCCAGTTGAGGGGTGTCGACGGTGGAAAAGTACAGT
ACTCGCCCAACTTAGCTACCTTGATAGGTATGCAAACGGGCTCCGTTAATGACGCGGTTT
ATTCGATCTACAAGTACATTTTGATCAACAATCTGTTTGTACGGAACAAACAGAGGCTC
AAGATGGTTCCAACGATGCCGAAGACAGCAGTAACGAGAATAACAATAAAAACGGTGCTG
GTGACGATGATGGCGTCGAGGGAAGTACTCCAAAGGATAAGCCCGAATTGGGTGAAGTGA
AGCTAGATTCACTCTTACAAAAGGTATTGGATACAAACGCCGCGCACCTCCCCTTGATGA
ATGTTGTGCAAACCGTGAACAACTGGTATCACCCCTACCGCCCATCATCCTAGATTATA
CAATTGATCTTTCCAAGATACCACCTATGGTGCTACCACCTTGATGTAGATGTGTCGC
ACATTCTCCACCAGCCTCAACCCAGCCAAATTTACAAAAGAGGAAGAAACAGATGCTG
AAGACACAGCAAACTACGTGAAATCACAAAGCTTGCTTGCAGTTGAACTCTAGTGCTC
AAAAATACCAGTTTTTCCACGAAGTGTCTTTCATCCAAGAGAAACGCTGACTCACTACT
TATGGTCTTCCAAGCAAAACGAGCTTGCTGCTGCAGGGCGACCAATACTTCAATGAAGATG
CTGCAAGAACGAGTGACATATACAGTAACAACAACATGACAGGTCACTAATGGGCAATA
TCTCACTACTGTACTCCCAAGGAAGACTATAA

YCR052W, 483 aa (SEQ ID NO 28)

MVTQTNPVPVPTYPTDAYIPTYLPDDKVSNLADLKKLIEMDSRLDLYLTRRRLDTSINLPT

NTKTKDHPPNKEMLRIYVYNTTESSPRSDSGTPADSGKTTWTLRIEGKLLHESANGKHPF
SEFLEGVAVDFKRLKPLGMGKKRKRDSLSLPLNLQQPEYNDQDSTMGDNDNGEDEDSEAE
AESREEIVDALEWNYDENNVVEFDGIDIKRQKGNLRCSITIQLRGVDGGKVQYSPNLAT
LIGMQTGSVNDAVYSIYKYILINNLFVTEQTEAQDGSNDAEDSSNENNNKNGAGDDDGVE
GSTPKDKPELGEVKLDSLLQKVLDTNAAHLPLMNVVQTVNKLVSPLPPIILDYITIDLSKD
TTYGATTLDVDVSHILHQPPQPNLQKEEETDAEDTAKLREITKLALQLNSSAQKYQFFH
ELSLHPRETLTHYLWSSKQNELVLQGDQYFNEDAARTSDIYSNNNNDRSLMGNISLLYSQ
GRL

YCR064C, 911 bp, CDS: 501-911 (SEQ ID NO 29)

AGGTTTTAACGCGTTATCTTTGTTCCGAAAAAACGGAATAATATTTTTTC
GCGTCGCGTTCTCGCGTCTGTTTTGTTTTTCGCGTTCCAATGACCAAATGGGAAAGTG
GTCGTCTTTGACGAAGGAGACGAAAACCTCTTCTAAAACGTTGGGAGAGAGATAATTACA
TGGCCAGAACAATACTGCAACGTGCATATAGTCGTTAGTCTGTGCTTGCACATCCACGGC
AGCCGCAGTGGACGCACTGATGGAAGGACACCTGTGTGCCCTTTTTGCGTGCTTCTTCCT
CTAACTGTGCACGAGGCACCCTGCAGATGCAAGTGCTACCGTTGTTAGTTTCGTTCTTTT
GAATGCAGCGCAGACAGCACAGTTTTTCATACCCGGTTTTGCGCCATTTGGCAATTAGCA
ATTTATCAGCATACTTTTCCTTTATCAACCAATCGTAAAGGTCTTTGGAGATGGCCTTTC
TCTTGTAAGTACAGAGTATATATGTATCTAGAGCGCTGGTGGTGGAGTTGCATTATCTCCC
AGAGCTGCTCATTTGGACTTTGCTGCGAGCTTAGACGACTTGTCTTTTGGGCATCTCTGA
GTTGGATTTTCGAAATCTGTGAGGGTTGGCTTGATTTTTTCGAACCCGTCAGGTGCAGGCT
TGGATCTTCTGGTCTTTATGCGCGGCATGTCGTTTTGTGAGGTGAGCTTTGCTAGTCTTG
ACGGCTGTAGAGGTGTTTACATTGATGATGAGTCCCTAAGAAAATTTTTCTTTTTTTTTC
AGTATTTCACTTTCCGTTGTGAACGACAAATGTACTATGCGTTCAAGAGCCAACGCAGTA
TCATCGTCAAAGTTCTTACCACAACGCGTGTGATTGATCTTGTACTGGTTGTAATGTGC
TAAGTCTGTGA

YCR064C, 136 aa (SEQ ID NO 30)

MYLERWWSCIISQSCSLDFAASLDDLSEFWASLSWISKSVRVGLIFSNPSGAGLDLLVFM
RGMSFCEVSFASLDGCRGVYIDDESLRKFFFFFQYFTFR CERQMYAFKSQRSIIIVKVPT
TTRVIDLVVNVLSL

YCR073W-A, 1448 bp, CDS: 501-1448 (SEQ ID NO 31)

GTTTATGGCTGGAATGACTTGATAATCTCTTCACGAGCTTACTTGAGATGGTATGAGGAG
CCAGAACTCTCCCGCCTTCAGCCGCTTTTTGTTGCTGTGTATTAGTATATCCATCATCA
TTTTACCTACAAGGAACCTTTTATAGCCACCCTAAGTAAAACAACATTAGCTTAGC
ATCCTCAATTCTTATCGTATGTTGTTGCTGCTATTTTTATCCTATTGTTCTTGGCATCGC
TTTTTTACATAAGGTACCAAGGCAAGAGAAAAGACCCGCGAAATTTTCAATTCGAGACAT
AGGGTTAATACGAAATATGTTAAGGTCTAGTTTCCAAAAAATGAAGAAAATGTGATTAGA
CATCCTGGGGAAATTAGGTTTAAATAGGGCGGGCGCTACAGGGGTTTTCTTAACAAATTT
CAATGATAATAGTGGCATCATCATCGTCATATCCAGTGTAGGTATGGACTAGAACAGAAA
GCAATTTGCAGCAAGACAATATGACTACGACGGTACCCAAGATATTCGCGTTTCACGAGT
TTTCAGACGTGGCAGAGGCCGTAGCTGACCATGTAGTCCACGCGCAAGACGGTGCATTGG
CTCCAAAGAACGAGAGGAAACACTCTGTTCCCAACATCAGCATGAATGCACTGGATATGA
CGAGAGAGGCCTCTTGCAAAAGCACAGCATCTGCCGCGGAAGGGAAAAGTGGTAGCAGTG
GTAGTGGCAGTGGTAGCAGTAAGCCCAAAAAGGAGAAACGGTTCAAGATTGCTCTCTCCG
GTGGGTCAATTGATCGAAGTGCTACACGAAGGTCTGCTAAAACGAGACGATGTACGGTGGG
GAGACTGGGACATTTACTTTGCAGACGAGAGACTTGTACCCTTCAGCTCGAATGAAAGCA
ATTATGGATGCGCCAAAAGGAAGATTTTGGACCTGATAGACACGGCGAAGTATGGAACTC
CGAAGGTGTACCACATTTGACGAGTCATTGATTGACGACCCGCAAGAATGCGTTGATAACT
ATGAAAAGGTGCTAATCCGCGGGTTTGCCGGTAGAGATTCCGTCAAACCTCCGATGTTCCG
ACTTGTTCTTCTGCTTGGTTGTGCCCCGATGGTCATATCGCATCACTCTTCCCTAACTTCC
AGGACAATCTACGTGAGAACTTGCAATGGGTGGTGGCCGTGGAGAACGCTCCTAGTGGGC
CCTCGACCAGAATTTTCGCTGACTATACCTGTAATCTGCCATTCTCACAGGGTTACTTTTCG
TTGTGCAAGGTGCAACCAAGGCGCCCATCATCAAGACCATTATGGAAAGGCCTGAAAAGG
GCCTACCTAGCAGTATTGTCAACGAAGGTGCTGCTGGTCTGTATCATGGTTTGTGACG
ACGATGCTCTTACGGACGTCCTCGTCACCAAAAAAAGTATAAATTCCACCAAGGTTTGT
CTATTTAA

YCR073W-A, 315 aa (SEQ ID NO 32)

MTTTPVKIFAFHEFSDVAEAVADHVVHAQD GALAPKNERKHSVPNISMNALDMTREASCK
STASAAEGKSGSSGSGSGSSKPKKEKRFKIALSGGSLIEVLHEGLLKRDDVRWGDWDIYF
ADERLVPFSSNESNYGCAKRKILD LIDTAKYGT PKVYHIDESLIDDPQECVDNYEKLIR
GFAGRDSVKLPMFDLFL LGCAPDGHIALFPNFQDNLREKLAWVVPVENAPSGPSTRISL
TIPVICHSHRVTFVVEGATKAPIIKTIMERPEKGLPSSI VNEGAAGRVSWFVDDDALTDV
LVTKKKYKFHQGLSI

YDL010W, 1196 bp, CDS: 501-1196 (SEQ ID NO 33)

TAGTAATTAGTTTCTTATGATGGATTTAATGGCGTAGTTCATCCGCGTTTAATTTAACTA
GAGGATAATCTACTTGCAGCATGAATGAAAATAGTAAGCCAGTAAGGATGCACTGACAGA
CTCAGCTACCGATTAGTGTGTTGACTTTTCCGCAAGATCCTTTTCTCCCTCTTTGGACC
TAGTCATCCCTCCACACAAGATTCGCTCTTAAGTAGTGGCGCAGGCTGTTTCGCTTTTAAG
CATAGTGCTTAATGTCGAAGGCTTTATAGATCCCAAATACTACGCCTTGAGAAATTGAAT
GCACTAGCAGTTAGTTAACTTTCTGGAACGCGCATGACGCGTCCCGGGGCGCCTGAGGCG
GAGCGTTCGCGAAATCGGGAAAACATTATACTGGGAAAGATCACTATCTATTCTCTAAAT
GAACTTTTAAGCAAATTATCGTAAGATAGAAAAGACGAAACCTTAGCAACCTAGCGGTTT
AATATAGAAACAATTTTATTATGATACCTTCCAATAAGAGAAATGCTAGAATTTTAAGCA
TTACAACGCTATTATTGTTGTTAGTGTTTTTCGTAGCGCAAAATGCGAACTTCTTGACGG
TAGAGATAAAAGAGGAACTTCTAAAGCATTTAGTACTAATATGGACAATATGGCTGGAG
GATCTTCCAGGGAATATGCTGCTATGCCGACTTCTACCACGAATAAGGGGAGCTCTGAAG
TAGACGAAGAAATTAATGAAATAAAACAGAAGGTGGGACTCCAACAGCCCATAGCATCGG
TTGATGATAGTTTGTGCGCCATTAAAAACGATAAAGGGTTCGCGAATAACCAAAGCTTTTA
ATGTTCAAAAAGAATACTCCCTCATACTAGACTTGTCTCCGATTATAATATTTAGTAAA
GCACCTGTTTATATAGCAAGGGCATGAAGGAAGTCTTGAAAATGAGTATCAGTTTATCC
CAAATACTATATTATAGAACTTGACAAACATGGACATGGGGAAGAGCTGCAAGAAATA
TCAAGTTGGTGACCGGTAGAGGAAGTGTCCAAACCTTTTGGTTAATGGAGTATCAAGAG
GAGGTAATGAAGAAATCAAGAACTGCACACTCAAGGGAACTTTTAGAATCATTACAAG
TCTGGAGTGATGGTAAATTCTCGGTTGAGCAACGTGAAAAACCTTCCAATAATTGA

YDL010W, 231 aa (SEQ ID NO 34)

MIPSNKRNARILSITLLLLL VFFVAQNANFLTVEIKEETSKAFSTNMDNMAGGSSREYA
AMPTSTTNKGSSEVDEEINEIKQKVGLQQPIASVDDSLSAIKNDKGSRITKAFNVQKEYS
LILDLSPIIIFSKSTCSYSKGMKELLENEYQFIPNYIIELDKHGHGEELQEYIKLVTGR
GTVPNLLVNGVSRGGNEEIKKLHTQGKLLSLQVWSDGKFSVEQREKPSNN

YDL036C, 1889 bp, CDS: 501-1889 (SEQ ID NO 35)

TCAAATCCAGCTTCTTTTCAAGCAATATTGTCACAAACGATGATGAGAATAGCATTGAAG
AGGATAAGAATTTACGCTATTTCAGATGCTAGTGCATCTGAAAATTATCTGGTCAAGCCCA
CAATACCAGGTACGACTCCTGATCCAATAATTGAGGCGCAGAACGATAATGATAGTAGTG
ATAGTAGCGGCATAGATTTGATAGCCTTCTTAAGAAATGGACCATTATAAAGTTTTTGTA
TCGCGATGTTTGAAAATGGAAAGTAAGGAACGTAATACAAATTGACAAGTAGCCGACATG
AATGACGCTCACTTCTCTTATATATGTTAGGTAGTATATGCATTATAGAATTTATTCATT
GAAGCAATGTGATTCCTCGATAAGTAAGCTTTTTTTCTGTCTGGCGGCGAACCATTAGAG
AACAAAAGACCGAGTTAAGAAAAAGTTCATAAAAACTTTTGAAAATGGATGAGTGCTCG
TATAATGGAATAGGAACTTATGCAAAGAAATAATAGGTAAAGAAATTTGTTTACAGTGC
CAGTAATAATGGCTCGACAACTCAAAGGAATGCATTATCTGCAGGTCTTGCTTTTGCAG
GTAATGCAACCTCAAATGAGTTTGATGAACATTTGCAAAATGAGGTTGAAAGAGAGAGGG
AAATTCAAAAGAAAAAAAATAAAGCGAACTCAATCAAAAAAATCGCCAGATTTGATTA
ATAAATCTACTTTTCAATCACGAACGATAGGCAGCAAAAAGAGAAACATAGACAACTAG
ATCCAGAGTATGAAATTGTCATCGATGGCCCTCTAAGGAAAATCAAGCCCTACCATTTTA
CGTACAGGACCTTTTGCAAAGAGCGTTGGAGAGATAAAAAATGGTTGATGTCTTTATAT
CTGAATTTGAGATCGTGAATCTGAATATTATAAAGAACAATCGAAAACGGGGACGTTT
ATATAAACGATGAACTGCGGACTTATCTACTGTAATTCGCAATGGTGACCTGATTACGC
ATCAGGTACATAGACATGAACCTCCAGTCACTTCCAGGCCTATCAAAGTTATTTTGAAG
ATGATAACATAATGGTTATTGATAAACCGAGCGGTATACCTGTTTACCCAACTGGCCGAT
ATCGGTTCAATACAATTACGAAAATGCTTCAAAATAATCTCGGATTTGTTGTGAACCCAT
GTAATAGGTTAGATAGGCTTACAAGTGGATTAATGTTTTTGGCAAAAACCTCCGAAGGGAG
CCGATAATATCGGCGATCAACTAAAAGCTCGAGAAGTCACTAAGGAATACGTGGCCAAGG
TAGTTGGAGAATTTCCAGAAACGGAAGTAATTGTTGAAAAACCTCTAAAACCTGATCGAGC
CAAGGCTTGCTCTTAATGCAGTTTGTCAAATGGACGAGAAAGGAGCCAAACATGCAAAAA

CTGTTTTTAACAGAATCAGCTACGACGGTAAACGAGTATTGTAAAGTGCAAACCGCTTA
CCGGGCGATCACATCAAATTAGAGTACATTTACAGTACTTAGGCCACCCAATTGCTAACG
ATCCTATTTATTCCAATGATGAAGTATGGGGTAACAATCTCGGAAAAGGCGGCCAGGCTG
ACTTCGATATAGTTATTACTAAGCTAGACGAAATAGGGAAAAGAAAACCTGCTAAAAGTT
GGTTCCATAGTAATGGCGGGTACGGTGAGGTATTAAGGCAAGAAAAATGTTCTATTTGTG
AATCTGATTTGTATACTGATCCTGGCCCCAATGATCTTGATCTGTGGTTACATGCCTATC
TATACGAATCAACTGAGACTGAAGAAGGAACCGAAAAGAAAAAGTGGTGCTACAAAACAG
AGTATCCAGAATGGGCTCTGAGAAGATAG

YDL036C, 462 aa (SEQ ID NO 36)

MQRNNRLRNLFVTPVIMARQLKRNALSAGLAFAGNATSNEFDEHLQNEVEREREIQKKKK
IKRTQSKKSPDLINKSTFQSRITIGSKKEKHRQLDPEYEIVIDGPLRKIKPYHFTYRTFCK
ERWRDKKLVDVFISEFRDRESEYKRTIENGDVHINDETADLSTVIRNGDLITHQVHRHE
PPVTSRPIKVIFEDDNIMVIDKPSGIPVHPTGRYRNTITKMLQNNLGFVVPNCNRLDRL
TSGLMFLAKTPKGADNIGDQLKAREVTKEYVAKVVGEFPETEVIVEKPLKLIIEPRLALNA
VCQMDEKGAKHAKTVFNRI SYDGKTSIVKCKPLTGRSHQIRVHLQYLGHPIANDPIYSND
EVWGNLKGKGQADFDIVITKLDEIGKRKPAKSWFHSNGGYGEVLRQEKCSICESDLYTD
PGPNLDLWLHAYLYESTETEEGTEKKKWYKTEYPEWALRR

YDL083C, 1364 bp, exon1: 501-909, intron1: 910-1341, exon2:
1342-1364 (SEQ ID NO 37)

TATTCCGACTAGAAAAAATTAAATTTTCTAACTACAAAAAATTGCCTGCATATATGTAA
GGATGTAAACAGGAAATGTATGGGTCACATATTAATAGCTTGTTTTACTCCATAAAAGAGT
CTGATATTCAGAAAAAACACCCATACATGTTGAAAAATAATGCATTGTGAAAAAAGTGG
TTGAAAAATGTATGCGATCTAGGAAAAACTGAATTTTCCTTAGGTTGTGCTCCTCCTCT
AGAAGGATGCTGTGGCCTTTGACCTGGGCGGAAATCTCTCTGTTTCCCTCTAGCTGAGG
GAAACAGAACTGGTAGCAGTTCGTTCCGGCCAGGCCGCGTGAGCCTATACCACCGAATAT
TATCCTAGCGCAGAGAGTAACACTGGCAAAGTCAAAAGTAAATGCCATGTAAATGTATA
GGTTACGCAGTAGACTATTTAATATATACCTTTTTTATTTAGCAGTGTTCGAAAAATACA
GCAAGAGAATAAGCAACAAGATGTCTGCCGTCCCAAGTGTCCAAGTATGTTAAATAATTT
AAACGATGTCACGAATTTGTGAGGGATATTGAAACCATGCAGTGAGATAATTTCAATTTA
AGAACCATATCACCTGAATAAGACGGGTGGGGCAAGCACTAGATGCGAATCATAGTTTTA
GAACAACGGATCACCATTTACACCGTTAAAGACCGAGTAGAAATAACCAATAAATTGTGT
GGGAAATATTATACTTAATTTCTCTGTGGAGTAAAGTAATGAGCGTCTTTTGCGGTCTT
ATTTATTCATTCGCTCCCCCTTGCAATGAATTTTGAACAGAATGCTCCAAAGAGGAAGTGC
CAGGGTACCTCACTTGTTCACCTTTTACACAGTTCATAATATTTTGGGATTTTGAA
TTTCTGTTTTACTAACATGTGACACGAAATGTTTTTCATTTTTGGTTTTATAACAGACTT
TTGGTAAGAAGAAATCAGCTACCGCTGTTGCCACGTCAGGCGGTAAGGGTTTGATTA
AGGTCAACGGTTCTCCAATCACTTTGGTTGAACCAGAAATCCTAAGATTCAAGGTCTACG
AACCATTATTGTTGGTTGGTTTGGACAAGTTCTCCAACATCGATATCAGAGTTAGAGTCA
CTGGTGGTGGTCATGTTTCTCAAGTCTACGCCATCAGACAAGCTATTGCTAAGGGTTTAG
TCGCTTACCACCAAAGTACGTTGACGAACAATCCAAGAACGAATTGAAGAAGGCCTTCA
CCTCTTACGACAGAACTTTGTTGATCGCTGATTCTAGAAGACCAGAACCAAAGAAATTCG
GTGGTAAGGGTGCTCGTTCTAGATTCCAAAAATCTTACCGTTAA

YDL083C, 143 aa (SEQ ID NO 38)

MSAVPSVQTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKKFGGKGARSRFQKSYR

YDL125C, 1088 bp, exon1: 501-597, intron1: 598-708, exon2:
709-1088 (SEQ ID NO 39)

TTCAAAATACGAGTAAAGGAGATCCTAGGTGTGGATTAGTAAGGGGAGTGTGGCAACTTC
CTTTTTCCGGTTAATTCTCCGCGCTTTTCGTTAGACTATTTTGCAAGGACCCAAATAGGAG
ACGCATGGAGGCTTCTACAAAACAGCGTGCCGTTTTGATGGCATGAGCAGGGGGCGCAA
GGAAACACCGGTAAATCGCGCAAGACCTTGTTGGCCACGTAGCCTCAAAGGTTGAATTGA
CACTTGTCTACAGAACTTGAAAAGTACAAAAGGAGGTCACATAAAACAGTAAGCTTGAGA
AGCTTTAAGATATGGTGCGAATCGTTACAGAATATTCCTTGCAGAAATAATGGCGGGTCC
GTTCTCTTCTGAAGAAGTTACCGCCCTACTGAAGCATTGCTGTACGATCGTGTAAATGTGA
TGTGTGTTCTGACTGGAAAGCGGAGAACATTATGAAGTAAAGGACAATCAGCACGCCTTC

CAGACTTTTAAGAAACATTGATGGAGCCATTGATATCGGCACCGTACCTAACAACAACAA
AAATGTCTGCTCCTGCTACGCTTGATGCTGCCTGTATTTTTTGCAAGATTATTAAAAGTA
TGTCACATTACTAATAAAGAGCTTACACTCACACCAATGATGGCGATAGTCTCTATGTAG
TACATATACATAAAGCAGAATACTAACAATCGATCCGCTATGCAACAGGCGAAATTCCAT
CCTTCAAATTGATTGAAACAAAGTACTCGTATGCTTTCTTGGACATCCAACCTACTGCTG
AAGGTCATGCTTTAATCATTCCTAAGTACCATGGTGCGAAGTTGCATGACATCCCGGACG
AATTCCTTACCGATGCTATGCCGATTGCCAAGAGACTGGCCAAGGCAATGAAGTTGGACA
CTTATAATGTGTTGCAGAATAATGGTAAAATTGCGCATCAAGAAGTCGACCACGTCCACT
TCCATTTGATTCCCTAAGAGAGATGAGAAAAGTGGTTTGATTGTAGGGTGGCCAGCCCAAG
AAACGGACTTCGATAAGTTGGGCAAGCTACACAAGGAATTGCTTGCCAACTAGAAAGGCT
CCGATTAG

YDL125C, 158 aa (SEQ ID NO 40)

MEPLISAPYLTTTKMSAPATLDAACIFCKIIKSEIPSFKLIETKYSYAFLDIQPTAEGHA
LIIPKYHGAKLHDIPDEFLLDAMPIAKRLAKAMKLDTYNVLQNNNGKIAHQEVDHVFHLLI
PKRDEKSLIVGWPAQETDFDKLGKLHKELLAKLEGSD

YDL133C-A, 578 bp, CDS: 501-578 (SEQ ID NO 41)

AAAGGTGGTTGGAGACTTTGTGTTGTAGCTTAGAATTTCTTCCACTATATGAAAGCCAAG
ACCTCTTCTCCTCTTTTCGACACTTCGTTTATTTCCACTTTCCCTTATTTAGTATTCATCG
TTCAGAATGCTTTCTTTATTTTACGACGGTTACCACACCCGTACACCCTTATCTCATTTTC
ACCAGTACCTTTCCCTTATTAGATTCATCTTATTTTATTTTAGGATTTTTAGGTCATTGTA
CGACGCGTGTGCGACCATGGAAAAGGTGTCGCAGCTGCGATGCTATCCATTTACCCGTCA
TCATTGCTGGCAGAAATCCCATCTTCTCTGCTGGGGTGATTTATATATATGAGAGAGTTA
ACGAATGTAATATTTCTGAATGTTAAATAATTGTTATCCGTCATTATTGTTTCACTTCTC
TCTTTGAAATTTTCGCTTGTTTTCTGTTTTCATCTTATATTTTACTTCAATCCTAAGATAG
TCATATCGACTTAATTCCAAATGAGAGCTAAGTGAGAGAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL133C-A, 25 aa (SEQ ID NO 42)

MRAKWRKKRTRRLKRKRRKVRARSK

YDL136W, 1268 bp, exon1: 501-503, intron1: 504-908, exon2:
909-1268 (SEQ ID NO 43)

CATGCGGACCTTGTGTGTTTTGTTTCTAGATTGTTTTATTTTTATGATTGTTGAAGATAT
AAACCACTGTATAGTTGTATAAGATAGGATAATGATGGTGCCTGAAAATAAACTTACTA
GCTCTTTAATATTGCAACGGCTTGTAACGGGCGCCATGATGACATTCAGAATTATACCAC
TACTATATGAAAAAATGAAAAGAGGCCCTGCTTTGAACCCGTACATTTTATTCTATAATA
TTGCATCTGTGGTTTGCCTGACGGCAGCGAGTCCAACACAAAGTCTGGCATATGCTACGA
ATTTTCCACCATGGATTCAGCACCCAAACATTTGAATTTTTTTTTCATGTCGATTGTGAAA
TTTTACTGAAGATGAGGGTAAATAGAGGCCTGCAATCGTCATCATATGAGAAATGGATAT
ATTGAAAATCTACTCACATCTCTTTTTTGGGGGTTTGGTAGTACAGTGAGAACACGATAA
AGAACCAAATAGGACTAAAAATGGTATGTAGAGATGAATATACATGAAACGGACGTGATA
TAATGTGCTATGGAAGAAAAAAGTCTCCTTTAATGTCTGCAGGATAAATAATCAAGTGGT
CTGAAGAAAATTTACAGCTACAGTATTACTGCAAACCTTGCAGGCAAATATCAGAGAGAT
CTCACCAGCTACAACCTTGGTAACAGAAATTTATAAGTTTATGGCACTTGTTAAAATTGTT
TGGAAGTTTTTCGAAATTATAATATTGGTCTTCAGAAACCTGGAACCACATGTGAACCTATT
TTTTTTGGATAATGCATTGCACAGAGCGTATTAGTGTATACGAGAATCTAAAAATTTGAA
ACTGGCTCATAAAAACAGGAACTTTTACTAACAGTTATGATTTTTTGTTCCTTTCTT
ATCAATAGGCCGCGCTTAAAGCTTACGAACCTAAGAACCAAATCCAAGGAACAATTAGCTT
CTCAATTGGTTGACTTGAAAAAGGAGTTGGCTGAATTGAAGGTCCAAAAGTTGTCCAGAC
CATCTTTGCCAAAGATCAAGACCGTCAGAAAGAGTATCGCCTGTGTCTTGACCGTCATCA
ACGAACAACAAAGAGAAGCTGTTAGACAATTATACAAGGGTAAGAAGTACCAACCAAAGG
ACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAGAGCTTTGACCAAATTCGAAGCTTCCC
AAGTTACCGAAAAGCAAAGAAAGAAGCAAATCGCTTTCCCACAAAGAAAGTACGCTATCA
AGGCTTAA

YDL136W, 120 aa (SEQ ID NO 44)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIKA

YDL167C, 2660 bp, CDS: 501-2660 (SEQ ID NO 45)

TGGGTGTCGTCAAACAGGATGCCGTGGAATCATAACGAACCGCACATTGTGGTAGAGCTAC
AAAGCGATACGAAAGAAGATATGGTATCTAACGTATCCCGTATTGTTGCTTGGGAAAAGA
TGTGGTTAGAACAACATCCAGATGGAGTCACAAATGAATATCAAGGGCCTCGTAGCGATG
ACGAAGACGATGAAGACAGTGAGTAGGCGTTCCATAACTTTGTGTATCTACATATATACA
TATATAATTGTAAATTAGTAACAGTAGTAATAGTAGTGCCTATTATAAAGGGTTTTCTTT
AAGTAATGTCATGTACTTGTTTAATGTGACTTTGGTAATATATTTTCATTCTCCGATGCC
GATGCCCAGTGGAAAAGTTTAAAGTGAAAAATTTTCAACACATACAAGTTTAATAAGTT
GGTTTTGATGCAAATAGCATTACTAAAGAAGAGCGCTAGGATAATTGTGCATTGCTATTG
TGATTTTTGATACAGAAATTATGCACTATGTGGTACTAGAGCTGCAAGTTGCGCATTTGC
CAGATACCCCCAAGGATCAATGTCGCATTGCGAATATAGCATTTCAAATTGTGAATGCTG
AAACATTAGTATGCCATTATGGGACCAATTCTTTACCGAGCATTGAAGTAAACGGGACGA
CAAAGAGTTTGGAGAGTGCAATGGTGCAATTGGACAAGGATATTCATGACGTTATTGGTA
ACGACGACTTTGTTCTTGTTCCTGTATTCAACATGGCATATCCGTGTTACCTTACCAC
GTCAAGCGAGAGATGATGGGTTTATTCTTACTTCTTATTTACAACATCCGAAAGTATTTG
ACTTATGGAAGGAATTCGATAGATGGTGTGTCAACCATCCGGAGATTTTGGGACAAAAGA
AAGCAATCTCCAACAACAATTGTAATACTAAAAGTATTAGTATTAATGCAGCCAAAAATA
CGAAGGATTTGGACGAAATAGTTAGAATATTGGAAGTTTCAATCCCAACTGAAGAGGCAG
GCTCTGTTCCAGAGATATACTCTCTTTTAAAAAGGACAACGGATATATTAATACAATTGC
ACAAAAAGTGTACTTCCCCTGAAGATATGGAATCTGTCTTAACAAAACCATATGACTCAC
ACACCGATATTAGAGCGTTTTTGGCAAGAGAAATCTAAGATTTTGTACATGAACAATTTAC
CGCCCGACACAACTCAAAGTGAGTTGGAATCATGGTTTACCCAATATGGTGTTAGACCAG
TTGGGTTTTGGACTGTCAAAAACATCGTAGAAGATACGTCTAACGTTAATAATAACTGGA
GTCTAAATAACAGTCCCTATGTGGAAGATCAAGATAGTATCTCAGGATTTGTTGTCTTCC
AAACACATGAAGAAGCAACTGAAGTACTAGCGTTGAATGGGAGATCAATCCTATCTAATC
TGGCAAACACTAAGCAACCAAGGGTGGTGGAACATGTCTTGAGCTTCAACCTTCTTCCA
CCGGAGTACTCGATAAGGCTCAAGAAATTTTATCGCCTTCCCTCAAAGTAAAAACAAAC
CAAGACCAGGTGACTGGAATTGCCCATCTTGTGGTTTTTCAAACCTTCAAAGACGTAATG
CATGTTTTAGATGTTCTTTTCCGGCACCATCAAATAGTCAAATACATACTGCGAACTCAA
ACAATAATGTTAACAGTAGTAGAAATAATTTAAACAATCGCGTGAACCTCGGGATCTTCAA
GCAATATTAGTAACACTGCAGCGAATCACCCCTATGGTGCCCTGAGTTCAACATGATTG
CTAACAACACGCCAGCAGCTTTAACATACAATAGAGCTCATTTTCCTGCAATTACGCCAT
TGTCGCGACAAAATTCATTGAACATGGCACCATCGAACAGTGGGTCGCCGATAATTATAG
CGGATCATTTTTTCGGGAAATAATAATATAGCCCCAAATTATCGTTATAATAATAATATTA
ACAATAACAACAATAATATTAACAATATGACCAATAATAGATATAACATTAATAACAACA
TCAACGGTAATGGGAATGGTAATGGGAACAACAGTAATAACAATAACAATCATAATAACA
ATCATAATAACAATCATCATAATGGTAGTATCAATAGTAATAGTAATACCAATAATAATA
ATAATAATAACAATGGTAACAATAGTAATAATTGTAATTCCAATATCGGTATGGGAGGAT
GTGGCTCCAACATGCCATTTAGAGCAGGAGATTGGAAGTGTTCCACGTGCACGTATCATA
ACTTTGCTAAAAACGTAGTGTGCTTACGCTGTGGTGGTCCAAAATCAATAAGCGGCGATG
CAAGTGAAACCAATCATTACATAGATTTCATCAACATTTGGACCAGCGTCGCGTACTCCCA
GTAATAACAATATTTCTGTTAATACTAATGGTGGTAGCAATGCTGGTTCGACCGATGGGA
ACGATAACAAAGGTCGTGATATTAGTTTGATGGAATTTATGTCACCACCGTTATCGATGG
CAACAAAGTCAATGAAGGAGGGAGATGGGAATGGTAGCTCGTTTAACGAGTTCAAAGTG
ACAAAGCTAACGTTAATTTTTTCCAATGTTGGTGATAATAGCGCTTTCGGTAATGGTTTTA
ATAGTTCAATACGTTGGTAG

YDL167C, 719 aa (SEQ ID NO 46)

MHYVVLELQVAHLPDTPKDCRIANIAFQIVNAETLVCHYGTNSLPSIEVNGTTKSLESA
MVQLDKDIHDVIGNDDFVLVSLYSTWHIRVTLPRQARDDGFILTSYLQHPKVFDLWKEFD
RWCNVNHPILGQKKAISNNCNTKSISINAANKTKDLDEIVRILEVSIPTEEAGSVPEIY
SLLKRTTDILILQLHKKCTSPEDMESVLTKPYDSHTDIRAFLQEKSKILYMNLPDQTQS
ELESWFTQYGVRPVGFVTVKNIVEDTSNVNNNWSLNNSPYVEDQDSISGFVVFQTHEEAT
EVLALNGRSILSNLANTKQPRVVEHVLELQPSSTGVLDKAQEILSPFPQSKNKP RP GDWN
CPSCGFSNFQRRTACFRCSFPAPSNSQIHTANSNNNVNSSRNLLNNRVNSGSSSNISNTA
ANHPYGAPEFNMIANNTPAALTYNRAHFPAITPLSRQNSLNMAPSNSGSPIIIADHFSGN
NNIAPNYRYNNNNNNNNNNNNNNNNMTNNRYNNNNINGNGNGNNSNNNNNNHNNNNHNNHH
NGSINSNSNTNNNNNNNNNGNNSNNCNSNIGMGCGSNMPFRAGDWKCSTCTYHNFKNVV
CLRCGGPKSISGDASETNHYIDSSTFGPASRTPSNNNISVNTNGGSNAGRTDGNNDNKG RD

ISLMEFMSPPLSMATKSMKEGDGNGSSSFNEFKSDKANVNF SNVGDNSAFGNFNSSIRW

YDL184C, 578 bp, CDS: 501-578 (SEQ ID NO 47)

AACAAGAAAACCCCTTCCGTTGATCTTAGATTCTTAGAGGTTTCATGAACTAGAAAGCGAC
TTGAACAAAGTCATCCTTCAAGAATCGAAATCTCAAGAGAAAAACAAATTTAATGTAGA
TTGTCCACTATCTCATGTAAATATACATAACAGGTATTCCTGAGCGTTCGAAAATTAGAC
TGTAATTTTCTGATGCGCTCCCGTACACCTTTGACATATACAAACATCCGCACATTTTAT
AGCTTTCTTTCTAGAATTTTTCACGCGCTCTCGATCAATGAACTCTTAAAAGTAACTG
ACCCCTAACTTTTCCAGGCAAGGCTGGCCTCATTACCCTACCCGAAAGTTTCACTTTA
CCCCATGGCAGATGGACGATATTTTAACAAGACGAACTGACCTCGTCTTCTATAAACT
GGACTTCTAAGCAACTCTCATTTATCTTATATCCGTTCCATTTTGTACTAAAAGAACCAG
ACCACATCGATTCAATCGAAATGAGAGCCAAGTGGAGAAAGAAGAGAACTAGAAGACTTA
AGAGAAAGAGACGGAAGGTGAGAGCCAGATCCAAATAA

YDL184C, 25 aa (SEQ ID NO 48)

MRKWRKKRTRRLKRKRRKVRARSK

YDL191W, 1354 bp, exon1: 501-503, intron1: 504-994, exon2:
995-1354 (SEQ ID NO 49)

TATTGACGTTTCGCTCTCAGGTCCACCGTGTCTCAAAAGATACTTTTAAAACCTAAAAC
ACACGAAATCATATTATGATAATTCAGAATGATAGTGTGGTACTGTGTCAATTGACTGTT
CAAGACTGAAGAGGATCTTTGATTTGTTGTTACTCAACAAATAATCTTCACGAAAACCTTT
CTCAATCTGGGGACTGTATTAATCTCAGACCCATACATATCTACACCCATAACTTTTAC
ATTTAATTTTTTATCACATAATAGGTAGCTTAAATTGTAAAGTCGCAAAAAAATGGCA
GCGCAGCCTCTCCGGGTGAACCCACGACAACCTTACCTGGCACTCCATGCACTAACGGGC
GGGTTTGGGCAGGATTCCAGCATCAATTTTGCAAAATTCACACCTGAGTAATTCATATAT
GTAATATAATGTTAAGCATACGCTGTCGATTAGCACTATTATTGACCGTAGAATAGGTAC
AGTGAGACAGTATATTGAAATGGTATGTTTGAGATGAACAAATAATAAAGACTGACAA
CTGCAGAACAGAGAGGATCATAGCAACCTAGTGCAAGAAAGAGCCTCGAAGCGTTAAACT
TTTGGAACGTAATTCATCCGTTGGCTATGTCTATTCAATACAGTTAGAATACGAAAGCTG
TAATCAAGTATATCGGATTATTCGCAAGCAAAGAATCAAGGAAAAGAAAGTGAAAATAGC
ATACATCTTTAAATTCAGAGGTTTGTGCTGAATTTTAATAGGGAAGTTTACGTTATGATTG
TTGGCCGTAGATCGCCTAGCGTTTGACCAAATTTAATTCCTCTAATTTTTTTATTGTAAA
AAAGCCTTCCAACGAAATAAATTAGTTATTGGTTTTTTTTCTCTGTTACGAGGGATATAT
GATGCCTGTGCTTGTAGTTCATTATAAGTGCTAATAAAATACTAACGTTAATAAAAATT
TGGAATATTATTTCAATTTTTTATCCTATTAATAGGCCGGTGTAAAGCTTACGAACTAAG
AACCAAATCCAAGGAACAATTGGCTTCTCAATTGGTTGACTTGAAAAGGAGTTGGCTGA
ATTGAAGGTCCAAAAGTTGTCCAGACCATCTTTGCCAAAGATCAAGACCGTCAGAAAGAG
TATCGCCTGTGTCTTGACCGTCATCAACGAACAACAAAGAGAAGCTGTTAGACAATTATA
CAAGGGTAAGAAGTACCAACCAAGGACTTGAGAGCCAAGAAGACCAGAGCTTTGAGAAG
AGCTTTGACCAAATTCGAAGCTTCCCAAGTTACCGAAAAGCAAAGAAAGCAAATCGC
TTTCCCACAAAGAAAGTACGCTATTAAGGCTTAA

YDL191W, 120 aa (SEQ ID NO 50)

MAGVKAYELRTKSKEQLASQLVDLKKELAEKLVQKLSRPSLPKIKTVRKSIACVLTVINE
QQREAVRQLYKGKKYQPKDLRAKKTRALRRALTKFEASQVTEKQRKKQIAFPQRKYAIIKA

YDR103W, 3254 bp, CDS: 501-3254 (SEQ ID NO 51)

ATCAAGTTTCCTTTAAAGGGATATATAACAGATTCTAAAACCTGACAGAAATATTTTCGAGT
GAAGAAGAAGCGTTAAATATTGGATCTTCCGCGAGTTCTACTCTGATACATTTTGAAGT
AGGAGAGTCATTTAGAAGGCGTATTGCTCAATAGTAGAAAGCAGGCCTGTGCACATGAAT
TAATTAATAAATATAAAGGTAGTGATTAGACGACACATGTCCATAGGTAACCTGTCATAA
TTTTGAACAATTTCCCTTCTTTTCTTTTTTTTTTTGGGTGCGGCGATATGTAGCTTGTT
AATTTACACATCATGTACTTTTCTGCATCAAAATATGAAAGGCGATAGTAGCTAAAGAAA
ATACCGAGAATTTCTCGAAAAGTTGACGACAAAAGAAAGGCATAAAAAAGTAATTTGAA
AATATTTTAAACCTGTTTAAACCCATCTAGCATCCGCGCTAAAAAAGGAAGATACAGGAT
ACAGCGGAAACAACCTTTTAAATGATGGAACTCCTACAGACAATATAGTTTCCCCTTTTC
ACAATTTTGGTAGCTCGACACAATATAGTGGTACCTTGTCGAGAACTCCCAACCAAATAA
TAGAGCTAGAGAAGCCAGTACTCTATCCCATTTGTCAAGAGGAAAAAATGGACGGAAA
AGTTAGCCAGGTTCCAAAGAAGTAGTGCTAAAAAGAAAGATTCTCACCTTCTCCTATTT

CCTCCTCTACATTTTCGTTCTCACCCAAATCTAGGGTCACTTCTTCAAACCTTCTGGCA
ATGAAGACGGTAACCTAATGAATACACCTTCTACGGTTTCCACTGATTATTTGCCACAAC
ACCCTCACAGAACATCGTCTTTGCCAAGACCTAATTCCAATCTCTTTCACGCAAGTAATA
GTAACCTATCCCGAGCAAATGAGCCCCCAAGGGCCGAAAATTTATCAGATAATATACCAC
CCAAGGTCGCTCCATTTGGCTATCCAATACAAAGAACCTCTATTAAAAAATCCTTTTGA
ATGCTTCTTGTACGTTATGTGACGAGCCTATTTCTAACAGAAGAAAGGGAGAGAAAATTA
TAGAGCTTGCATGTGGCCACTTAAGTCACCAAGAATGTCTTATTATCTCTTTTGGCACCA
CTTCAAAGGCAGACGTTTCGTGCGCTATTTCTTTTGTACCAAATGTAAAAAAGATACTA
ACAAAGCCGTTCAATGCATTCAGAAAATGATGAACATAAGGATATTCTAATTTCTGATT
TTTTGATTTCATAAGATTCCTGATTCTGAGTTATCAATCACACCTCAGTCCCGCTTTCCTC
CTTATTCACCACTCTTGCCTCCTTTTGGGTTATCCTATACACCTGTTGAAAGACAAACGA
TATATTCTCAAGCTCCAAGTCTAAACCCAAATCTCATATTGGCTGCACCCCCCAAGGAAA
GAAACCAAATTCACAAAAAAATCAAACTATACATTTTACATTCACCCCTGGGGCACA
GAAGAATTCCGTCCGGAGCAAACCTCTATCTTAGCAGACACCTCTGTAGCGTTGTCAGCTA
ATGATTCTATTTCTGCTGTTTCCAATTTCGGTAAGAGCAAAGGATGACGAAACCAAACAA
CGTTGCCGCTGTTAAGGTCATATTTTATTCAAATTCCTTTTGAACAATTTCCAGGAAGAAT
TGCAGGATTGGAGAATAGACGGGGACTATGGATTACTAAGGTTGGTAGACAAATTGATGA
TTTCCAAAGATGGTCAGAGATATATACAATGCTGGTGTTCCTTATTTGAAGACGCATTTG
TAATAGCAGAAGTGGATAACGATGTTGATGTTTGGAAATTAGACTAAAGAATTTAGAAG
TATTTACACCTATTGCCAAGTGGAGAATGACTACACTCGAAGCTTCAGTACTCAAATGCA
CCTTAAATAAACAACATTGCGCCGATTTATCAGATCTTTACATTGTTTCAGAATATAAATT
CTGACGAAAGCACAACCTGTACAGAAATGGATATCAGGTATATTGAATCAGGATTTTGTAT
TCAATGAGGACAATATCACTTCGACCCTGCCTATTCTTCCCATTATAAAGAACTTTTCAA
AAGATGTTGGTAATGGTAGGCACGAGACGAGTACCTTTCTAGGTTTAATCAATCCTAACA
AAGTTGTTGAAGTTGGAAATGTGCACGATAATGATACTGTAATCATAAGGAGGGGATTCA
CCTTAAATTCAGGAGAATGTTCTAGGCAGAGTACTGTGACAGTATACAATCTGTTCTAA
CCACGATAAGCTCAATTCCTTTCCCTTAAACGAGAAAAACCTGATAATTTGGCAATAATCT
TACAGATCGATTTTACGAAATTGAAGGAAGAAGACAGTTTAATTGTTGTTTATAACAGTC
TAAAAGCTTTAACCATTAAATTTGCGCGTTCGAGTTTGTTCGTTGATCGAAATAATT
ATGTTCTGGACTATGGATCGGTATTACACAAGATAGATTCACTAGATTCCATCTCAAATC
TCAAATCAAAGAGTTCTCTGACACAATTTTACCTATTTGGTTGAAAAATACTCTATATC
CCGAAAATATTCATGAACATTTGGGTATTGTTGCTGTATCAAATAGTAATATGGAAGCAA
AAAAATCCATACTATTTCAAGATTACAGATGCTTTACAAGTTTGGGAAGAAGAAGGCCCA
ATGAATTGAAGATTAAGGTGGGCTATTTGAACGTTGACTACAGTGATAAAATTGATGAAC
TAGTCGAGGCCAGCTCCTGGACTTTTGTTTTAGAACTCTTTGCTACAGTTTCGGTCTAA
GTTTTGATGAACATGATGACGATGACGAAGAGGATAATGATGATTGACCGATAATGAAC
TTGATAATAGTTTCAGGATCACTGTGCGATGCTGAATCTACAACCTACTATTTCATATTGATT
CTCCATTTGATAATGAAAATGCTACCGCAAATATGGTGAATGACAGAAACCTTCTCACTG
AGGGTGAACATAGCAATATAGAAAACCTAGAACTGTCGCTTCTTCAGTACAGCCAGCTC
TGATTCCTAATATTAGATTTTCACTTCATTCTGAGGAGGAAGGTACTAATGAAAATGAAA
ATGAAAATGATATGCCAGTATTATTACTTAGTGATATGGATAAAGGAATCGATGGCATAA
CCAGACGCAGTTCATTCTCGAGTCTTATAGAGAGCGGTAATAACAACCTGTCCCCCTCCATA
TGGATTATATATAG

YDR103W, 917 aa (SEQ ID NO 52)

MMETPTDNIVSPFHNFGSSTQYSGTLSRTPNQIIIELEKPSLSPLSRGKKWTEKLARFQR
SSAKKKRFSPSPISSTFSFSPKSRVTSNSSGNEDGNLMNTPSTVSTDYLPQHPHRTSS
LPRPNSNLFHASNSNLSRANEPRAENLSDNIPPKVAPFGYPIQRTSIKKSFLNASCTL
DEPISNRRKGEKIIELACGHLSHQECLIIISFGTTSKADVRLFPFCTKCKKDTNKAVQCI
PENDELKDILISDFLIHKIPDSELSITPQSRFPYPYSPLLPPFGLSYTPVERQTIYSQAPS
LNPNLILAAPPKERNQIPQKKSNYTFLHSPGLHRRIPSGANSILADTSVALSANDSISAV
SNSVRAKDDETKTTLPLLSYFIQILLNNFQEELQDWRIDGDYGLLRVLVDKLMISKDGQR
YIQCWCFLFEDAFVIAEVDNDVDVLEIRLKNLEVFPIANLRMTTLEASVLKCTLNKQHC
ADLSDLIVQNINSDESTTVQKWISGILNQDFVFNEEDNITSTLPILPIIKNFSKDVGNR
HETSTFLGLINPNKVVEVGNVHDNDTVIIRRGFTLNSGECSRQSTVDSIQSVLTTISSIL
SLKREKPDNLAILQIDFTKLKEEDSLIVVYNSLKALTIKFARLQFCFVDRNNYVLDYGS
VLHKIDSLDSISNLKSKSSSTQFSPIWLKNTLYPENIHEHLGIVAVSNSNMEAKKSILFQ
DYRCFTSFGRRRPNELKIKVGYLNVDSKIDELVEASSWTFVLETLCYSFGLSFDEHDD
DDEEDNDDSTDNELDNSSGSLSDAESTTTIHIDSPFDNENATANMVNDRNLLTEGEHSNI
ENLETVASSVQPALIPNIRFSLHSEEEGTNENENENDMPVLLLSMDMDKGIDGITRRSSFS

SLIESGNNNCPLHMDYI

YDR238C, 3422 bp, CDS: 501-3422 (SEQ ID NO 53)

CCGTGTCAAGATCTAACACGGTAGTCAGCTACTACACAAGGTCTCAGAACAGAATGAGAA
GTGGAACACTGGATAATGATTACGTGAACAGACAAAAGCTTCCTACACATATCTCTCTTC
AAGATTATCGTGATGCTAATGCTAGAAAGTAATATATCGCGTCAGGACTCTGTCTCCACAA
CGAACTCTGATGTGGTAGACCTCAGCTATTCTCTGGGGCATGGCTTGCGTGTGGCAAACC
CTGATTCAGACCCAGAATGATATCCTTCTCTGTAGTTTGTAGATGTCATATATGTACGT
TTATGGAACAGCATTTTAGAAAAGTATTACCCAGCTTATCACTTCGTTTTTTTTTCTTT
CCGTGTACTCGCTACACGTAGAAAGAAATCAGAAAACAACAGCTCGACAAGTGAAATTTG
ACGTTTCATTAAGACTCAGTTAAGATTGCCTTGAGAATAAACAAAAGTAATCACAGTTAAC
TATTGAACAAGAGTGCACCTATGACTTCACCTTCTTCACAGCCAGCGTACACGTTGGTTT
TCGATCCTTCTCCGAGTATGGAGACTTACTCGAGTACCGATTTTCAGAAAGCTCTTGAAA
AGGGATCTGATGAACAAAAAATTGACACGATGAAATCAATTTTAGTTACAATGCTGGAAG
GAAATCCAATGCCTGAATTGTTGATGCACATAATAAGATTTGTCATGCCTTCTAAAAATA
AGGAATTA AAAAAGCTTTTGTACTTCTACTGGGAAATTGTTCCCAAAC TAGCTGAAGATG
GAAATTTGAGACATGAAATGATTCTTGTCTGTAATGCCATTCAACACGATTTGCAACATC
CTAATGAATATATTAGAGGTAACACATTAAGGTTTTTAACGAAATTGAGAGAGGCCGAAC
TCTTAGAACAGATGGTTCCCTCTGTCTTAGCGTGCTTGGAATACCGTCATGCATATGTTT
GTAAGTATGCAATCCTAGCAGTTTTCTCCATTTTCAAGGTCAGCGAACATTTACTTCCCG
ATGCTAAAGAAATCATCAATTCGTTCATAGTAGCTGAAACTGATCCAATATGTAAAAGAA
ATGCATTTATTGGGTTAGCTGAATTAGATCGTGAAAATGCCTTACACTATTTAGAGAACA
ATATTGCTGATATAGAAAACCTAGACCCTTTATTACAAGCTGTCTTTGTTCAATTTATCA
GACAAGATGCAAACAGGACCCCTGCTTTGAAAGCCCAATATATCGAATTATTGATGGAAC
TGCTTTCGACCACGACTTCCGATGAAGTCATCTTCGAGACCGCATTAGCCCTAACTGTGT
TGTCTGCCAATCCAAATGTCTTGGTTCTGCGGTTAACAAATTGATTGACTTGGCCGTCA
AGGTTTCTGATAATAACATTAAGTTAATTGTTCTAGACCGTATTCAAGACATCAATGCTA
ATAACGTAGGTGCTTTGGAAGAGTTAACCCTGGATATTTTGAGAGTCTTGAATGCAGAAG
ATTTAGACGTTTCGTTCAAAGGCGCTTGATATTTCAATGGACTTGGCCACATCCAGAAATG
CTGAAGATGTTGTTGAGCTTTTGAAGAAAGAGCTGCAAACAACCGTAAATAACCCAGATC
AAGACAAGGCAATGCAGTACAGACAATTGTTAATAAAAACCTATTCGTACCGTGGCTGTAA
ACTTTGTAGAAATGGCAGCAAGTGTTGTTTCGCTATTATTAGATTTTCATCGGTGATTTAA
ACTCGGTTGCCGCCAGTGGTATCATTGCCCTTATCAAAGAAGTGATCGAAAAATACCCAC
AACTTAGAGCCAATATCCTTGAAAACATGGTTCAAACGCTAGACAAAGTGAGATCTGCTA
AAGCTTACCGCGGTGCATTATGGATTATGGGTGAGTATGCTGAAGGAGAAAGTGAGATAC
AACATTGTTGGAAGCACATTCGTAACAGCGTAGGTGAAGTTCCTATCCTTCAATCAGAAA
TCAAAAAGTTAACACAAAACCAAGAACACACCGAAGAAAATGAGGTTGACGCTACCGCCA
AGCCAACCTGGTCCAGTTATTCTACCAGACGGTACGTATGCCACTGAAAGCGCTTTCGATG
TGAAGACTTCTCAAAGTCAGTTACCGATGAAGAACGTGATTCTAGACCTCCAATTCCGCC
GGTTTGTTTTAAAGTGGTGATTCTTACACAGCTGCCATTCTGGCCAACACCATCATTAAC
TTGTTTTTAAATTCGAAAACGTTTCCAAGAACAACCTGTCATCAATGCTCTAAAGGCGG
AAGCTTTACTAATTTTAGTTAGTATTGTAAGAGTGGGTCAAAGCTCTTTGGTGAGAAAA
AAATTGATGAAGATTCTTTAGAGAGAGTTATGACATCTATTTCTATTTTATTGGATGAAG
TTAATCCTGAGGAAAAGAAGGAAGAAGTTAAACTTCTGGAGGTTGCATTCTTGACACCA
CCAAATCCTCATTCAAGAGACAAATTGAAATTGCAAAGAAGAACAAGCATAAGAGAGCAT
TAAAAGACAGTTGCAAAAACATCGAACCAATTGATACGCCGATTTCTTTCAGGCAATTTG
CTGGTGTGGATTCTACTAATGTGCAAAAAGATAGTATTGAAGAAGATTTACAACCTGGCAA
TGAAAGGAGATGCAATCCACGCTACTAGCAGCTCTAGTATTTCGAAGCTGAAGAAGATAG
TACCTTTATGTGGCTTTTCTGATCCAGTTTACGCCGAGGCTTGATTACAAACAATCAAT
TTGACGTCGTATTAGATGTTCTTCTTGTTAATCAAACGAAAGAAACATTGAAAAACCTAC
ATGTGCAATTTGCAACTCTTGGTGATTGTAAGATTATTGACACACCACAGAAGACCAACG
TGATTCCTCATGGCTTCCACAAATTCACCTGTACTGTCAAAGTTTCCTCTGCTGACACAG
GTGTCAATTTTCGGTAATATTATTTATGATGGTGCGCATGGTGAAGATGCTCGTTATGTTA
TTTTAAACGACGTTTCATGTTGACATTATGGATTATATCAAACCAGCCACTGCTGACGATG
AACATTTCCGTACCATGTGGAATGCATTTGAGTGGGAGAACAAAATATCGGTCAAATCAC
AACTACCAACATTGCATGCTTATTTGAGAGAAGTGGTCAAGGGAACATAATATGGGTATTC
TAACACCATCAGAGTCGTTGGGAGAAGATGATTGTAGGTTCTTAAGTTGTAATCTGTATG
CGAAGTCGTCTTTTGGTGAAGATGCCCTAGCCAACTTGTGTATCGAAAAGGATTCCAAAA
CCAATGATGTCATAGGTTATGTTCTGATCCGATCAAAGGGACAAGGTTTGGCTCTGTCCC
TAGGTGACAGAGTGGCATTGATTGCTAAGAAGACCAATAAACTTGCTCTCACTCATGTTT

GA

YDR238C, 973 aa (SEQ ID NO 54)

MTSLSSQPAYTLVFDPSPSMETYSSTDFQKALEKGSDEQKIDTMKSILVTMLEGNPMPEL
LMHIIRFVMPSPKSKNELKKLLYFYWEIVPKLAEDGKLRHEMILVCNAIQHDLQHPNEYIRG
NTLRFLTKLREAELLEQMVPSVLACLEYRHAYVRKYAILAVFSIFKVSEHLLPDAKEIIN
SFIVAETDPICKRNAFIGLAELDRENALHYLENNIADIENLDPLLQAVFVQFIRQDANRT
PALKAQYIELLMELLSTTTSDDEVIFETALALTVLSANPNVLVPAVNKLIDLAVKVSNNI
KLIVLDRIQDINANNVGALEELTLDILRVLNAEDLDVRSKALDISMDLATSRNAEDVVQL
LKKELQTTVNNPDQDKAMQYRQLLIKTIRTAVNVFVEMAASVVSLLLDFIGDLNSVAASG
IIAFIKEYIEKYPQLRANILENMVQTLDKVRSKAYRGALWIMGEYAEGESEIQHCWKHI
RNSVGEVPILQSEIKKLTQNEHEEENEVDATAKPTGPVILPDGTYATESAFDVKTSQKS
VTDEERDSRPPIRRFLVSGDFYTAAILANTIILKVLKFENVSKNKTVINALKAEALLILV
SIVRVGQSSLVEKKIDEDSLERVMTSISILLDEVNPEEKKEEVKLLEVAFLDTTKSSFKR
QIEIAKKNKHKRALKDSCKNIEPIDTPIFRQFAGVDSTNVQKDSIEEDLQLAMKGDH
ATSSSSISKLKIVPLCGFSDPVYAEACITNNQFDVLDVLLVNQTKETLKNLHVQFATL
GDLKIIDTPQKTNPVPHGFHKFTVTVKVSSADTGVIFGNIYDGAHGEDARYVILNDVHV
DIMDYIKPATADDEHFRTMWNFAFEWENKISVKSQPLTLHAYLRELVKGTNMGILTPSESL
GEDDCRFLSCNLYAKSSFGEALANLCIEKDSKTNDVIGYVRIRSKGQGLALSLGDRVAL
IAKKTNKLALTHV

YDR259C, 1652 bp, CDS: 501-1652 (SEQ ID NO 55)

AAACTTTGTTCAAGATTATGCTTTCTTTGTAATTTTAAACATAGTCTTGCACTTATTTTT
ACTGCATGTGGATAAAAGTTTTTCGAATCGTTTGCAAGCAAATGTAAACTATTACTTTTT
AATGATTTCTGATACTCTTTGATTCCATTCTGTCTACTTTTTTTCTGCATTTGAAACGCT
AATTAAGTATTTCTTGCCCTGCTTCTTTTCCTTTTGATTTCTTTTTTTTATTCTCAAGTT
TTTAATTTCTGGAGAATCTCTTTTTTTTGTTTATTTTGTTAACACAGTTAGTGGAGCCTTG
TAGTATCGAGAGTAGACTATCTTTGGAAAGCAATGCGAGTTGAGAGATTGTGGAGTGTAC
TACAGAACCAATATTAACACAATCTTTCTCTCAAACCTGTAACACCGAGTTTTTTTCCCA
CCAATCGTGAATCCGATAGCATATACTTTTGCTAGAAATTTCAATAAACACAGAATAA
CGAAGAGTGCTAAGGGACAAATGCAAAACCCTCCGTTGATTCGTCCTCGATATGTATAATC
AGGGAAGCAGCTCAATGGCTACTTATAATGCCTCTGAGAAGAATCTAAATGAGCATCCTT
CTCCGCAAATTGCACAGCCAGCAGCTCCCAAAAGTTACCTTATAGAATAAATCCTACAA
CCACTAATGGGGACACCGACATATCTGTTAACAGCAATCCTATCCAGCCTCCTTTGCCAA
ACTTGATGCATCTATCTGGTCCGTCTGACTATAGATCGATGCATCAAAGTCCTATACATC
CATCTTATATCATCCCTCCGCATTCAAATGAAAGAAAACAATCAGCTTCTTACAACAGAC
CTCAAATGCTCATGTAGTATTCAACCTTCCGTGGTATTCCCCCTAAAAGTTATTCCA
TATCTTATGCACCTTATCAAATAAATCCCCCTTTACCAAATGGACTTCCGAACCAGAGCA
TATCTTTGAATAAGGAGTATATTGCAGAGGAGCAACTATCAACCCTCCCATCTCGCAATA
CCAGTGTTACTACTGCACCTCCTTCTTTTCAAAACAGTGCTGATACCGCTAAAAATTGAG
CTGATAATAATGATAATAATGATAATGTAACCAAACTGTTCTCTGATAAAGACACCCAAC
TCATAAGTAGTTCAGGCAAACTTTAAGAAATACTAGAAGAGCTGCTCAAAATAGAACCG
CTCAAAAGGCATTTAGACAAAGGAAAGAAAAATACATCAAGAATCTCGAACAAAAATCAA
AGATATTTGACGATTTACTAGCAGAAAATAAATACTTCAAATCATTAAACGATTCATTAA
GAAATGACAACAACATTTTAATAGCTCAGCATGAAGCTATAAGGAATGCAATTACTATGT
TAAGAAGTGAGTATGATGTCTTATGTAACGAAAACAACATGTTGAAGAATGAGAATAGTA
TAATAAAAAATGAACACAACATGTCAAGAAATGAAAATGAAAACCTAAAACCTGAGAATA
AACGCTTCCACGCTGAATATATACGAATGATCGAGGATATTGAAAATACTAAAAGAAAGG
AACAGAACAACGAGATGAAATAGAGCAACTAAAAAATAAGATCCCTGGAGGAAA
TAGTAGGGAGACACTCGGATAGTGCCACGTAA

YDR259C, 383 aa (SEQ ID NO 56)

MQNPPLIRPDMYNQGSSSMATYNASEKNLNEHPSQIAQPSTSQKLPYRINPTTTNGDTD
ISVNSNP IQPPLPNLMHLSGPSDYRSMHQSPIHPSYIIPHSNERKQSASYNRPQNAHVS
IQPSVVFPPKSYSISYAPYQINPPLPNGLPNQSIISLNKEYIAEEQLSTLPSRNTSVTTAP
PSFQNSADTAKNSADNNDNNDNVTKPVPDKDTQLISSSGKTLRNTRRAAQNRTAQKAFRQ
RKEYIKNLEQKSKIFDDLLAENNNFKSLNDSLRNDNNILIAQHEAIRNAITMLRSEYDV
LCNENMLKNENSI IKNEHNMSRNEENENLKENKRFHAHEYIRMIEDIENTKRKEQEORDE
IEQLKKKIRSLEEIVGRHSDSAT

YDR294C, 2270 bp, CDS: 501-2270 (SEQ ID NO 57)

CCGACAGTACGACTTAAAAAACAAAAACAACGTCCAGGTGGAAAAAGCTGCCGCAAATGG
TACACGGTTTAGATCAACAAGATCCAATACCCCTAATTACACATGAATGTGACGTTTCCT
AAAAGAAGTAGCCTGTATAATATAGAGAGATTTTATATACTTTCTTAATGAATTAGACTG
TTTCTACAAGTATTTGACACTGGAAAAAAGAGAAAGTACATAGAGATTGGCCAAATATT
TAAATCTACACAGTTGCCTATCGTTTATCGCCTTATTCTTCAGAAACATTTTCATCAACTA
CTCTGGTGCATTATTTTCATGTTAGTTACCATATATACCGGCCGCGCATCGGGGTTTTT
TGATTGAAAAAATTGGTATATTTTCAGTACACATATAAATAAAACCCCTCAATTTGCCTCT
CCAACCGTTATAACTATTCCAGATCCTCTTTACCGAGCAAGTAGGCTAGCTTCTGTAAAG
GGATTTTTCATCTAATAACAATGAGTGGAGTATCAAATAAAACAGTATCAATTAATGGTT
GGTATGGCATGCCAATTCATTTACTAAGGGAAGAAGGCGACTTTGCCCAGTTTATGATTC
TAACCATCAACGAATTAAAAATAGCCATACATGGTTACCTCAGAAATACCCCATGGTACA
ACATGTTGAAGGATTATTTGTTTGTGATCTTTTGTGTTACAAGCTAATAAGTAATTTTTTTT
ATCTGTTGAAAGTTTATGGGCCGGTGAGGTTAGCAGTGAGAACATACGAGCATAGTTCCA
GAAGATTGTTTCGTTGGTTATTGGACTCACCATTTTGTAGGGGTACCGTAGAAAAGGAAG
TCACAAAGGTCAAACAATCGATCGAAGACGAACATAATTAGATCGGACTCTCAGTTAATGA
ATTTCCACAGTTGCCATCCAATGGGATACCTCAGGATGATGTTATTGAAGAGCTAAATA
AATTGAACGACTTGATACCACATACCCAATGGAAGGAAGGAAAGGTCTCTGGTGCCGTTT
ACCACGGTGGTGATGATTTGATCCACTTACAAACAATCGCATACGAAAAATATTGCGTTG
CCAATCAATTACATCCCGATGTCTTCTCGCCGTACGTAAAATGGAATCCGAAGTGGTTT
CTATGGTTTTAAGAATGTTTAATGCCCCCTCTGATACAGGTTGTGGTACCACAACCTTCAG
GTGGTACAGAATCCTTGCTTTTAGCATGTCTGAGCGCTAAAATGTATGCCCTTCATCATC
GTGGAATCACCGAACCAGAAATAATTGCTCCCGTAAGTGCACATGCTGGGTTTGACAAAG
CTGCTTATTACTTTGGCATGAAGCTACGCCACGTGGAGCTAGATCCAACGACATATCAAG
TGGACCTGGGAAAAGTGAAAAAATTCATCAATAAGAACACAATTTTACTGGTCCGGTCCG
CTCCAACTTTCCTCATGGTATTGCCGATGATATTGAAGGATTGGGTAAAATAGCACAAA
AATATAAACTTCCTTTACACGTCGACAGTTGTCTAGGTTCTTTTATTGTTTCATTTATGG
AAAAGGCTGGTTACAAAAATCTGCCATTACTTGACTTTAGAGTCCCGGGAGTCACCTCAA
TATCATGTGACACTCATAAATATGGATTGACCAAAAAGGCTCGTCAGTTATAATGTATA
GAAACAGCGACTTACGAATGCATCAGTATTACGTAAATCCTGCTTGGACTGGCGGGTTAT
ATGGCTCTCCTACATTAGCAGGGTCCAGGCTGGTGCTATTGTCTAGGTTGTTGGGCCA
CTATGGTCAACATGGGTGAAAATGGGTACATTGAGTCGTGCCAAGAAATAGTCGGTGCAG
CAATGAAGTTTAAAAAATACATCCAGGAAAACATTCCAGACCTGAATATAATGGGCAACC
CTAGATATTAGTCATTTTCAATTTTCTTCAAAGACCTTGAACATACACGAACATCTGACA
GGTTGTCCAAGAAAGGCTGGCATTTCATGCCCCACAAAAGCCGTTGCACTACACATGG
CCTTCACGAGATTGAGCGCTCATGTTGTGGATGAGATCTGCGACATTTTACGTACTACCG
TGCAAGAGTTGAAGAGCGAATCAAATTCTAAACCATCCCCAGACGGAAGTAGCGCTCTAT
ATGGTGTGCGCGGGAGCGTTAAAACTGCTGGCGTTGCAGACAAATTGATTGTGGGATTCC
TAGACGCATTATACAAGTTGGGTCCAGGAGAGGATACCGCCACCAAGTAG

YDR294C, 589 aa (SEQ ID NO 58)

MSGVSNKTVSINGWYGMPIHLLREEGDFQFMILTINELKIAIHGYLRNTPWYNMLKDYL
FVIFCYKLISNFFYLLKVYGPVRLAVRTYEHSSRRLFRWLLDSPFLRGTVKEVEVKVKQS
IEDELIRSDSQLMNFPLPSNGIPQDDVIEELNKLNDLIPHTQWKEGKVSAGVYHGGDDL
IHLQTIAYEKYCVANQLHPDVFPVVRKMESEVSMVLRMFNAPSDTGCGTTTSGGTESLL
LACLSAKMYALHHRGITEPEIIAPVTAHAGFDKAAYYFGMKLRHVELDPTTYQVDLGKVK
KFINKNTILLVGSAPNFPHPGIADDIEGLGKIAQKYKLPLHVDSCIGSFIVSFMEKAGYKN
LPLLDLFRVPGVTSISCDTHKYGFAPKGSSVIMYRNSDLRMHQYYVNPWTGGLYGSPTLA
GSRPGAIVVGCWATMVNMGENGYESQEIIVGAAMKFKKYIQENIPDLNIMGNPRYSVIS
FSSKTLNIHELSDRLSKKGWHFNALQKPVALHMAFTRLSAHVVDEICDILRTTVQELKSE
SNSKPSPDGTSALYGVAGSVKTAGVADKLIVGFLDALYKLGPGEDTATK

YDR430C, 3470 bp, CDS: 501-3470 (SEQ ID NO 59)

ACGTCATTTTGTTCCTTGTGGAGCTGGTGGTTCTTGTGGAGCAGATTCTGTGGAGCAGAT
TCCTGTGGAACCTTGTGGTTCTTGTGGAGCATCTGGAGCCTGTGGTGGTTCTTGGTGCTGT
TCTTCGACTGGGGCATCGACAACAGATTCTGGTAGTTGCTCTACGTGAGTTTCTTGAGCT
TCAGACATTATCCTTATGGTTTACGCTAATTGCTTAATTTTGATTCTTCAAAGTATA
TATATTTAGAAGAGAGGAAATTATTTTTCTCATGTCTTTTTTAAATCCCTTTGGGTGGCG
AAAAAAAAGAATGTAAAAAATTTGCCCTTCGTTTACAGTGATAAATATACGGAGGGGCT
CTATGATAAAGGTAGTAGTAAATCATTGAATTGTTGAACAAGCATTGACAGATATGATAA

CAAGCAATTGTAATCAATAAGCCACCAATTAGAAGGCTACTCAAAAGAATAAAGTTACTA
TAAAATATACTGCGGTATATATGTTGCGGTTTCAGCGATTTGCGTCCTCGTATGCCCAAG
CACAGGCCGTTAGAAAATATCCAGTTGGAGGTATATTCCATGGTTATGAAGTGAGAAGAA
TTCTACCGGTTCCGGAGCTGAGACTCACTGCGGTAGATTTGGTGCACTCCCAGACAGGAG
CCGAGCATTTGCATATTGATAGAGACGACAAGAATAATGTGTTTCAGCATTGCTTTTAAAA
CCAACCCTCCAGATTCCACTGGGGTCCCTCATATTCTAGAGCATACAACGTTGTGTGGGT
CTGTTAAATATCCAGTTAGGGACCCTTTTTTCAAAATGCTAAATAAATCTCTAGCTAATT
TCATGAACGCTATGACAGGTCCAGATTATACATTTTTTCCCTTTTCCACTACGAACCCTC
AAGATTTTCGCTAATTTAAGAGGTGTTTATTTAGACTCCACCTTGAATCCGCTACTTAAAC
AAGAAGATTTTGATCAGGAGGGTGGAGGTGGAGCATAAAAACATCACAGACCCGGAGA
GTAACATTGTTTTCAAGGTGTTGTCTATAACGAAATGAAAGGTCAAATATCAAATGCCA
ATTACTATTTCTGGAGTAAATTTCAACAGTCTATTTATCCTTCCCTGAATAACTCCGGCG
GAGATCCTATGAAAATTACAGACTTGAGATACGGCGATCTCTTGGATTTCCATCACAAAA
ATTACCATCCCTCCAATGCAAAAACCTTTCACGTACGGTAACTTGCCATTGGTGGATACGT
TAAAGCAATTAAATGAGCAGTTCAGTGGTTACGGGAAGAGAGCTCGAAAGGATAAGTTGT
TAATGCCTATTGATTTAAAAAAGACATAGATGTCAAGTTACTGGGTCAAATAGATACTA
TGCTTCCACCGGAGAAGCAGACAAAAGCCTCAATGACGTGGATTTGTGGAGCGCCACAGG
ACACATATGATACCTTTTTGTTAAAAGTACTGGGGAATTTATTAATGGATGGCCATTCTT
CTGTAATGTATCAAAAATTAATAGAATCAGGAATTGGTTTGGAGTTCTCCGTAAATTCAG
GTGTTGAACCAACTACAGCAGTAAATTTGCTAACTGTTGGTATACAGGGCGTGAGTGATA
TTGAAATATTTAAAGACACTGTAAATAATATTTTTCAAAACCTGTTGGAAACAGAACATC
CTTTTGACCGCAAGCGTATCGATGCCATAATTGAACAATTGGAATTATCTAAGAAGGATC
AAAAGGCTGACTTTGGACTTCAATTACTCTATTCTATACTACCTGGTTGGACAAACAAAA
TCGATCCTTTTGAGAGCTTGTGTTTGAGGACGTTTTGCAAAGATTTAGAGGTGACTTAG
AAACGAAAGGTGATACTTTATTCCAAGATTTAATCCGTAAATATATCGTTCATAAACCTT
GTTTCACGTTTTCCATTTCAGGGATCTGAAGAGTTCTCTAAATCTTTGGATGATGAAGAAC
AAACAAGACTGAGAGAAAAAATTACTGCCTTGGATGAACAAGACAAGAAAAACATCTTTA
AACGTGGTATACTGTTACAGGAGAAACAAAATGAAAAAGAAGATTTATCCTGTTTACCTA
CCTTACAAATAAAAGACATCCCAAGAGCTGGTGATAAATATTCAATCGAACAGAAGAATA
ATACAATGTCTAGGATTACTGATACCAATGGTATCACATATGTCAGAGGTAAACGTTTAC
TAAATGACATAATACCCTTTGAACCTTCCCATACTTACCTTTATTTGCTGAATCGTTAA
CTAACCTAGGGACAACAACAGAATCCTTCAGTGAAATAGAAGATCAGATAAAATTACATA
CGGGTGGTATATCAACACATGTAGAGGTTACATCTGACCCTAACACCACAGAGCCTCGCC
TGATTTTCGGGTTTGACGGATGGTCTTTAAATTCGAAGACCGACCACATTTTTGAATTCT
GGTCTAAGATCTTACTAGAACTGATTTCCATAAAAACAGCGATAAATTGAAAGTTCTTA
TCCGCTTATTAGCATCTTCAAACACATCTTCTGTAGCAGATGCCGGTCATGCATTTGCAA
GGGGCTATTCTGCCGCACATTATAGATCAAGTGGAGCTATAAATGAGACCCTCAATGGTA
TTGAGCAACTACAATTTATAAATAGATTGCACAGCTTGTTAGACAATGAAGAACTTTCC
AAAGAGAAGTTGTGACAGCTAACTGAATTGCAAAAGTACATTGTTGATACCAATAACA
TGAATTTTTTTTATCACCTCAGACTCTGATGTTCAAGCGAAAACAGTAGAAAGCCAAATTT
CAAAATTCATGGAGAGATTACCTCATGGCAGCTGCTTGCCCAATGGACCAAAGACTTCAG
ATTATCCTCTTATTGGATCCAAATGTAAACATACTTTGATAAAATTTCCCTTTCCAGGTCC
ATTACACATCCCAAGCTTTATTGGGTGTGCCGTATACACATAAGGATGGCTCTGCACTTC
AAGTTATGTCAAATATGCTAACATTCAAACATTTGCACAGAGAAGTCAGAGAAAAGGGTG
GTGCTTATGGTGGTGGTCTTCTATAGCGCCTTAGCGGGTATTTTCAGTTTCTATTCTT
ATAGGGATCCTCAGCCTTTGAAGAGTTTAGAAACCTTCAAGAATAGCGGGCGTTATATAC
TGAACGATGCCAAGTGGGGCGTCACAGACCTTGATGAAGCTAAATTGACAATATTTCAAC
AAGTAGACGCACCTAAAAGTCCCAAGGAGAAGGCGTGACGTATTTTCATGAGCGGTGTTA
CAGACGATATGAAACAAGCAAGAAGGGAACAACTCTTAGACGTATCTCTCCTGGACGTTT
ATAGAGTCGCCGAAAAATATCTACTAAACAAGAAGGGGTGAGTACGGTCATTGGACCTG
GAATCGAGGGGAAGACTGTTTCACCAAATTGGGAGGTGAAGGAACTGTAG

YDR430C, 989 aa (SEQ ID NO 60)

MLRFQRFASSYAQAQAVRKYPVGGIFHGYEVRRILPVPELRLTAVDLVHSQTGAEHLHID
RDDKNNVFSIAFKTNPPDSTGVPHILEHTTLCGSVKYPVRDPFFKMLNKSLANFMNAMTG
PDYTFPFSTTNPQDFANLRGVYLDSTLNPLLKQEDFDQEGWRLEHKNIIDPESNIVFKG
VVYNEMKGQISNANYFWSKFQQSIYPSLNNSGGDPMKITDLRYGDLLDFHHKNYHPSNA
KTFTYGNLPLVDTLKQLNEQFSGYGKRARKDKLLMPIDLKIDVKKLGQIDTMLPPEKQ
TKASMTWICGAPQDQTYDTFLLKVLGNLLMDGHSSVMYQKLIESGIGLEFSVNSGVEPTTA
VNLLTVGIQGVSDIEIFKDTVNNIFQNLLETEHPFDRKRIDAIIEQLELSKKDQKADFGL

QLLYSILPGWTNKIDPFESLLFEDVLQRFGRDLETKGDTLFDLIRKYIVHKPCFTFSIQ
GSEEFKSLDDEEQTRLREKITALDEQDKKNIFKRGILLQEKQNEKEDLSCLPTLQIKDI
PRAGDKYSIEQKNNTMSRITDTNGITYVRGKRLNDIIPFELFPYLPLFAESLTNLGTTT
ESFSEIEDQIKLHTGGISTHVEVTS DPNTTEPRLIFGFDGWSLNSKTDHIFEFSKILLE
TDFHKNSDKLKVLIIRLLASSNTSSVADAGHAFARGYSAHYRSSGAINETLNGIEQLQFI
NRLHSLLDNEETFQREVVDKLTTELQKYIVDTNNMNFITSDSDVQAKTVESQISKFMERL
PHGSCLPNGPKTSDYPLIGSKCKHTLIKFPFQVHYTSQALLGVPHYTHKDGSALQVMSNML
TFKHLHREVREKGGAYGGGASYSALAGIFSFSYRDPQPLKSLETFKNSGRYILNDAKWG
VTDLDEAKLTIFQQVDAPKSPKGEVTFYFMSGVTDDMKQARREQLLDVSLLDVHRVAEKY
LLNKEGVSTVIGPGIEGKTVSPNWEVKEL

YDR438W, 1613 bp, CDS: 501-1613 (SEQ ID NO 61)

CTTTTCTCAGCACCTGTCCAGAGACATAACATCACATCGCCCCAGTAAATGCA
TACGCAAGATAAGATACAAACCTGGCTACGGGAACACTACGCCAACGTGATTGGCAATTGT
GCTCTAATAGTTACTCTATTATTGCTGTTAATTGACAATGTTTAGTCACGTGCAACACAA
TTCAAGTCACGTGGAAAGGCCTTCACATGGTGATCCATCTTCTACATCTTCATCGGTCTT
GCATAAAGTCATAATATCGGGCTACTGGAATGTATGCACCTAACAGTACTATTATATGGT
GAGGCTGTAATGCTTACCGTTTTGTGGCTATTCTCGTATTCTGTAGGCCCCCCCCATACAC
ATTTTTTCGGTAACTGCGGCATATAGATGAAAGTTGAAATGAATATTCAAAAGAATATATA
TAATAATGCAGGAGATCAAGGAAGAATTAGATATGTATAAGAGTGATGGTAGAGGCAAAA
AATAAAAAGTAAGCAGGAGAATGAATCGTGTGGTATAGACGTAGATCATATGATAGGGG
TCCTGCTTCTGGCCGTAGTGGTGGTGTGTTTGGGTGGCGCTTCGTGTTTGACTAATGAAT
TGCTCGAGACAAACGCGTACAATAAACCTTCTTCTTACTTATCTAAACATATCATCGT
TTGCTCTTTATTTGACGCCAGATCTATGGAGGATAATCCAATCAAGAAGGAAGAGCTTGC
AGGAACGGACAGAACGAACATTACCTATTCACACACAAGAATCTTTTTCAGAGTTCCTAC
CTTTACTATCTTCAACTCCTTCTACTTCTTCAAATTTGTCTTCGATAGCGGACACGAAAG
TGAAGGATACAATGAGGTTGAGTCTGCTATTTTGGCTCTTGTGGTTCGTGGCAAATTTGG
CGGCTAACGCTGCTTTGTCGTATACCACAGTGGCTTCGTCAACAATTCTTTCATCGACAT
CCTCATTTTTTACCTTATTTCTTGCCACTAGTCTAGGAATAGAACTTTTTTCGACAAAAA
AACTGCTGGGGTTATTTGTGTCTTTGTTTGAATATCTTAATTGTGATGCAATCCTCGA
AGCAACAGGATTCTGTGAGTGCCTTCCTCCTTTTGGTAGGTAACACTTTAGCACTGCTGG
GGTCATTGGGTTACAGTGTCTATACAACCCTTTTGAATACGAAATATCATCCAAAGGTC
TCAGACTAGACATTACAGATGTTTCTTGGTTATGTTGGTATCTTCACGTTTCTGTTGTTTT
GGCCAATTTTAATAATCCTGGATATAACACATATGGAACTTTTGAACACCAAGTAACT
TCCACATTTCTTTTCTTGTCTATGTTAAATTGTATCATTATCTTTGTTAGTGACTATTTTT
GGTGTAAGCCCTCATTTTGACATCACCCCTTGGTGGTTACCGTTGCCTTAACCTTTACTA
TCCCGTTAGCCATGTTCCGTGATTTTGTATGGCGAGAGGCATTTTTTACGCCTTGGTATA
TCATTGGTGTATTTTTCATTTTGTGTTTCTTCTAGTTAACCATCGGGGAGAATCTG
CTGTTGAAAAGGACTGTGCTGCGGTTGAAAAGGACCTATCTTGATGCCTAA

YDR438W, 370 aa (SEQ ID NO 62)

MNRVGIDVDHMGVLLLVVVVFWVGASCLTNELLETNAYNKPFFLTLYLNISSFALYLTP
DLWRRIQSRKSLQERTERTLPIHTQESFSEFLPLLSTPSTSSNLSSIADTKVKDTMRL
SLLFCVLWFVANLAANAALSYTTVASSTILSSTSSFFTLFLATSLGIETFSTKKLLGLFV
SLFGIILIVMQSSKQQDSVSASSFLVGNLALLGSLGYSVYTTLLKYEISSKGLRLDIQM
FLGYVGIFTLLFWPILIIILDITHMETFELPSNFHISFLVMLNCIIIFVSDYFWCKALIL
TSPLVVTVALTFTIPLAMFADFVWREAFFTPWYIIGVIFIFVSFFLVNHRGESAVEKDCA
AVEKGPILDA

YDR450W, 1376 bp, exon1: 501-547, intron1: 548-982, exon2:
983-1376 (SEQ ID NO 63)

CGGCCCATGAGCATAAATTGAGAACGATATTATTAATTCTAGTATATTTTAGGAACAGCA
GGCCATTATATCCAAAACCTTTTTTAAATAGCATCCACATCACTTACTGGCGTACAGTTT
CGTGTCTGGCAACAAAAAGTACATTTAATTTCAATGATTAAAAAGACATTAAACATCCG
TACATTACGCACCCATGCATGCTATCTGAAAATATTCTACATGCTGCTTTTAGAAATTTG
AAGCGGCATATGGTGTTTCCTTGCGGAGACGCGCGCTCAGGGGAAGTGGGATTCCGAAAG
ATGCCTTTCCAGTCCCATATGCCCATCCCAAGATCATGCCCGGGAGAGCAAATGTCGCC
CCAGCCAGGTCGGACACATCTGTCAATTCGACCACTAAGTATTGTCAAAGCTAGGGTTAAT
TGAAGATAGCTCTACATGTTATTAGTAGAGTTTTTAAACGTTGAGATACTAGTGAACGTA
TACACAAGAGCGGATAAAAGATGTCTTTAGTTGTCCAAGAACAAGGTTCTTCCAACACA

TTTTACGGTATGTTTATTATTACTAGTGAGCTATGACAAAATCGGCTAAAAACTTAAAA
TATGACAGACAAGAAAGGAAATTCATTCACCTCTTTAATCGTGGCGATTATTCGCTAACG
ACGTGATTAAATATAATAATGATGTTCCCGGGCTGGACTAAGAACGTAATAATAAGGCTG
ATGAACAAATTTATGGTTTATGCATCAAAAAGGAACATGAATTTGGCATAAGCGCACATA
ATTACGGAACATTGCAATAGCGGTCGGAGGTAAAGTACCGGGAATGCTTTACAATGAATC
AGCTATTGGCGGATATTGACCAACCAACACTAAAATTTTATATCCTGCTCCGATTTTGT
CTTGGCCGTGAAATCCATTATGCACATTTTACTAACGTTTATCAATAAGTTCGGTTTC
CCGTCTAAATTTTACGCGAGTTTGTGTAACACTAACGTTGACGGTAACATTAAGATCG
TTTACGCTTTGACCACTATCAAGGGTGTGGTTCGTCGTTACTCCAACCTTGGTCTGTAAGA
AGGCTGATGTTGATTTACACAAGAGAGCTGGTGAATTGACCCAAGAAGAATTGGAAAGAA
TTGTTCAAATTATGCAAAACCCAACCTCACTACAAAATCCCAGCTTGGTTCTTGAACCGTC
AAAATGACATCACTGATGGTAAGGACTACCACACTTTGGCTAACAACGTCGAATCCAAAT
TGAGAGATGACTTGGAAGATTAAAGAAAATCAGAGCTCATCGTGGTATCAGACACTTCT
GGGGTTTGCGTGTTAGAGGTCAACACACCAAGACCACTGGTAGAAGAAGAGCTTAA

YDR450W, 146 aa (SEQ ID NO 64)

MSLVVQEQGSFQHILRLNLTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLERLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YDR486C, 1289 bp, CDS: 501-1289 (SEQ ID NO 65)

ACTGCATACACAATAACTGTAGATGTAGCCCAAGGCACTACCACAGGTATTTCTGCTCAC
GACAGGTCGATGACTTGTAGGGCTCTTGACAGACTCTTCCTCTACGCCAAAATCATTTTAA
AAACCAGGGCACATCTGTCCCTTGAGAGCCGCTGATGGCGGTGTTTTGCAGAGAAGAGGC
CACACTGAGGCCGGTGTGATTTGTGTAACTAAGTGGACTAAGTCCCGTCGCTGTTATT
GGCGAATTGGTTAACGATGACGAACAAGGAACATGATGAGATTAAATGACTGCCAAGCG
TTTGGTAAGAAACATGGCATTCTTTGATCTCCATCGAAGAATTGGCCCAATATTTGAAG
AAATAATCTGGTGAACATTTTCTCCATTCTATCACAACAGACTCACACATATATAC
ATGTATATATTTGTAACCTTTGTATATATCTTTTGTGTTTTTGACCTTTTCTTCTCTATG
TTTTTCAGCCATACAAAATATGGGATTTTGTAGCAAGAGAAAAAGTACATCTAAAAAAG
TAGTAATAGGAGGAAGCCAAGATTGGTTGAAACACAGTTATAAACTCTTCAAGGCAATTA
TGAACAGGATTTTCGGATATGGGAACAAAAGAGCCATGATCAGCTCTTACAAGAGTCGA
ATCAGTCCATGAATCAGGCCCAACAATCACTATCGAACAGAATATCCCAGTTAGATACTC
AAATCGCCCAGTTAACTTCCAGCTGCAAAATATTCAAAGAATTGCAAAGATCAAACA
ACAAGCAACCCTCGTTAAGAAAACAGGCTTTGAAGATTTTAAATAAACGTAAACAGTTAG
AAAATATGAAGGATTCTTTAGATTCTCAATCCTGGTCCATGACGCAAGCCCAGTTAAACA
ATGATAACTTACAGAACACAATGATCACTATAAACGCACTAAAGCAAACAACAATGCCA
TGAAGGCTCAATACGGCAAGATAAATATCGACAACTACAGGACATGCAGGATGAGATGC
TGGATTTAATAGAACAAGGGGATGAGCTGCAAGAAGTCTTGGAATGAATAATAACAGTG
GCGAGCTCGACGACATTAGTGATGCAGAGCTGGATGCAGAGCTGGATGCTCTGGCACAAG
AGGATTTCACTTTGCCAACCAGCGAAAACCTATTAGGTAACGATATGCCCAGTTACTTAC
TAGGTGCGAATGCGCCACCGGCTTTTATTGATGAAGAGCCAACTTAGATACTGAAGACA
AAAATAAAGCTTTAGAAAGCGCTCAGTGA

YDR486C, 262 aa (SEQ ID NO 66)

MGFLAREKVHLKKVVIGGSQDWLKHYSYKLFKAIMNRIFGYGNKKSHDQLLQESNQSMNQA
QQSLSNRISQLDTQIAQLNLFQLQNIQKNLQSRNNKQPSLRKQALKILNKRKQLENMKDSL
DSQSWSMTQAQLTNDNLQNTMITINALKQTNAMKAQYGKINIDKLQDMQDEMLDLIEQG
DELQEVLAMNNNSGELDDISDAELDAELDALAQEDFTLPTSENSLGNDMPSYLLGANAPP
AFIDEEPNLDTEKKNKALESAQ

YDR471W, 1295 bp, exon1: 501-531, intron1: 532-915, exon2:
916-1295 (SEQ ID NO 67)

GGCAAATCAATTAAAATTCCTTTTCTCTCTACCTTTGCTAATATTAAAAACCATAGTTGT
AAAGGGTACTTAATGCTATATTCCTGTAAAGTTTCCTATTTACCTTGTTTTTCCAATT
CTTACCAATTTGAAGACTATGTTTTTAAACACCCAATCATTTTCCACCCACACATATATT
ACCCTTTTTTTGGGTGAAGAGAAGTAGTATTTTGTGTTTTTCATGGGAGTGGAAGTCCTTTC
AAAATAATCCGAGCAGTAGTGCTGTCTAGGCGGAGATTATTGAAAGTCGGCATTGGCTG
CAGCTAGCGTTTTGTTTTTGGTACTACCTGTCAAACCCGGCGTCTGCCTAGATTGCGCGG
AGGGTACGTTGAAACTTTTGCCTTTCCACGTCAGTTTATAATATCAAAGCAGCAATATA

CACATTTAATGGTTTGCCCTTAGTGACTATTAGGGCGTTTTGGTGAAAAGAAAGAGTCGC
TCAAAGAAATCAATATAACCATGGCTAAATTTTTGAAAGCAGGTAAAGTTGGTACGTAAA
TTTAACAGAGCAAACGCTCTAATTAAGATATCGAATAAAAGGGGACTTTCAGGTGCATAA
GATGGGAAATTGTACAATCTGAGGGACAAACAATATGGAAAGCAGTACATGATTGTATTG
TCATTGTAGGAGGTACCAATTGTGCCAGTAAAAAAGAGAGGGCCCGGGGAGCACCACATT
CACGACCAATCGTGTGATCTGCAAAAAGGCACATGGAAAATGTAATTTATCAGTGTTT
AACACTGAGTTGAACAGATAGCTATCTAATCAATGTTAACTTTCCAGGGAACAAAAAGCT
AAATCCACTTCTCTTTTATTTCAAAATATCATTAGAAATAGAAAAATTTACTAACAAATT
TTCGTATTATCGTAGCTGTGCTTGTTCGTGGTTCGTTACGCTGGTAAGAAGGTTGTGATCG
TTAAGCCACACGATGAGGGTTCTAAATCTCATCCATTCGGTCACGCTTTGGTTGCCGGTA
TTGAAAGGTACCCATCAAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTCGCTAAGAGAA
CTAAATCAAGCCATTCATCAAAGTCGTCAACTACAACCACTTATTGCCAACCAGATACA
CCTTGGATGTTGAAGCTTTCAAGAGCGTTGTATCTACAGAGACTTTTGAACAACCATCCC
AACGTGAAGAAGCCAAGAAGGTTGTAAAGAAGGCATTTGAAGAAAGACATCAAGCTGGTA
AAAACCAATGGTTCTTCTCCAAGTTGAGATTCTAA

YDR471W, 136 aa (SEQ ID NO 68)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYP SKVTKKHGAK
KVAKRTKIKPFIKVVNYNHLLPTRYTL DVEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YDR499W, 2744 bp, CDS: 501-2744 (SEQ ID NO 69)

TAACAATAGAAAAAATACACACACATTAGATTGGAATTAGAGCTTAAGTGGTACAACT
AGGGCTAATAAAGAGGTAACGGTCGGTTCTCTACTAAGGTTTCGTATTGTGTGGCACCGAT
GTTAAGCACTTTTAAGCGGAATAACTCGAGTGGAATTTTATGTTTATGTTAGGTTTACC
TTGAATTTTTTTAAAAAAAAGAGTCAGACAGGCTCGCTCTTCTCTACTAAATATTAGG
AGCAAAGCAGTAAAAAGTCTCTGAATAAGGATAGTAACCTGTAGTAACCTCCAAATTTAT
CTTACAAAGAGCTATTAGTATCTTGGTTCTTCTATTTTCTTTCGATTATTGGTGATTTTTC
CCGCCTCTAGCCAAATCCGAGCGTTCATCGATTTTTTGGGGAAACAGCACATGCAATA
AAATAAAAAGCAAACAAATACGCGATAGTGCACGAAACGTCAACACAATCATCAAATCT
TTTGATATTTCTATTATAGATGAGACGAGAAACGGTGGGTGAATTTTCTTCAGATGACG
ATGATGATATTCTTTTGAATTAGGCACCAGGCCTCCAAGGTTTACTCAAATACCGCCAT
CATCAGCAGCATTACAAACACAAATCCCCTACTTTGGAGGTTACAACGACCACATTAA
ACAATAAACAGAGTAAAAATGATAACCAACTGGTTAACCAACTGAATAAAGCTCAAGGTG
AAGCAAGCATGCTTCGTGATAAAATAAATTTTGAACATTGAAAGGGGAAAAGGAAAAGA
ATATTCAAGCCGTCAAAGTTAATGAATTGCAAGTCAAGCATCTTCAAGAGTTGGCTAAAT
TAAAACAAGAATTACAGAACTGGAAGATGAGAAGAAGTTCTTACAGATGGAAGCGAGAG
GAAAATCGAAAAGGGAAGTTATTACGAATGTAAAACCAACCGTCAACAACATTATCAACAA
ACACAAACACTATAACGCCAGATTCGTCTCTAGTTGCAATCGAAGCAAACCTCAATCAC
CACAATCAAAAAACGTAAGATAAGTGATAATTTACTGAAAAAATATGGTTCCCCTAA
ACCCAAATAGGATTATTCCCGATGAAACGAGTTTATTTCTAGAGTCAATATTACTTCATC
AAATAATAGGCGCTGACCTGAGCACAATAGAAATATTAAATAGATTGAAGCTTGACTACA
TCACAGAGTTTAAATTTAAGAATTTTCGTCAATTGCTAAAGGAGCCCCCATAGGGAAGTCCA
TAGTTTCTCTACTTTTGGGATGTAAAAGACGTTGACCCTCGACAGGTTTCATAGATACTT
TGCTAGAGGATATAGCTGTTTTGATCAAGGAAATATCAGTTCATCCAAATGAATCGAAAT
TAGCTGTCCCATTTCTCGTTGCATTGATGTATCAGATTGTACAATTTTCGTCTAGTGCCA
CTCATAATTTAGCACTGAAGGATTGTTTTCTTTTATTTGCGATTTAATAAGAATCTATC
ATCATGTATTGAAAGTACCGATACATGAATCAAATATGAATTTGCATGTAGAACCCTCAGA
TTTTCCAATATGAACGTATAGACTATTTGATAATTTTCGTATTCCTTTGATCTCCTAGAAG
GTATATTAAGGGTACTGCAGTCGCATCCTAAGCAAACCTTATATGGAATTTTTTGTATGAAA
ATATTCTAAAATCATTTGAATTTGTCTACAACTAGCACTAACCATTTTCATACAAGCCAA
TGGTAAATGTAATATTTAGTGCAAGTCGAGGTCGTTAATATTTATCACTAGTATAATATTAA
ATATGGACAATTCCTCAGATCTGAAATCCTTGATAAGCGGTAGTTGGTGGAGAGATTGTA
TTACAAGATTATACGCTCTTTTGGAAAAGGAAATTAAGAGTGCGGACGTATATAATGAAA
ATGTGGATACTACAACCTTTCATATGTCGAAGTACCATGACTTTTTTGGGTTAATCCGAA
ATATAGGTGATAATGAATTGGGAGGATTGATATCAAAGCTGATTTATACTGACCGATTGC
AAAGTGTCCCAAGGGTAATTTCTAAAGAGGATATTGGGATGGATAGCGACAAATTCCTG
CCCCTATAATAGGTTACAAGATGGAATAATGGCTTTTGAAGTTAAAGATGAAGTTTTAA
ATATTTTTGAAAATTTATTAATGATCTATGGAGACGATGCGACCATAGTAAATGGAGAAA
TGCTCATCCACTCCTCTAAATCTTATCCAGGGAGCAAGCGTTAATGATAGAAAGGTACG

TGGGACAAGACTCCCCGAACCTTGGACCTCAGATGCCATCTTATTGAACATACTTTAACCA
TAATATATAGGCTATGGAAAGACCATTTCAAACAATTGCGTGAAGAACAATCAAGCAGG
TAGAAAGCCAATTGATTATGTCACCTATGGAGGTTTCTCGTATGCCAAACCGAAACTGTGA
CAGCAAACGAAAGAGAAATGAGAGATCATCGACACCTTGTAGATAGTTTGCATGATCTGA
CGATAAAGGATCAAGCCTCTTATTACGAAGATGCCTTTGAGGATTTACCAGAATATATCG
AAGAAGAATTGAAGATGCAATTGAATAAAAGAACGGGGAGAATAATGCAAGTAAAGTACG
ATGAGAAATTTCAAGAAATGGCAAGAACTATTCTTGAGTCAAAATCATTCGATCTAACCA
CACTAGAGGAGGCCGATTATTATATATCTCAATGGGACTGTAA

YDR499W, 747 aa (SEQ ID NO 70)

MRRETVGEFSSDDDDILLELGTRPPRFTQIPSSAALQTQIPTTLEVTTLNNKQSKN
DNQLVNQLNKAQGEASMLRDKINFLNIEREKEKNIQAVKVNELOVKHLQELAKLKQELQK
LEDEKKFLQMEARGKSKREVITNVKPPSTLSTNTNTITPDSSSVAIEAKPQSPQSKKRK
ISDNLLKKNMVPLNPNRIIPDETSFLLESILHQIIGADLSTIEILNRLKLDYITEFKFK
NFVIAKGAPIGKSIVSLLLRCKKTLTLDRFIDTLLEDIAVLIKEISVHPNESKLAVPFLV
ALMYQIVQFRPSATHNLALKDCFLFICDLIRIYHHVLKVPIHESNMNLHVEPQIFQYELI
DYLIISYSFDLLEGILRVLQSHPKQTYMEFFDENILKSFEFVYKLALTI SYKPMVNVIFS
AVEVVNIITSIIILNMDNSSDLKSLISGSWWRDCITRLYALLEKEIKSGDVYNENVDTTL
HMSKYHDFGLIRNIGDNELGGLISKLIYTDRLQSVPRVISKEDIGMDSDKFTAPIIGYK
MEKWLLKLKDEVLNIFENLLMIYGDATIVNGEMLIHSSKFLSREQALMIERYVGQDSPN
LDLRCHLIEHTLTIIYRLWKDHFQQLREEQIKQVESQLIMSLWRFLVCQTETVTANEREM
RDHRHLVDSLHDLTIKDQASYEDAFEDLPEYIEEELKMQLNKRTGRIMQVKYDEKFKQEM
ARTILESKSFDLTTLEADSLYISMGL

YDR507C, 3929 bp, CDS: 501-3929 (SEQ ID NO 71)

CTCTTTAAATATTCTATGTACTTTGTGCAAACATCATTGTCATCACATAAATGCATTCCT
ACTATTACTAACTTGAACCTTCACTTCACTGGAAGAACTGGGTATTCAAGGTAAAGAAAT
CATTTGTTTTGCGCCAAGTTTCGTCTGACAAGAATTTTTATTATTATTTCCTACTTTTC
ATCGAAGGAAACGCGTCAAATCCATTTCGTTACTACGCGCAATCTGCGTTATTTCCTTTTT
CGGCATACCATCGCGAAATATCAACGGCCACACCATAGATTCTTTTGATGTTAAATTAA
AAGCGACTGAATGAAGTGCACACATTTTTTATTCTTCTTGATTTTCTTTTCTATTTTGT
TTTGCTTTCTCTTCTGTCGACAACGTCTCAACTGTACTCACCATTAGTATTCTCGAAGGC
TTTAGCAGACTTGTGAATAATTAATTGCCCACTTTGATCAAGAAAGATATTCGCAGCACA
ATACAATAATAACATTCAAAATGGCAATCAATGGTAACAGTATTCCTGCCATAAAGGATA
ATACCATCGGTCCATGGAACTAGGTGAACTCTCGGTCTAGGGAGCACTGGTAAAGTCC
AGCTTGCTCGTAATGGATCCACAGGACAAGAGGCGGCAGTTAAGGTAAATATCAAAAGCAG
TATTCAATACCGGTAATGTCAGCGGTACTTCGATTGTTGGCTCCACCACCCCAAGTGCTC
TACCATATGGTATAGAACGCGAAATAATCATTATGAAGTTGTTAAACCACCCCAATGTGT
TACGTTTATATGATGTCTGGGAAACAAATACAGATTTATACCTTGTTTATAGAATACGCGG
AGAAAGGTGAGTTGTTCAACTTATTGGTTGAGAGAGGTCTCTGCCAGAGCATGAAGCTA
TCAGGTTTTTTAGACAAATTATTATTGGTGTGTCGTACTGTCATGCGTTGGGTATTGTCC
ATCGTGATCTAAAACCGGAAATCTATTATTAGATCATAAATATAACATCAAGATTGCAG
ATTTTGGTATGGCTGCTTTGGAACTGAAGGAAAGCTACTGGAGACGTCGTGCGGATCAC
CACATTATGCTGCACCAGAAATTGTATCTGGTATACCGTATCAAGGTTTCGCAAGTGATG
TGTGGTCATGCGGTGTGATCCTATTGCCCCCTTCTTACTGGTTCGGTTACCCTTTGACGAGG
AAGATGGAAATATAAGAACACTATTACTTAAAGTTCAAAAAGGTGAGTTCGAAATGCCTT
CTGATGATGAAATTTGCGGTGAAGCTCAGGATTTGATTAGAAAAATCTTAACCGTTGATC
CTGAAAGAAGAATCAAGACCAGAGATATACTCAAACATCCGCTATTACAAAAATATCCAA
GTATAAGAGATTCTAAAAGTATTAGAGGCTTACCAAGAGAAGACACATATCTCACGCCAT
TATCAGAAAGTAATTCTTCTATTGACGCTACGATTTTGCAAAATTTAGTAATATTATGGC
ATGGAAGAGATCCTGAAGGAATTAAGGAAAACTAAGAGAACCTGGCGCTAATGCAGAAA
AGACATTATATGCACTACTGTATAGATTTAAGTGTGACACTCAAAAAGAGCTTATTAAGC
AACAGCAAGTTAAGAAGAGGCAGTCAATTAGTAGCGTTTCTGTTTCCCCATCTAAAAAAG
TATCGACAACCTCCACAACGCAGAAGAAATAGAGAATCTTTAATTAGTGTAACATCTTCTC
GTAAAAAGCCAATATCCTTCAACAAATTCAGTGCCTCCAGTGCCTCCTCCAGCAATCTAA
CTACACCCGGTTCTTCAAAACGCCTTTCAAAAACTTCTCTTCAAAGAAGAAATTATCTA
CAATCGTTAACCAATCTTCTCCAACACCAGCATCACGTAATAAAAGAGCTTCGGTTATAA
ATGTGGAAAAGAATCAAAAAGAGCCTCTATCTTTTCTACTACCAAGAAGAACAAGAT
CTTCTAGATCTATCAAGAGAATGTCATTGATACCAAGCATGAAACGTGAATCGGTGACAA
CAAAATTAATGTCAACATATGCGAAATTGGCAGAGGATGACGATTGGGAATACATTGAGA

AGGAAACAAAGAGAACGAGCTCAAATTTTGCAACTTTGATAGATGAAATTTTGTAGTACG
AAAAGTACGAACAAATAAGGAAAGAGAAGGAAGAGCTAGAACGTAAAGTGAGAGAAGCAA
AAGCACGTGAAGAGCTGGAACGTAGAAGACGTAAACAAGAAGAAAAAGAACGTGCAAGAA
AATTACTAGAAAAGGAAGATCTGAAAAGAAAACAGGAGGAAGTCAAGAAGCAAATTGAAA
TTGATATAAGTGATCTAGAGCAAGAGCTGTCCAAACACAAAGAGGAAAAACTGGATGGTA
ATATTAGATCTATCTCTGCTCCTATGGAAAATGAAGAGAAAAATATCAATCATTTGGAGG
TTGATATTGACAATATTCTCCGTCGCCGCAACTTTTCTTTACAACTAGACCTGTGTCAA

GGCTTGATCCGGGTATAATGTTCTCCAGTCCAAGTGAAGTAAGTCCAGTGGAAACCAA
AGAGAACAGAAAATGAAAGACTTACAACAGAAAAGAAAATTTTAGAACTATCAGAAGAT
CAAAATTTCTTGGGTTTCATCATTTAATATCGATAAAGAGTTGAAATTGTCTAAAATGGAAT
ATCCAAGTATAATTGCACCACAAAGATTGTCAGAGGAGCGAGTGGTGTGAGATTCTAATG
ATGGATATGAATCTTTGATCCTCCCGAAGGATGGGAATGGCGTATCTCAATTAAAGGATA
GTACCGCAACAACTGCTCCCGTCTCTGATGGTAGGTTGAGGAAGATCTCTGAAATTAGAG
TACCACAATTTACTAGAAAATCAAGGCATTTTAGTGAGTCCAATAAAAGGCTATCTGTCC
TGTCGATGTACTCTACCAAGGAGTCGTTTACCAACTTGGTTGATATTTTGAAAAACGGTA
ACCTTGATGTCAATAACCAACAAAGCCAAAGAATTCCAACACCAAGAAGTGCGGATGATT
CAGAATTTCTTTTGAAGTGTCAACGAAGAAGCTGAATATACAGGAAATAGTTTGAACG
ATGAGAGATTGTACGATGTCCGTGATTCCACTATCAAAGACAAATCCGCGTTAAAGCTGA
ACTTTGCAGATCGTTTAAATGGATCGAACGAAGCGAAACAACTGATAACTTACATCTTC
CGATCCTTCCCTCCGCTTAATGGTGACAATGAATTGCGTAAACAGAATAGCCAAGAGGGTG
ACCAGGCACATCCAAAGATTAAATCGATGATACCAGAATCAGGCTCTTCTTCACATACTG
AAAAGGAAGAAGAAAATGAGGAAAAGGAAGAGAAAAAGCCAGAACAACACAAACAAGAAG
AGGATCAAGAAAAAAGAGAGAAAGTAGTAGATGATATGGAGCCACCATTGAACAAATCTG
TGCAAAAAATTAGGGAAAAAAATGCTGGCTCGCAGGCAAAGGATCATTCAAAGATCACT
TAAAAGAGCATAAGCAGGATAAAAAATACAGCAATTGGAAATGGTTCCTTCTTTAGAAAAT
TCTCAAATCTTTCGGACAAAACAATGGAATTGTATGCCAAGATTTCTGCAAAACAATTGT
TTAATGGTTTAGAGAAGCTGTTGCGTGGTTGGACTCAGTATGGTTTAAAAAATATAAAT
CGCACCCCAACAATCTGACCTTAACGGGTAAACTATCGAGTGATAATATATTCTCACTAC
GTTCAACACTCTTTGAGGTTAATATTTATCCGAGAGGTAAGATGAGCGTTGTGCAGTTCA
AGAAAGTTTCTGGTTCATTCAAAGCTGTCAAAAAGTTGGTCAATGAAGTTGAGAACGTCC
TGAATAAGGAAGGCGTTCTACAAAAATAG

YDR507C, 1142 aa (SEQ ID NO 72)

MAINGNSIPAIDNTIGPWKLGETLGLGSTGKVQLARNGSTGQEA AVKVISKAVFNTGNV
SGTSIVGSTTPDALPYGIEREIIIMKLLNHPNVLRLYDVWETNTDLYLVLEYAEKGELFN
LLVERGPLPEHEAIRFFRQIIIGVSYCHALGIVHRDLKPENLLLDHKYNIKIADFGMAAL
ETEGKLLLETSCGSPHYAAPEIVSGIPYQGFASDVWSCGVILFALLTGRLPFDEEDGNIRT
LLLKVQKGEFEMPSDDEISREAQDLIRKILTVDPERRIKTRDILKHPLLOKYPsirDSKS
IRGLPREDTYLTPLSESNSSIDATILQNLVILWHGRDPEGIKEKLREPGANAECTLYALL
YRFKCDTQKELIKQQQVKKRQSISSSVSPSKKVSTTPQRRRNRESLISVTSSRKKPISF
NKFTASSASSSNLTTPGSSKRLSKNFSSKKKLSTIVNQSSPTPASRNKRASVINVEKNQK
RASIFSTTKKNKRSSRSIKRMSLIPSMKRESVTTKLMSTYAKLAEDDDWEYIEKETKRTS
SNFATLIDEIFEYEKYEQIRKEKEELERKVREAKAREELERRRRKQEEKERARKLLEKED
LKRKQEEELKKQIEIDISDLEQELSKHKEEKLDGNIRSISAPMENEENKINHLEVDIDNIL
RRRNFSLQTRPVSRLDPGIMFSSPTEEVSPVEPKRTENERLTTEKKILETIRRSKFLGSS
FNIDKELKLSKMEYPSIIAPQRLSEERVVSDSNDGYESLILPKDGNGVSQLKDSTATTAP
VSDGRLRKISEIRVPQFTRKSRHFSSESNKRLSVLSMYSTKESFTNLVDILKNGNLDVNNQ
QSQRIPTRPSADDSEFLFETVNEEAETGNSSNDERLYDVGDSTIKDKSALKLNFADRFN
GSNEAKQTDNLHLPLPPLNGDNELRKQNSQEGDQAHPKIKSMIPESGSSSHTKEKEENE
EKEEKKPEQHKQEEDQEKREKVDDMEPPLNKSQKIREKNAGSQAKDHSKDHLKEHKQD
KNTAIGNGSFFRKFSKSSDKTMELYAKISAKQLFNGLEKLLRGWTQYGLKNIKSHPNLTL
LTGKLSSDNIFSLRSTLFEVNIYPRGKMSVVQFKKVSFSKAVKKLVNEVENVLNKEGVL
QK

YDR515W, 1844 bp, CDS: 501-1844 (SEQ ID NO 73)

GAGTTGAATCTATGCGTAACCATTTTGAAGTACCGCTTCGTATGCTTTCTTGCACTTTGTG
GAGCTACTCATACAATAGCTTATAATCTGTGTAGTCAAAGTATATACTAGGCAAATTACT
AGTAAATGCAGTATTCATATGTCCTCAAACCGTTTTTTGTCAGTATGTTATTGATCCATCG
AATCAAAATTTTTTACCAGCAAGAGAAAAAGATCTTACTATTTTGTGCTTATGAAAAAA

TTAGTAAAAGTAAAGCTGGAAGCACATACAAGCGCAGCTGAATCACAAAGGAAAATTGGC
ACATCCTTGGTTGACACTTGTCTATTTATTTAAAAGGTTTTTAAAAAGTAGTGTTTCAGCAGT
TCTATCATATTTTTTTTATTTAAAAAAAATACTGAGAGGAAGCGTATTGTTAAGACACAA
TTTAGGGTGGCGTTAAATAAACGAGAGAGCCCAAAAATATAACCAAGATAAAGAAAATCA
ATCATAAAGTGAATTCAAAAATGTCATCGCAAAACCTCAATGATAATCCAAAAAATACAT
CCTCAGCAGCTGAAGATAAGAAGAAACAACTTCATCCTTAAAGTTGGCACCAATACCAA

CCACATCGCCATGGAAATCATCTTCGCCAGATAGCAATACAGTAATTCCTGTAGAGGAAC
TAAGAGATATATCAAAGACTGCAAAGCCAAGTAAAAATGGTTCGGGGTCAATTAAATTAA
CAAGCAATACCAAATGGACTCCAATTACGCCGTCTGTTATAATCTCAGGTTCCAAGGACA
CAAATTCAAAGTCAGGAAAGAACTCTAAAAATTTCTAAGACTAATAAAAAAATGAAAAAGC
GTGGCAAATATAATAACGATATCAATAAAAAGGACTTTAACGGTCAAACCAACAGTACAT
CGGAAATAAGTAACGTTTCCAATCTTGAATCCAAACCTTTAGATGCTAACGCTAAAGTAA
ACATACATTCAAGCTCAGGAGCAACTGCCAATGGGAATATAAAGAGGATAACAAACAACA
ACAATTCAACCAACGGTAGACAATCAAGAAATTATCAAAACAGGAATGGCAAAACAAGAT
ACAACAACAATAGTAGACACAGTCAGGCGGCTAATAATGCCATCTCCTTCCCAAATAATT
ATCAGGCTAGACCTGAATATATTTCCAATGCCAGCCACTGGTTGAACAACAATTCAAGAA
ATAGCTATAAACAACCTGTCATACTTCCGTCAACAGCAGTATTATAATAACATCAACTATC
AACAACAATTGCAAACACCATATTATTACTCAATGGAACCTATTTTTTAAATCTATCGAAA
GTATCAAAAACCAAATTGAATTTCTATTTTAGTGAAGAGAACTTGAAAAACAGATGAATTTT
TAAGATCTAAATTCAAAAAAGCCAATGACGGATTATCCCCATGAGTTTGATAGGGAAAT
TTTACCGTATGGTTAATTTATCTCTTGGTGGAGACCCAAATTTAATTTTGGCATCTATGA
GAGAAGTTTTACAACATAAAGAAACAAACCATTGGAATTTGCCCTTGGAAGCATAGAAG
GTGCTCAGAAGAACATGGCAGATGATTTCAATCCATTGGAAAACCTATTTTATTAGGCGCG
AAAATTGGGCTGAATACGCTATGGAAAGTAATTTTGATGAAAATGATGACGAAACTGAAA
AATACAACATTGAGAAACTATTGGGACCGAACGATTTAGACAATTATTCCTTATATGGGCT
ATCCAAACTTCTTTCCAGTAATGAAAATGGGAAAAAGAGTCAGAGCTATGACCAAGGTG
AAATTAGCAGGCAGTTTGAACAAAACCTTACAAATAAATGATTAA

YDR515W, 447 aa (SEQ ID NO 74)

MSSQNLNDNPKNTSSAAEDKKKQTSSLKLAPIPTTSPWKSSSPDSNTVIPVEELRDISKT
AKPSKNGSGSIKLTSTNTKWTPITPSVIIISGSKDTNSKSGKNSKNSKTNKKMKKRGKYNNND
INKKDFNGQTNSTSEISNVSNLESKPLDANAKVNIHSSSGATANGNIKRITNNNNSTNGR
QSRNYQNRNGKTRYNNNSRHSQAANNAISFPNNYQARPEYIPNASHWLNNNSRNSYKQLS
YFRQQQYYNNINYQQQLQTPYYYSMEPIFKSIESIKNQIEFYFSEENLKTDEFLRSKFKK
ANDGFIPMSLIGKFYRMVNLSLGGDPNLLILASMREVLQHKETNHLEIALGSIEGAQKNMA
DDFNPLENYFIRRENWAEYAMESNFDENDDETEKYNIEKLLGPNDLDNYSYMGYPNFFPS
NENGKKSQSYDQGEISRQFEQNLQIND

YDR518W, 2054 bp, CDS: 501-2054 (SEQ ID NO 75)

GCAGCAGGGGCAAGATGACAACCCTGTTCTGTTCTGTTCCAGTAGAATCTGAGACGGC
TTTTGTGCCATCAGCATTACAGCACCACCGGTGCCAACAAAGAAGAAATCAAAAAATAA
AAAGGGTACCCAGCCATTGGCAATGGATGACTATTTTAATGAAGGCAGAGATAAGTCATC
TACCGCTGCGAAGTCAGCAGAATCTGACATCCTCGCCCCACCACCACAAAAACAGTCATC
CTCTGATTAACCTTTCCTGGTTAGTCTTTTGGTTTTGTTTTCATAGCAAAATTAAATATATA
TATATAAGCTTGCTTTCCCTTCAAACACGTAACGATAGTTGGCAATGTACGAAAAGTA
CCGAGACTTTTTTTCAAAGGCACGCGTGTCCTTTTTTTGTTAAGACAATAGATATTTTAGC
ATTCAGAAAGTTTCAATTTCCAAGACTTGACGTTTCAATTATATGGCAATCTCCCAACAA
GCACCCGCTCATATAATACCATGCAAGTGACCACAAGATTTATATCTGCGATAGTCTCGT
TTTGCCTGTTTGCTTCTTTACGTTGGCTGAAAACAGCGCAAGAGCTACGCCGGGATCAG
ATTTACTCGTTCTAACAGAGAAGAAATTTAAATCATTCATCGAATCTCATCCGTTAGTCC
TCGTGAGTTTTTTGCTCCATGGTGTTTGCAATCTCAGATCTTACGCCCTCACTTAGAAG
AGGCCGCCTCTATTTTAAAGGAGCATAACGTCCAGTTGTTCAAATTGATTGTGAGGCTA
ACAGTATGGTTTGCCTGCAACAACTATAAATACCTACCCAACCTTGAAAATCTTTAAAA
ATGGTCGTATTTTTGATGGTCAAGTCTATCGCGGTGTCAAGATCACCGATGAAATCACTC
AGTACATGATTCAGCTATACGAGGCTTCTGTCAATTTATTTAAATTCCGAAGATGAAATCC
AACCATACTTGGAATAATGCAACTTTACCAGTAGTAATAAACAGAGGCTTGACAGGCTTGA
ATGAAACGTATCAAGAAGTCGCACTGGACCTTGCTGAGGATTACGTCTTTTTTATCCCTTC
TAGATTCAGAAGATAAGTCATTATCAATCCACTTGCCAAACACTACAGAACCAATTCTGT
TTGATGGAATGTAGACTCTTTGGTCGGAAATTCCGTTGCTCTAACTCAGTGGTTAAAG

TGGTAATTTTACCTTACTTTACCGACATCGAACCTGATCTCTTCCCCAAGTACATTTCTA
GCAATTTGCCGTTGGCTTACTTCTTTTATACTTCTGAGGAAGAATTGGAAGATTACACTG
ATCTTTTTCACGCAGTTAGGTAAGGAAAATCGTGGCCAAATAAATTTTCATTGCATTAAACT
CTACAATGTTCCACACACCACGTTAGATTCTTAAATATGAGAGAACAGTTCCCATTTATTTG
CTATCCATAATATGATCAATAATCTGAAATATGGTTTACCACAACCTACCAGAAGAAGAGT
ACGCGAAATTAGAAAAACCACAACCACTAGACAGAGATATGATCGTTCAGTTGGTAAAAG
ATTACCGTGAAGGTACTGCCAAGCCAATTGTTAAGTCAGAAGAGATTCCAAAAGAACAAA
AGTCCAATGTTTATAAAAATAGTTGGGAAGACACATGACGACATTGTTTCATGATGATGACA
AGGATGTCCTTGTCAAATATTACGCGACATGGTGTATTTCATAGTAAAAGGTTTGCGCCTA
TTTACGAAGAAATTGCAAATGTCTTAGCATCTGATGAATCTGTTTCGCGATAAAATCTTGA
TCGCCGAAGTAGATTTCAGGGGCAAATGATATCTTAAGTTTTCTGTGACAGGATATCCAA
CCATTGCTTTGTATCCTGCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAA
ATTTGGAAGATGTTTTCGAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGG
CAATTTATGATAAATTGCACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTAC
ATGATGAATTATAA

YDR518W, 517 aa (SEQ ID NO 76)

MQVTRFISAIVSFCLFASFTLAENSARATPGSDLLVLTEKKFKSFIESHPLVLVEFFAP
WCLHSQILRPHLEEAASILKEHNVPVQIDCEANSMVCLQQTINTYPTLKIFKNGRIFDG
QVYRGVKITDEITQYMIQLYEASVIYLNSEDEIQPYLENATLPVVINRGLTGLNETYQEV
ALDLAEDYVFLSLLDSEDKSLSIHLNPTTEPILFDGNVDSL VGNSVALTQWLKVVLIPYF
TDIEPDLFPKYISSNLPLAYFFYTSEELEDYTDLFTQLGKENRGQINFIALNSTMFPHH
VRFLNMREQFPLFAIHNMINNLKYGLPQLPEEYAKLEKPQLDRDMIVQLVKDYREGTA
KPIVKSEEIPKEQKSNVYKIVGKTHDDIVHDDDKDVLVKYYATWCIHSKRFAPIYEEIAN
VLASDESVRDKILIAEVDSGANDILSFPVTGYPTIALYPAGNNSKPIIFNKIRNLEDVFE
FIKESGTHHIDGQAIYDKLHQAKDSEVSTEDTVHDEL

YDR519W, 908 bp, CDS: 501-908 (SEQ ID NO 77)

GGGGCAAATGATATCTTAAGTTTTCTGTGACAGGATATCCAACCATTTGCTTTGTATCCT
GCCGGAATAACTCTAAGCCTATTATCTTCAATAAAATTAGAAATTTGGAAGATGTTTTC
GAATTTATCAAGGAATCAGGTACACATCACATTGACGGCCAGGCAATTTATGATAAATTG
CACCAGGCCAAGGATTCTGAAGTGTCTACTGAAGATACCGTACATGATGAATTATAATCA
ATAAATAAAGCATATATAATGCACATTTTTAACATCTGATTACTCGCATCGTTTCTGGAA
GAAAATAGCTAATATTCGTTATTTATGGCATCACGATTATTCTCACCAGTTACCCGTTTA
TGCTCTTGAAGAGATTTAGCATTACTGCCAGCGCATCTTCAAATACAGGTTTATATGAGA
CCCATTACTATAACCTAAGAAGAGAAAAAGGAGTGCTTTCGTTTTCAATCACATTCTAG
TTTACAGTAATTGAGTCTCGATGATGTTTAATATTTACCTTTTCGTCACTTTTTTTTCCA
CCATTCTTGCAGGTTCCCTGTCAGATTTGGAAATCGGTATTATCAAGAGAATACCGGTAG
AAGATTGCTTAATTAAGGCAATGCCAGGTGATAAAGTTAAGGTTTATTATACAGGATCTT
TATTAGAATCGGGAACTGTATTTGACTCAAGTTATTCAAGAGGCTCTCCTATCGCTTTTG
AACTTGCGGTTGGCAGAGTAATTAAAGGTTGGGATCAAGGTGTTGCCGGCATGTGCGTTG
GCGAAAAAAGAAAGCTGCAAATTTCAAAGTTCTTTGGCCTACGGAGAAAGAGGTGTCCAG
GCGTCATTCCTCCAAGTGCTGATTTGGTGTTTGATGTCGAATTGGTAGACGTGAAATCAG
CCGCCTAG

YDR519W, 136 aa (SEQ ID NO 78)

MMFNIYLFVTFSTILAGSLSDLEIGI IKRIPVEDCLIKAMPGDKVKVHYTGSLLES MTV
FDSSYSRGSPIAFELGVGRVIKGWDQGVAGMCVGEKRLQIPSSLAYGERGVPGVIPPSA
DLVFDVELVDVKSAA

YER102W, 1103 bp, CDS: 501-1103 (SEQ ID NO 79)

CGAGCTTGCCAGCATTTCCAATGCCCATCGTATTGTACTCAATGGTGAAACTTACCACCAT
ATTGTTAAAGCTATTATTTATGATTTTTACTTACCAAACATTGAAAGGAGACTGAACAC
ACCACGATAAAACGTATGTTCTGATACCCAGCAAATGAGAAAGTAGAAGGAGAAACCTAA
AAACCTGTGGCGGTCAAGACTGCTAGCAAGATGGATATTTAGATCATAAATTCTAACGCA
TGCATCCTGAGCAATGAAATCATGCAACCTAACATTTGAGGTTAATATATGAGAATTAAC
TAGCGTTGAGGAGGTACTGCAATTTAAAAGACCGAAGAATTATCGATGCAAGGAAAAATG
GGTCTAGGATGAATACGAGCAATTGAAATACATTTGGAATACCTTGTGAAAATATCACAT
ACTTTGCCTTCTATCTCGATGCGTTATTACAAGAAAATAGTTTTACTAACAAATTAACA
AAAATTAATAAGTGTAATAAATGGGTATTTCTCGTGATTCTCGTCACAAAAGATCAGCCA

CTGGTGCTAAACGTGCTCAATTCAGAAAGAAGAGAAAGTTCTGAATTAGGTCTGCAACCAG
CCAACACAAAAATTGGTGCTAAGAGAATCCACTCTGTCAGAACTAGAGGTGGTAACAAGA
AATACAGAGCTCTAAGAATTGAAACCGGTAACCTTTTCTTGGGCTTCTGAAGGTATCTCCA
AGAAGACCAGAATTGCTGGTGTTGTTTACCATCCATCCAACAATGAATTGGTTAGAATA
ACACTTTGACCAAGGCTGCCATTGTCCAAATTGATGCTACTCCATTCAGACAATGGTTCG
AAGCTCACTACGGTCAAACCTTGGGTAAGAAGAAGAACGTCAAGGAAGAAGAACTGTTG
CCAAGAGCAAGAACGCTGAAAGAAAGTGGGCTGCTAGAGCTGCTTCTGCCAAGATCGAAT
CTTCCGTTGAATCTCAATTCAGCGCCGGTAGATTATACGCTTGTATCTCTTCCAGACCAG
GTCAATCCGGTAGATGTGATGGTTACATCTTGAAGGTGAAGAATTAGCTTTCTACCTAA
GAAGATTGACTGCTAAGAAATAG

YER102W, 200 aa (SEQ ID NO 80)

MGISRDSRHKRSATGAKRAQFRKKRKFELGRQPANTKIGAKRIHSVRTRGGNKKYRALRI
ETGNFSWASEGISKTRIAGVVYHPSNNELVRTNTLTAAIVQIDATPFRQWFEAHYGQT
LGKKKNVKEEETVAKSKNAERKWAARAASAKIESSVESQFSAGRLYACISSRPGQSGRCD
GYILEGEELAFYLRRLTAKK

YER153C, 1265 bp, CDS: 501-1265 (SEQ ID NO 81)

ACCCTATATGGGAGGACAACCTCGCCCACTGTTTGGGTCGTGTTAGCGATAAGGTCCGAAG
TAGAAGCGGAAAGAGAAGGAGCTGAAGAGGTTAATTCATCGATGGAAGGCAACTGGGTTT
GGATTTCCGAGACATCGTTGGCATTGTTGGGCCGTCGAATTAAATCTTTTGGCCTGAAAAG
AGATCCATGACGGATGGGGCCGGGGCAATACTATGGTTTCGAGCGGTGGCCAGTCTGGAAG
AGGCAGCAAACCTTGACGTGACGAGTCGAGAGGTGAGTTTGAACATCGTCGGGGAGGTTA
TTCTGTGGCTCCGCTTGTACGTGAACAGATACGTATAGAGGGCGAGCCACTGGTTAAATT
TTTCATGGCTCGGATTACTTCCGTACTGCTGGCTAAAATCGAAATCTCGGCCTGCTGAGA
GTGTTTTGAGCAATCAAGGGAACATCTGAACGTGGAAGAGCAGACGAGGCATTAGCTCGA
ACATAAGAACGGAACACGTCATGTTGACTATCACGAAAAGACTGGTGACCACCGATGTGC
GGTCGCGAATACTGTTAAGCAGTTTAAACGGGAAAATGTCCGATGCACTGGCGCTGCTGC
GTCAGCAGCAGCAGACCAGCGTGATGTGGAGCTGCTGCACACGATGCTAGCGCGAGCCG
CTGCGCTTGCCCATGCCGACACTATAGCATAATGTGGTATCAGCATGTGATGCCACGCC
GGTTGCCAGTAGAGGGCCGCTGCTATGTGAAATGGCTGGCGTAGCATTGTACCAGGACA
GGCTCTTCTTACCCGCGCAGTTCTCCAGCACTACCAGGCGATGAATCGCGATCGTCGCA
CCAGCCCAGAAGATGAACCTGATTGAGTATGAGCTTAGACGGATTAAAGTCGAAGCGTTTG
CGCGTGGCACAATGCACTCCACGGCGCTCAGGGAAAAGTGGAAGGTATTCTTGCAGGAGA
TGGATACGCTACCAGGGCAGCCGCCATTAAGGCTGCGCGACTTCCCGCAAATGACCAAGG
CTATGGGCATAGCATTGATGCAGCAAGATGAGCAAGCAGCTGCCCTGGCGTTGTTTGGAC
GACAGCCCCTAGTGATAAAGAACGAATGGTCACTACCGCTACTACTGGCTGGTGTCTTT
GGCATGTTCCCGGCCCGAGCGCAGGCGCGACGTGTGCTGGCGGAGTTCCGTCAAAGTTATC
GCGGGCTGCCGCTGCTGGATGCCGAAGTACTGATAAAGAGAAGAGGATTTGAAATCAACA
CATAA

YER153C, 254 aa (SEQ ID NO 82)

MLTITKRLVTDDVRSRILLSSLNGKMSDALALLRQQQOTSVDVELLHTMLARAAALAHAD
TIAYMWYQHVMPRRLPVEGRLLCEMAGVALYQDRLFLPAQFLQHYQAMNRDRRTSPEDEL
IEYELRRIKVEAFARGTMHSTALREKWKVFLQEMDTLPGQPPLRLRDFPQMTKAMGIALM
QQDEQAAALALFGRQPLVIKNEWSLPLLLAGVLWHVPGPAQARRVLAEFRQSYRGLPLLD
AELVIKRRGFINT

YFL014W, 830 bp, CDS: 501-830 (SEQ ID NO 83)

GGACTAGAAGCCAAAAGCCAGAGGCGGTAAAAATAGCAAGACTAGAATATTGCTGGCATC
TGTTAAGGGGATATGTTGCAACTTGCAGGGGGCGGCACAAAATAACATAGAAACGTAGTA
AAGAGGGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGGAAAAGG
TGAAAGAAGGAAAGGTATACGCAAGCATTAATACAACCCACAAACACAGACCAGAAGCAC
TCTAGACGGAGAGTAAGTATGATCTACAGCCCTTGAAAATCGTTTGGTCAACTTTGAGGT
TCCGGTCGTCCCCCTCTTGATCTGAAAGGTCTTTCTCTAAATCTATATTAACGTATAA
ATAGGACGGTGAATTGCGTTCTACTTCCCTCAATTGCGTTTGATCTTATTTAATCTCTCTC
TAATATATAGAAAAAAAACCATCTGATTATTCGATAATCTCAAACAAACAACTCAAAAC
AAAAAACTAAATACAACAATGTCTGACGCAGGTAGAAAAGGATTCGGTGAAAAGCTT
CTGAAGCTTTGAAGCCAGACTCTCAAAGTCATACGCTGAACAAGGTAAGGAATACATCA
CTGACAAGGCCGACAAGGTCGCTGGTAAGGTTCAACCAGAAGACAACAAGGGTGTCTTCC

AAGGTGTCCACGACTCTGCCGAAAAAGGCAAGGATAACGCTGAAGGTCAAGGTGAATCTT
TGGCAGACCAAGCTAGAGATTACATGGGAGCCGCCAAGTCCAAGTTGAACGATGCCGTCG
AATATGTTTCCGGTCGTGTCCACGGTGAAGAAGACCCAACCAAGAAGTAA

YFL014W, 109 aa (SEQ ID NO 84)

MSDAGRKGFGKASEALKPDSQKSYAEQGKEYITDKADKVAGKVQPEDNKGVFQGVHDSA
EKGKDNAEGQGESLADQARDYMGAASKLNDAVEYVSGRVHGEEDPTKK

YFL015C, 995 bp, CDS: 501-995 (SEQ ID NO 85)

GACCTTCAGCGTTATCCTTGCCCTTTTTCGGCAGAGTCGTGGACACCTTGGAAGACACCCT
TGTTGTCTTCTGGTTGAACCTTACCAGCGACCTTGTCGGCCTTGTCAGTGATGTATTCCT
TACCTTGTTTCAGCGTATGACTTTTGAGAGTCTGGCTTCAAAGCTTCAGAAGCTTTTTCAC
CGAATCCTTTTCTACCTGCGTCAGACATTGTTGTATTTAGTTTTTTTGTGTTTGAGTTGT
TTGTTTGAGATTATCGAATAATCAGATGGTTTTTTTTTCTATATATTAGAGAGAGATTAA
ATAAGATCAAACGCAATTGAGGAAGTAGAACGCAATTCACCGTCCTATTTATACGTTTTA
ATATAGATTTAGAGAAAGACCTTTCAGATCAAGAGGGGGACGACCGGAACCTCAAAGTTG
ACCAAACGATTTTCCAGGGGCTGTAGATCTAGTTACTCTCCGTCTAGAGTGCTTCTGGTC
TGTGTTTGTGGGTTGTATTAATGCTTGCGTATACCTTTCCTTCTTTCAATTTCTACGTCA
ATGGGTTTTTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT
ATGTTATTTTGTGCCGCCCCCTGCAAGTTGCAACATATCCCCTTAACAGATGCCAGCAAT
ATTCTAGTCTTGCTATTTTTACCGCCTCTGGCTTTTGGCTTCTAGTCTTGTCCCAAGAG
CCAAGGGCCCGTCAACACGTCGTCATTGCTACCGCCAGCTGGCACCCACACATCACCGAC
CCTTTTTTTTCCATTTTTCGGCTGGGCCGTTAGTGGGATCCGCCCGCTCCCGGAGATTTTCA
CTTGGAATTTGCGCGTCCCCTTTTTTTTCTTCAATCTCTGACTCCCCCTACCTTCTCCCCT
TTTCTGTGTATCAAGAGGAAAAGAAGGAGAAAAGGAGAACTCCGAAAAATACCGAACAAG
AGGGTAACAGAAATGTGCATTTGGATGAGCGGGTAA

YFL015C, 164 aa (SEQ ID NO 86)

MLAYTFPSFNFYVNGFFSFLFLFLFLFPSLLRFYVILCRPLQVATYPLNRCQQYSSLAIF
TASGFWLLVLPRAKGPSTRRH CYRQLAPTHHRPFFSIFGWAVSGIRPLPEIFTWICASP
FFLHSLTPPTFSHF SVYQEEKKEKRRTPKNTEQEGNRMCIWMSG

YFR022W, 2702 bp, CDS: 501-2702 (SEQ ID NO 87)

CTGCCTTCCGTACGTACACAAACGCATACACAATATAGTTTATATAAACTCCTGCGTATAAT
CTATCCTTTTGCATAATATTTTCGTACCATTTATCTTGTGCGGTGTTTTATTTAAAC
AATAGAACTCGCCTAAAGGGGAAATTTTCGATATAAAAATTCAAAAAAATGGCTTTCATG
GATCGAGTATTTGTTTGTGCGAAAAAGGATCACTGGAGTGACGTTACTACGCTACGAAGCC
TCCTTCCGGCTTAGCCCTGTTGATTACGAATTTGGATCAGTTGGTATTTGATTCCTCGGA
AGAGTTAACTTCACGCGGGTAAATCACTTGTGATGCGGTATATTTCTCTATACGGCTAATA
GATGAATCAGGGTGTTTTAAAGTGCGTATAAACCTTTTGTCTATTTTCGTTTATATAATT
GGCGTTGATAAAGAGCCAATATCTATTGTTGCTACATAGAGGCAGCTCTCTTAGCAAAAT
AAAAATACAAAAAGTTTCGACATGGGCTTCAGTAGCGGTAAATCAACTAAGAAAAAGCCTC
TGCTTTTTCGATATCAGACTTAAAAATGTTGACAACGATGTAATACTCCTCAAAGGTCCTC
CAAACGAGGCCCCCTCGGTGCTTTTATCTGGTTGCATCGTTTTATCGATTAAACGAACCCA
TGCAGATCAAAGCATATCATTGAGACTTTATGGGAAGATACAAATAGACGTACCATTAG
AGAGGCCCCAGGACGCTAGTTCTTCGTCGTTGTCTTCATCGCCGCCAAAGATCAGAAAGT
ACAACAAAGTTTTTTTATAATTACGCATGGGATAATGTTAACCTCAAGGAGTATCTGAGTG
GTTTAAGAGGGCAATCTGGCCTTGCGGGCAGTAGCTCATCAAGTAATATCTTGGGCACTC
GCCAAAGAGCTCAGTCCACAAGTTCTTGAAGTCTTTAAAGGGGTCTCCTCACCCCTCTT
CATGTACTTTAGATAAAGGGCAACTACGATTTTCCCTTTAGTGCTATTTTGCCTGGTTCTG
TACCAGAGAGCGTAGAATCTTTGCCAAATTGCTTCGTGACATATAGCATGGAATCCGTTA
TTGAACGCAGCAAAAATTATAGTGATTTGATCTGTAGGAAAAATATTAGAGTTCTGAGAA
CCATTTCAACCGCAGCAGTGGAGTTATCAGAACTGTTTGTGTAGATAACTCATGGCCCCG
ACAAAGTGGAATTATCTATTTTCACTACCCAACAAAGCCGTAGCTATTGGTTTCAGCCACCC
CTATAAATATTTCCATTGTACCTCTTTCGAAAGGTTTGAATTTGGGCTCAATCAAAGTCG
TATTATTTGAGAATTATCAATATTGTGACCCCTTCCCTCCAGTAATTTCTGAAAATAGGC
AAGTGACAGAACTAAATCTTGAAGATCCCTTGAACGAGTCATCTGGAGAATTTAATGGTA
ATGGTTGCTTTGTAAATAACCCCTTTTTTTCAGCCTGATCATTCATCCAAGACAAGTGGG

AGATTGATACCATCCTGCAAATCCCGAACAGCTTATCAAACCTGTGTGCAAGATTGTGATG
TCCGCTCTAACATTAAGGTTTCGCCATAAGCTCAAATTTTTCATCATCCTAATTAACCCAG
ATGGTCATAAATCTGAGTTAAGAGCGTCTTACCGATTCAACTTTTTATTTACCATTTG
TGGCACTTTCAATAAAACCATTTGTCATCCTCGAATTTGTATTCGCTTTTTTAGCACCCTA
ACCAGAAAGACGAAAACCTCATCACAAGAAGAGGAAGAGGAATATCTGTTTTCTAGATCAG
CATCAGTCACAGGGTTGGAATTATTAGCGGATATGCGTAGCGGTGGCTCTGTTCCCTACCA
TTTCAGACTTGATGACGCCCCCAAATTATGAAATGCACGTATATGATCGTCTTTATAGCG
GTTCTTTCACTCGCACGGCTGTGGAAACGTCTGGAACATGTACTCCTTTGGGAAGCGAAT
GTTGCGACTGTCGAGGATCAGCAACAGGATTTAGAAGATTTACGTATACGGTTGACAAAAA
TTAGAAATCAACGTGACAATCTAGGGCTACCACCGTCTGCCTCGTCTGCTGCCGCTTCCA
GATCGCTATCTCCATTACTAAACGTTCCAGCACCAGAGGATGGCACGGAGAGAATCTTAC
CTCAGAGTGCTCTTGGTCCCAATAGTGGCTCTGTGCCAGGAGTACATAGTAACGTATCAC
CTGTTTTACTTTCAAGATCCCCAGCCCCAAGCGTGTACGCCATGAAGTGTACCAGTGC
CCTCGGGCTTAAATTATCCAGAGACTCAAACCTGAACAAGGTTCCATCGTATGGCAAGG
CAATGAAATATGATATCATTTGGTGAGGACCTTCCTCCTTCCCTACCTTGTGCGATACAAA
ATGTGCAACCAAGAAAACCCAGTAGGGTACATTCAGGAACCTTCGACAACATTTGTCAT
CTTCTATACCAACTAGCTTTTCATTCCTCTAGTTTTATGAGTAGCACTGCTTCCCCTATTT
CCATAATTAATGGCTCTAGAAGTAGTTCTAGTGGGGTATCTCTTAATACACTTAATGAGT
TAACTTCGAAAACCTTCGAATAACCCATCCAGTAATAGTATGAAAAGGTCACCAACAAGAC
GGAGGGCTACTTCTTTAGCTGGGTTTATGGGAGGTTTCTATCAAAGGGTAACAAACGAT
AG

YFR022W, 733 aa (SEQ ID NO 88)

MGFSSGKSTKKKPLLFDIRLKNVDNDVILLKGPPNEAPSVLLSGCIVLSINEPMQIKSIS
LRLYGKIQIDVPLERPQDASSSSLSPPKIRKYNKVFNYNVDNVLKEYLSGLRGQSG
LAGSSSSSNILGTRQRAQSTSSLKSLKGSSSPSSCTLDKGNYPFSAIPLGSLPESVES
LPNCFVTYSMESVIERSKNYSDLICRKNIRVLRTISPAVELSETVCVDNSWPKVDYSI
SVPNKAVAIGSATPINISIVPLSKGLKLSIKVLFENYQYCDPFPVISENRQVTELNL
EDPLNESSGEFNGNGCFVNNPFFQPDHSFQDKWEIDTILQIPNSLSNCVQDCDVRNLIKV
RHKLKFFIILINPDGHKSELRASLPILQFISPFVALSIKPLSSSNLYSLFSTTNQKDENS
SQEEEEEEYLFERSASVTGLELLADMRSGGSVPTISDLMTPPNYEMHVDRLYSGSFTRTA
VETSGTCTPLGSECSTVEDQQQDLEDLRIRLTKIRNQRDNLGLPPSASSAAASRSLSPLL
NVPAPEDGTERILPQSALGPNSGSVPGVHSNVSPVLLSRSPAPSVSAHEVLPVPSGLNYP
ETQNLNKVPSYKAMKYDIIGEDLPPSYPCAIONVQPRKPSRVHSRNSSTTLSSSIPTSF
HSSSFMSSTASPIISIINGSRSSSSGVSLNTLNELTSKTSNNPSSNSMKRSPTRRRATSLA
GFMGGFLSKGNKR

YGL011C, 1259 bp, CDS: 501-1259 (SEQ ID NO 89)

AGACAATAAAATATGGAAAATAAAACGCTTAGCACAGCAGTCAATGAAATACTCTGATAT
ATTTTGACTCTGTGGAGCATACAGCTACCACTAAATAGGATTGTGGGGACAAATATGGAA
TGATCAAAACGTTCTTAGGATTGTGGTGGTAAACTTGTAATCCAAGCTGAGATCTT
AAATCCAGCAAACCTTCGCCCATATTTATTCTTTTATAACAGAAGAAGAGACTATATTCT
CAAAACCTCGTATATTTATATACATATCCTCCAAACAACTCCCAAGTTTCACTTTCCTG
GATTTACCTTGGCATTCTTTTCCCCATCCTCTTATAATGGTAATCGCGATCCTTAATTA
TGATATCACAATAGACGAAGGGCACACACCAATTTGCCACCGTAAGGATAGAGTAAGTTA
AATGGCTAACTCATTATAATCTTCATGCTAAATCATATAAGGGCAGAGACGAAGCAAAGC
GAAAAAACATATTACAATCATGTCGGGTGCTGCTGCTGCATCTGCTGCTGGTTATGACA
GGCACATCACTATCTTTTCCCCGAGGGTCGTTTATATCAAGTAGAATATGCCTTTAAAG
CGACTAATCAAATAACATAAACTCACTAGCGGTCAGAGGTAAAGATTGTACAGTGGTGA
TAAGTCAGAAAAAGGTCCCTGATAAACTGTTGGATCCAACCTACTGTTTCGTATATTTTTT
GTATTTCAAGAACAAATTGGTATGGTAGTGAACGGACCAATACCGGATGCAAGAAATGCGG
CCCTAAGAGCCAAGGCTGAGGCTGCAGAATTCGGTTATAAATATGGTTATGATATGCCAT
GCGATGTATTGGCTAAGAGAATGGCTAACCTTTCCCAAATCTATACTCAAAGAGCATATA
TGAGACCATTAGGTGTTATACTCACATTTGTTTCGGTAGATGAAGAATTGGGTCCCTCCA
TTTACAAAACCTGACCCTGCAGGTTATTACGTTGGCTACAAAGCTACTGCGACAGGACCAA
AACAAACAGGAGATCACAACAACTTAGAAAACCATTTCAAAAAGAGTAAATCGACCATA

TTAATGAAGAATCATGGGAGAAGGTGGTAGAATTTGCTATTACTCATATGATTGACGCAC
TGGGTACCGAATTTTCAAAGAATGACTTGGAAGTCGGTGTCTGCTACAAAGGACAAATTCT
TTACCTTGAGTGCTGAGAACATCGAAGAAAGGCTAGTAGCAATTGCTGAACAAGATTAA

YGL011C, 252 aa (SEQ ID NO 90)

MSGAAAASAAGYDRHITIFSPEGRLYQVEYAFKATNQTNINSLAVRGKDCTVVISQKKVP
DKLLDPTTVSYIFCISRTIGMVVNGPIPDARNAALRAKAEAAEFYKYGYDMPCDVLAKR
MANLSQIYTQRAYMRPLGVILTFVSVDEELGPSIYKTDPAAGYVVGKATATGPKQQEITT
NLENHFKFSKIDHINEESWEKVVEFAITHMIDALGTEFSKNDLEVGVA TKDKFFTL SAEN
IEERLVAIAEQD

YGL031C, 968 bp, CDS: 501-968 (SEQ ID NO 91)

CCAAGTTAAGCAAGACACCAAGACAATAACTTGAGAGGTATGTCCCTATATGATGATGAT
TCATAATTAATGGCGACCGAGGGCAGCGTTGTGCTAGAAAGCAATGTATTAATATATGAG
AGAGCTTCAGATAGCCAATACACCGGAATTTAGACTTTGACAGGATTGTGGCTTGTTCCA
GTATAACTTATAATATATGTCAACCTTTGAGCAGGAAACCCAATGAAAATGCTTCATTAC
ATATATACGATATGGAGAAGCATGAAAAATAACAGCGTGAGATGTTATCCATGTTGCAAG
AACCTAGTAAATGAATTCTGAATTTGCAAAAAGTCCATATTTCCACGTTCTCCTCTTCC
TACAATTTTGC GAACGCCTGAACAACCATGCGGATTACCATTATTTATATTGACAAGATG
GCTACCTATGAAAAGCATAGACTTACTAACATTTTTTTTTTCAAATATGTTTGAAAACG
TGGATTAATATAGTGATAAAATGAAGGTTGAAATCGATTCTTTTTTCAGGTGCCAAAATCT
ACCCAGGCAGAGGTACCTTGTTGTCCGTGGTGACTCCAAAATCTTCAGATTCCAAAACCT
CCAAATCTGCCTCTTTGTTCAAGCAAAGAAAGAACCCAAGAAGAATCGCTTGGA CTGTCT
TATTCAGAAAGCATCACAAGAAGGGTATCACCGAAGAAGTTGCTAAGAAGAGATCTAGAA
AAACCGTTAAGGCCCAAAGACCAATTACCGGTGCTTCTTTGGACTTGATCAAGGAAAGAA
GATCTTTGAAGCCAGAAGTTAGAAAGGCTAACAGAGAAGAAAAATTGAAGGCCAACAAAG
AAAAGAAGAAGGCTGAAAAGGCTGCTAGAAAGGCTGAAAAGGCTAAGTCTGCTGGTACTC
AAAGTTCTAAGTTCTCCAAGCAACAAGCTAAGGGTGCTTTCCAAAAGGTTGCTGCTACTT
CTCGTTAA

YGL031C, 155 aa (SEQ ID NO 92)

MKVEIDSFSGAKIYPGRGTLFVRGDSKIFRFQNSKSASL FKQRKNPRRIAWTVLFRKHHK
KGITEEVAKKRSRKT VKAQRPI TGASLDLIKERRSLKPEVRKANREEK LKANKEKKKA EK
AARKAEKAKSAGTQSSKFSKQQA KGA FQKVAATSR

YGL032C, 764 bp, CDS: 501-764 (SEQ ID NO 93)

CTCCCATATTTTTTTTATTCACAGGCTAGACAATGGTAATGGTGCTTTAGATGATTT CAGT
GGATTACATTCGCACAATAGATAAATGACTAATTTTCAAGAATTTGTTTCAACCTGCCG
GCATT CAGTTATTATAAGTTATTGTTTGATGGTAAACTTCGCCATCACCGGTTGCTGCG
TTTATTGCAAAATTACTGAAACCATGTAATTTCCGAATACGGTAATTACACGCAGTTTGA
AATTTGACATGCAAGTTTAACAAAAAACTTCTGTCCGCATCTAAAGCTTAATTAAGGGA
CTGTTTCATACCTTCAGATCCAATATACTGAATATCAGGCAATTGATTTCCCTTGTAAT
ATACAATATAAATAGTTGTAAGAAGAGGTGATATGTTAAGTTTCCATTTTGACGTATTCC
TCATTCTAGAATGATTGTAAGCTCTCAACAGTCACTTGTGTGCCAAAATATTATACCTAC
TTCATACATTTTCAATTAAGATGCAGTTACTTCGCTGTTTTTCAATATTTTCTGTTATTG
CTTCAGTTTTAGCACAGGAAGTGAACACTATATGCGAGCAAATCCCCCTCACC AACTTTAG
AATCGACGCCGTACTCTTTGTCAACGACTACTATTTTGGCCAACGGGAAGGCAATGCAAG
GAGTTTTTGAATATTACAAATCAGTAACGTTTGT CAGTAATTGCGGTTCTCACCCTCAA
CAACTAGCAAAGGCAGCCCCATAAACACACAGTATGTTTTTTGA

YGL032C, 87 aa (SEQ ID NO 94)

MQLLRCSIFSIVIASVLAQELTTICEQIPSP TLESTPYSLS TTTILANGKAMQGVFEYYK
SVTFVSNCGSH PSTTSKGS PINTQYVF

YGL043W, 1430 bp, CDS: 501-1430 (SEQ ID NO 95)

TCGGGATGGTGGGTGTTCTGTACCCCGCATTCACACCGCTCTGCCTATTCATTTTATC
GTTTTCGTCTTTTCTTTCAATGTATTGATAATTAACGTGTCTATGTGATGCTATTGGTAT
ATAGCCTTTCTTGATATATCCCTCTAACAATTATTACAAGTGTTTCTGTTTAAAGCAAGTG
CTAGAAGTGACTCGGTTCTCTTAGGAAATTCTAAACGCAAGATTTCTCTTATGGTGATTG
TAACAATTATGAGATACTTCACTAGCCACCTTAAC TTTACGGACCTTCTTTTGAAACGA

TGCTTCGAATGACAACGCCTTTTTGATATATAATATCCAATTTTCATTATAGGGAAATTTT
CAACTCTTACCCGCCCCACTGTGCTGATATGACCAAGTGATCACTCGATGATGGGACTAC
GTATTGAAAAATATTGAATGAAAAATTACTCAAGCAGCAGAACATTCACAGTGTAGTCAG
TCCGCATAAGAGCATTCATCATGGATAGTAAGGAAGTACTGGTACATGTTAAGAATCTAG
AAAAGAACAAAAGTAATGATGCTGCAGTCTTAGAAATCTTACATGTCTTGGATAAAGAAT
TCGTCCCCACTGAAAAGTTACTGAGAGAAACAAAAGTTGGTGTGGAAGTCAACAAGTTTA
AAAAATCCACTAATGTAGAGATCAGCAAACCTCGTGAAGAAAATGATTAGCTCTTGGAAAG
ACGCAATTAATAAAAAATAAGCGTTCCAGGCAAGCACAGCAGCATCATCAAGATCATGCGC
CAGGCAATGCAGAGGACAAGACAACCTGTAGGTGAGTCCGTGAATGGTGTTCACAGCCGG
CCTCCTCCAGTCAGATGCCATGAAACAAGACAAGTACGTCAGCACTAAACCAAGAAATA
GTAAGAACGATGGTGTGGATACAGCTATATACCACCACAAATTACGTGATCAGGTACTAA
AAGCACTCTACGACGTTTTGGCCAAGGAAAGTGAGCATCCACCTCAATCTATTTTGCATA
CTGCAAAGGCCATAGAAAGTGAAATGAATAAAGTTAACAACCTGTGACACCAACGAAGCCG
CTTACAAAGCCAGGTATCGTATAATTTATTCAAACGTCATATCAAAGAATAACCCAGATC
TCAAACATAAAATTGCCAACGGTGATATAACACCTGAATTCTTAGCTACATGCGATGCCA
AGGATCTGGCACCAGCGCCCTTAAAGCAAAAGATAGAAGAAATTGCCAAGCAAAACTTAT
ACAACGCACAGGGTGCCACCATAGAAAGGTCAGTCACCGATAGATTTACATGTGGTAAAT
GTAAAGAGAAGAAGGTATCTTACTATCAATTGCAAACAAGATCTGCGGATGAACCATTGA
CCACTTTCTGTACATGTGAAGCATGTGGTAACAGATGGAAATTTCTCTTAG

YGL043W, 309 aa (SEQ ID NO 96)

MDSKEVLVHVKNLEKNKSNDAVLEILHVLDDKEFVPTKLLRETKVGVENVNKFKKSTNVE
ISKLVKKMISSWKDAINKNKRSRQAQQHHQDHAPGNAEDKTTVGESVNGVQQPASSQSDA
MKQDKYVSTKPRNSKNDGVDTAIYHHKLRDQVLKALYDVLAKESHPQSILHTAKAIES
EMNKVNNCDTNEAAYKARYRIIYSNVISKNNPDLKHKIANGDITPEFLATCDAKDLAPAP
LKQKIEEIAKQNLNAQGATIERSVTDRFTCGKCKEKKVSYQLOTRSADEPLTTFCTCE
ACGNRWKFS

YGL102C, 929 bp, CDS: 501-929 (SEQ ID NO 97)

TGTTACGATCAACATTCTTGTCCGTAATCAGCATGGTAGTTAAACCCATTCTGTACATAT
GGTCAGATATACTTTTCGCATGGGTCAATACCATGGTCAACCCAACCAGTTCTTCTTTGCG
TTTTCAAAAGTTGTATAATATTCAAAAACGCTAACTGATAATTTGGGTGAGGTTTCGAAA
GAATTGCCAAAATCTCCCTAGGTATATTATCTTCTGGCTTCCAGATGTAACTGCAGTCA
TTTTGTTTTTCTTGGTCTTTTACCTCGAATAGGTTTTCTTGTTTTTGTTATTTGTTTTCTTT
TTGGACCCTATGTTTATATATATGGATTTTGAAAATCTTTTAAAAAAGCGATAAAAGCGTTG
GGATCTGCCACTGGTAACTTCAAAATAGACAAGACGAAAAAACGGTGAAAATGGGTGATA
GAAATAATACAGAAGTAGATGTTGAATTAGATTAACTGAAGATATATAATTTATTGGAA
AATACATAGAGTTTTTGTGTGATGCGCTTAAGCGATCAATTCAACAACACCACCAGCAGCT
CTGATTTTTTCTTTCAGCCAACCTTGGAGACGAATCTAGCTTTGACGATAACTGGAACATTT
GGAATTCTACCCTTACCCAAGATCTTACCGTAACCGGCTGCCAAAGTGTCAATAACTGGA
GCAGTTTCCTTAGAAGCAGATTTCAAGTATTGGTCTCTCTTGTCTTCTGGGATCAATGTC
CACAATTTGTCCAAGTTCAAGACTGGCTTCCAGAAATGAGCTTGTGCTTGTGGAAGTAT
CTCATACCAACCTTACCGAAATAACCTGGATGGTATTTATCCATGTTAATTCTGTGGTGA
TGTTGACCACCGGCCATACCTCTACCACCGGGGTGCTTTCTGTGCTTACCGATACGACCT
TTACCGGCTGTACAAAAAAATATTGTAA

YGL102C, 142 aa (SEQ ID NO 98)

MRLSDQFNNTTSSSDFFFSQLGDESSFDNWNINWSTLTQDLTVTGCSVNNWSSFLRSR
FQVLVSLVFDQCPQFVQVQDWLPEMSLLLVEVSHTNLTEITWMVFIHVNSVVMLTTGHT
STTGVLVSLDTTFTGCTKKIL

YGL103W, 1461 bp, exon1: 501-549, intron1: 550-1060, exon2:
1061-1461 (SEQ ID NO 99)

AACAAGCTATAATATTGTTAAATATAGTTGATCAACAGCATTGTAATGATTACAAGAGAC
GAGGTGGAATGAACCTTATGAAATGCGTATTATATATAAACTGTAATAAGAGCTAAGTTG
AATTGAAATCTACGATACTTGATGTTGACATTATAGCACTAGTTCCCAGGAAACCCTTTC
GAAAAACACAGCAAAAACAAGAGTACTGTAACCAATGTAACATCTGTACACCAGGGACCC
ACACATTACCAAAATCAAAATTATTTTCTAATGCCTGTTATTTTTCCTATTTTTCCTCT
GGCGCGTGAATAGCCCGCAGAGACGCAACAATTTTCTCGCAGTTTTTCGCTTGTTTAA
TGCGTATTTTCCCAGATAGGTTCAAACCTTTCATCTGTATCCCGTATATTTAAGATGGCG

TTTGCTTTCTCCGTTGATTTTTTTCCTTCTTAGTGATTTTTTTGCATTAAATCCCAGAAC
AATCATCCAACATAATCAAGAATGCCTTCCAGATTCACCTAAGACTAGAAAGCACAGAGGTC
ACGTCTCAGGTATGTAGTTCCATTTGGAAGAGGGAATGAAAGAACCAAGACGGTGACTTT
TTTTTTAGTGTTGTGCAACCAATATGTCGTGTGTATATCATGGTACAGGAGAATGTCAAT
CAGCTAAGTGACTCAACATATTTCTTTGTGTTTTGATTGCGAACTTTGTATTACCATCT
CACTGTTGAGACGGCTTATTTGAGGTAATAGCTCGAGTAAATGTACTCTTCCATCGCAA
CTGAGCAAAAAGAAAGTGTGCATAGCCTTTGTCATACTTCTCCTTTATTATAACCATGATA
TTCAGAACAGTCATACTGTCTACTCATTTTACGGCTATAAAAGGTAACTTTCATTTAGAT
TATGGAAAGCACTAATTATCGCTGTATCAAATGGTGTAGAGAGCGCAATTATGAAAAAG
AGTTACCACGTTTCTTTTGTTCGATAAAATGTCCAGTTGAAAACCTGTTTTACTAACGA
TTTAAAAATTGTATTTTATTACAATATTTTTTTTGTACAGCCGGTAAAGGTCGTATCGGT
AAGCACAGAAAGCACCCCGGTGGTAGAGGTATGGCCGGTGGTCAACATCACACAGAATT
AACATGGATAAATACCATCCAGGTTATTTCCGGTAAGGTTGGTATGAGATACTTCCACAAG
CAACAAGCTCATTTCTGGAAGCCAGTCTTGAACCTGGACAAATTGTGGACATTGATCCCA
GAAGACAAGAGAGACCAATACTTGAATCTGCTTCTAAGGAACTGCTCCAGTTATTGAC
ACTTTGGCAGCCGGTTACGGTAAGATCTTGGGTAAGGGTAGAATTCCAAATGTTCCAGTT
ATCGTCAAAGCTAGATTCGTCTCCAAGTTGGCTGAAGAAAAATCAGAGCTGCTGGTGGT
GTTGTTGAATTGATCGCTTAA

YGL103W, 149 aa (SEQ ID NO 100)

MPSRFTKTRKHRGHVSAGKGRIGKHKHPGGRGMAGGQHHHRINMDKYHPGYFGKVGMR
YFHKQQAHFVKPVLNLDKLWTLIPEDKRDQYLKSASKETAPVIDTLAAGYGKILGKGRIPN
VPVIVKARFVSKLAEEKIRAAGGVVELIA

YGL130W, 1880 bp, CDS: 501-1880 (SEQ ID NO 101)

TTTTGGTACTTGAATTTCTCGTTTCTACTAGCTGGATTGCTTGTCTTTTACAATTCCTG
GGAGTTTGGCTATTGCTACCTTGGTCTTAGCACCCTTTTCCGCTATTTGTATTGT
TGAACATAATTTAGTATCTATTTCCATTTTATTATAATTCACGTTTTTAGCAGCCTCTCTT
CTTCTAGGTAATTGGAAATCTTCTTCTTAGGCATAGCGTGACCAGCTGAAAGGCAGATG
ATCTCAATATGTCCCGATAGGCCAATTTTGCCACCAGATAGTTCGATGGCATTTTATTTT
TAGTCCTTTTGAAGCAATATCATAAAATATATATAGTTCCTCATGATGTTCCGGTCAGT
CGCTCCGAAGCGTAACCTAGTATAATAAATAGTTTCATTGCAGAAAATAACGAAAGAAATG
GTGGAATACGATCTGTTATATCTAAACTAAAGCTAACTAACGGAATAAGCAAATACGAAT
CGACCGCTAATTTAACAAATATGGTTTCTAGCAATGGAAAGTAGAGTGGCACCAGGAAATTC
CTGGGCTCATTTCAACCTGGGAATGTCACGCAAGACTTGAAGATGATGGTCTGTAAATTAT
TGAATTTCCCAAAACCTACGAAACATTCCCTGGTTCCAGCCTGTGTCTTTTACGATT
CTGATGTGGAAGAGAAGCTGCTTGGCATGATTACTACGTTTGTGAGAAAACAGATGGTC
TGCGGGTGTGATGTTTATAGTGATAAATCCTGTGACGGGTGAGCAAGGATGCTTTATGA
TTGATAGGGAAAATAACTATTATCTGGTTAATGGATTTAGGTTTCCAGATTACCCCAA
AGAAGAAAGAAGAGCTGCTAGAGACTCTTCAAGATGGCACCTTATTAGATGGTGAACCTG
TCATACAACTAACCCAATGACAAAATTACAAGAGTTGCGTTATTTAATGTTTCGATTGTC
TTGCTATCAATGGTAGATGTCTCACACAATCACCAACAAGTTCTAGACTAGCCACCTTG
GAAAAGAATTTTTTAAACCATACTTCGATTTAAGAGCAGCGTACCCTAATCGTTGTACTA
CTTTTCCGTTCAAATTTCCATGAAACATATGGATTTTCAAGTTACCAATTAGTAAAAGTTG
CTAAAAGTTTAGATAAACTACCACATCTTCTGATGGTCTGATATTTACTCCTGTGAAGG
CACCTTACACTGCCGGCGGAAAGATTCAATTGTTATTAAATGGAAGCCAGAACAGAAA
ACACCGTGGACTTCAAATTGATTTTAGATATCCCAATGGTGGAGGATCCTTCTTGCCTA
AAGATGATCGGAACAGGTGGTATTACAATTATGACGTTAAGCCAGTTTTTCAGCTTATATG
TCTGGCAAGGCGGAGCTGATGTCAATTACGTTTAAACATTTTCGACCAGCCTTTCGATA
GGAAGGAATTTGAAATATTAGAAAGAACATACAGAAAATTTGCAGAGTTGAGCGTTTCAG
ATGAGGAATGGCAAATTTGAAGAACCTAGAACAGCCATTAAATGGTAGAATAGTAGAGT
GCCAAAAAACCAAGAGACTGGGGCGTGGGAAATGTTAAGATTCAGGGATGATAAGTTAA
ATGGTAATCATACATCGGTGGTCCAGAAAGTTTTGGAGAGTATCAACGATTCAGTTTCAT
TGGAGGACCTCGAGGAAATTGTTGGTGATATTAAAGGTGCTGGGACGAGAGAAGAGCAA
ATATGGCTGGTGGTAGTGGGAGACCCTACCGTCTCAAAGTCAAATGCGACATTATCTA
CCTCTAAGCCAGTCCATTACAGCCCCCAAGTAATGATAAGGAGCCAAAATATGTAGACG
AGGATGATTGGTTCGGATTAG

YGL130W, 459 aa (SEQ ID NO 102)

MVLAMESRVAPFIPGLIQPGNVTDLKMVCKLLNSPKPTKTFPGSQPVSFQHSDVEEKL

LAHDYYVCEKTDGLRVLMFIVINPVTGEQGC FMIDRENNYYLVNGFRFPRLPQKKKEELL
ETLQDGTLLDGELVIQTNPMTKLQELRYLMFDCLAINGRCLTQSPTSSRLAHLGKEFFKP
YFDLRAAYPNRCTTFPFKISMKHMDFSYQLVKVAKSLDKLPHLSDGLIFTPVKAPYTAGG
KDSLLLKWKPEQENTVDFKLILDIPMVEDPSLPKDDRNRYNYDVKPVFSLYVWQGGAD
VNSRLKHFDQPFDRKEFEILERTYRKFAELSVSDEEWQNLKNLEQPLNGRIVECAKNQET
GAWEMLRFRDDKLNGNHTSVVQKVLESINDSVSLEDLEEIVGDIKRCWDERRANMAGGSG
RPLPSQSQNATLSTSKPVHSQPPSNDKEPKYVDEDDWSD

YGL147C, 1076 bp, CDS: 501-1076 (SEQ ID NO 103)

CAATATTATAGTTACTACCTATTTGATTATTAAGATCAAAAGTAATCCTTCATCTCATAT
CAAAAAGAAAGGTTTGTAAGAGAGCATTGGGCAGAGAGTATTTGTCCTGCGTATAGAGGA
GAAAAAATTGTACTGATGCTAATTTTGGTGTCTCTCTTTTATTTTGTAAAGACTGT
TTTCCAGAAATGTTTGGGTTTATTTTAAATTTTGTAAACATTTTTCATCCTTTCTC
ATTTTGTCAATTTTCTGTGGAAAATTTCACTGACGCGAAGAAGCGATGAAATTTT
CAACATCCTCCCATCATCCCAATATTGGCATAACACACATGCAGCACAGCGGAAGTGG
GAGGTCAGAGGCAATGTGGCAGAGACGCTGGCGCGCCTGTATTGTATAATAGTATATTT
ACACTCAATTCAATTTTGTATTAATTAAGTGTGTAAAGCTTCTGAAATCAAGAAG
CCCGTACCAGAAGTTCAATCATGAAATACATCCAACTGAACAACAAATCGAAGTCCAG
AAGGTGTCACTGTGACATCAAGTCCAGAATCGTCAAGGTTGTTGGTCCAAGAGGTAAT
TGACCAAGAACTTGAAGCACATTTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTTGCTGTTTACAACGGTGGCAGAAAGCACGTTGCTGCTTTGAGAACCGTCAAGTCTT
TGGTTGACAACATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTTGTTGAAAAGGATGGTGCCAAATTCATTGAAG
TCAGAACTTTTGGGTGACAAGAAGATCAGAAACGTTCCAGTTAGAGATGGTGTTACTA
TCGAATTTTCCACCAACGTTAAGGACGAAATTTGCTTGTGAGGTAACCTCTGTCGAAGACG
TTTCCCAAAACGCTGCTGACTTGCAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTA
AATTTTGGACGGTATCTACGTTTCTACAAGGGTTTATTACTGAAGATTTATAA

YGL147C, 191 aa (SEQ ID NO 104)

MKYIQTEQQIEVPEGVTVSIKSRIVKVVGPRGTLTKNLKHIDVTFTKVNNQLIKVAVHNG
GRKHVAALRTVKS LVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKEFIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVNRNKDIRKFLDGIY
VSHKGFITEDL

YGL213C, 1694 bp, CDS: 501-1694 (SEQ ID NO 105)

AATCAAAACGATCGTTATACAATTCATTGAGGAACCTCTCTAGTCCGATCCGTCTTTCAT
CGATCATTTCCGGATCATCATATCTTCTTGGCCACCTCCTGTCCAATACACCGGGCTTTT
CAGGGAAGTCATATGGGATGGTGTCTTCTACATCTCTCTCCAATCGTGTCTTCAGTTTCC
AAACTCGGAATACCTTTTGTAAAGGCGCTTGTGTTGGTGTACTAACACCGTATAAAACAT
ACTTGGGGTTGATTTTAACATCGTCCACCTTGATTCTTAACCTTTTCACTCATTTTCCCTA
CAGAATTAGCTGCCATCAATATCAATTATCAACCCTTATATGACTTTATTGTTTTTGT
TTGTTGGCTAATTAATTGATACAAATCTTTAGCGGAAAAATAAAAAAATATAAAGTAAA
GAAGGAAAAATTAGGCGATATTAAACAAATCTAAAATAAAGACAAGAAACGAAAAAGAG
GTTAATCAAGTATTGGAAAAATGTCCAAAGTGTTTATTGCCACAGCAAATGCAGGTAAAG
CTCATGACGCTGATATTTTCTCGGTTTCTGCTTGCAATTCATTTACGGTAAGTTGTTTCA
GTGACGGTTACTTAAAGGTGTGGGATAATAAGCTGTAGATAATGAAATCCAAAAGATA
AGTCATATTCTCACTTTGTCCATAAGTCCGGATTGCACCATGTCGATGTCTTGCAAGCTA
TTGAGAGAGATGCATTTGAATTATGCCTTGTGCTACCACTTCATTTTCTGGCGATTTAC
TCTTCTATCGTATCACTAGAGAAGATGAGACTAAAAAGTTATATTCGAGAAATTGGATC
TTCTAGACTCAGACATGAAAAAGCATTCCTTTTGGGCATTAAATGGGGTGCCTCAAATG
ACAGACTACTTTCCCATAGGCTGGTTGCTACAGACGTCAAAGGGACCACTTACATTTGGA
AGTTTCAACCGTTTGCAGATGAGTCAAATCTTTAACACTAAATTGGAGCCCCACGTTAG
AATTACAAGGCACTGTGCAATCGCCTATGACTCCAAGTCAATTTGCCACTTCTGTGGATA
TCTCTGAACGAGGACTAATTGCCACAGGTTTAAATAATGGAACAGTACAAATTTCAGAAC
TATCTACATTACGCCCCGTTGTACAATTTGAATCTCAGCATTCATGATTAATAATTGCA
ATTCCATCAGATCGGTGAAATTTTCTCCTCAAGGATCCTTATTAGCCATTGCTCACGATT
CAAATTCATTTGGTTGCATCACTCTATATGAACTGAATTTGGTGAAAGAATAGGCTCCT
TATCCGTACCAACCCATAGCTCGCAGGCAAGTCTGGGTGAATTTGCACATTCCTAGCTGGG
TCATGAGTCTATCGTTTAAATGATTCTGGTGAAACATATGCAGTGCCGGATGGGATGGTA
AATTGAGATTTTGGGATGTAAAAACAAAGGAAAGAATCACTACATTGAATATGCATTGTG

ATGATATTGAAATTGAAGAGGATATCTTAGCTGTTGATGAACATGGAGATTCTTTAGCTG
AACCTGGTGTCTTTGACGTGAAGTTTTTGAAAAAGGTTGGAGATCTGGTATGGGAGCTG
ATTTAAATGAAAGTTTATGCTGTGTTTGTTTAGATAGAAGCATCAGGTGGTTTAGAGAAG
CTGGCGGTAAATAA

YGL213C, 397 aa (SEQ ID NO 106)

MSKVFIATANAGKAHDADIFSVSACNSFTVSCSGDGYLKVWDNKLDDNENPKDKSYSHFV
HKSGLHHVDVLQAIERDAFELCLVATTSFSGDLLFYRITREDETKKVIFEKLDLLDSMK
KHSFWALKWGASNDRLLSHRLVATDVKGTTYIWKFHPPFADESNSLTLNWSPTLELQGTVE
SPMTPSQFATSVDISERGLIATGFNNGTVQISELSTLRPLYNFESQHSMINNSNSIRSVM
FSPQGSLLAIAHDSNSFGCITLYETEFGERIGSLVPTHSSQASLGEFAHSSWVMSLSFN
DSGETLCSAGWDGKLRFDVVKTKERITTLNMHCDDIEIEEDILAVDEHGDSLAEPGVFDV
KFLKKGWRSGMGADLNECLCCVCLDRSIRWFRFAGGK

YGL235W, 1037 bp, CDS: 501-1037 (SEQ ID NO 107)

CTGGTTCCAACCATATCTTATGGGAAGATCTATCAGGAAACCTTAGAATCTTAGCTTCGA
TGGAGGGACAATAGCGGGGGCCTTTGATGGTCGTGTCCTGAATATGAATGGATTGATGCA
AGTTATTGCGCAAAAAGTCGTGCATTTGAGGTGTGGTATGTGTGCCAAAGCAATCCAGTT
GCTTCGTGGGTTCTGACTGACACGGTTTCATTCAGAAACTCATAGGGACAGGCAACGCAT
CTCCCTTCTGGACCTCCAGAGCGCTGAAATCAATGGATTCTTGGCCAGCCTAGCCGGAG
TGCCTGTTTTCAAACGCCCTAACTGAAAGCCACCTCATTTTGTAGAGTATTGCTGATCC
CATATGTTGGCTGCTCGCCAATTCTTCCTGCTGCAATACGCTTGTGCGCCGATGTGAATTT
CTGCACTGAGAAACGTACCTGTAGTGATTATGACCTGATCTGCCCCAACCTGGGTACCGT
CATCCAGAACCACACCTTTGATGACCTTGTGGCCACATCCGGGGTCATACAAGATCAAGT
CAGCAACTTTGTTCTGCAGCAGAGACAAGTTGGGGTGTGCTTTCTTGTGCGAAAGTTCCC
TTTGTCATGTATTTCTTATATACTCTCTGTCTATCTGGGCTCTGGGCCCCCACACAGCAG
GACCCTTGCTTCTGTTTCAGCATTTTGAATTGCACTCCAGCGAGATCAGTTACTTTGCCCA
TCAGCCCATCGAGAGCGTCGATTTCTTTACAAGGATGCCCTTACCCACTCCACCAATAG
AGGGGTGCACGAACACTTACCAATATCTGTTAACGATGGTGTAAATGAGAGTAGTATGCG
CACCAGTCCTAGATGACGCAGCTGCAGCTTCGCAGCCTGCATGTCCAGCACCGATGACCA
CGACCTGTGTCTTGGTTGTGGGTTGGAAGCTTGTCAAAGAAGATATGGTCAACCGCCTCC
TGAGGACCTGTAAGGGAAATGAAGTACACGAAGACGCCAAGGTTGTTACACGCAGCATCG
TTCTTTGGGGCGTTTAG

YGL235W, 178 aa (SEQ ID NO 108)

MTLWPHPGSYKIKSATLFCSRDKLGCAFLSESSLCMYFLYNSLSIWALGPHTAGPLLLFS
ILNCTPARSVTLPISPSRASISFTRMPLPTPIEGLHEHLPISVNDGVMRVVCAPVLD
AAASQPACPAPMTTTCVLVVGWKLKEDMVNRLRLRTCKGNEVHEDAKVVTRSIVLWGV

YGL260W, 731 bp, CDS: 501-731 (SEQ ID NO 109)

TACCATGGAACACCGGTGATCATTCTGGTCACTTGGTCTGGGGCAATACCAGTCAACATG
GTGGTGAAGTCACCGTAGTTGAAAACGGCTTCAGCAACTTCAACTGGGTAGGTTTCCGTT
GGGTGGGCGGCTTGGAACATGTAGTATTGAGCCAAGTGAGCTCTGATATCAGAGACGTAG
ACACCTAATTCAACCAAATTGACTCTTTCGTGAGCTGAGCTAGAGTGGTGGTTGCGGAA
GCAGTAGCAGCGATGGCAGCGACACCAGCGCGATTGAAGTTAATTTGACCATTGTATTT
GTTTTGTTTTTTAGTGCTGGTATAAGCTTAACAGGAAAGAAAGAAATAAAGATATATTCT
CAAAAGCATACAGTTGAAGCAGCTCTATTTATACCCGTTCTCTATCAGTCATCACTACT
TAAACGATTCTGTTAACAGATGCTCATTTAGCACCTCACATATCCTCCATATCTCATCTTT
CACACAATCTCATTATCACTATGGAGATGCTCTTGTCTTGAACGAATCATACTCTTTC
ATAGACTTCGTATGTGGAGTATTGTATTATGGCACTCATGTGTATTCGTATGCGCAGAAT
GTGGGAATGCCAATTATAGGGTGCCGAGGTGCCTTATAAAACCCTTTTCTGTGCCTGTGA
CATTTCTTTTTCGGTCAAAAAGAATATCCGAATTTTAGATTTGACCCTCGTACAGAAG
CTTATTGTTAA

YGL260W, 76 aa (SEQ ID NO 110)

MEMLLFLNESYIFHRLRMWSIVLWHSCVFVCAECGNANYRVPRCLIKPFSVPVTFPFSVK
KNIRILDLPRTAYC

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 111)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTT

TTTTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTTCCT
GTGTAGCCTAATGTTTAATGCCTAATTTTTTTCTAAAATGCAGCAACATACATATGTTGA
GTCGTATAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTCAGGACA
TTTTAAACATCCGTACAACGAGAACCCATACATTACTTTTTTTAATATTCTTTTTGT
CACCGCCTTCTTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAA
GCTAGGATACCAAATTGAACTTGGACATAACTCATTAAGAAGTATACTGTAAAGA
GAGGCATTCATTTTCGTGTATTATAACGTTTAGCATCAGTTACCCTTGAAAGCCCAACATA
TACAAAAATACGCGTCCAAGATGTCTACTAAAGCCCAAAACCCTATGCGTGATTTGAAGA
TCGAGAAATTGGTCTTGAACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCT
CCAAGGTTTTAGAACAAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTTCGGTATCAGAAGAAACGAAAAAATTGCTGTTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGGAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACTGTTGGTAACTCCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAAGTACGACGCTGATGTGCTCGATA
AATAA

YGR085C, 174 aa (SEQ ID NO 112)
MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRFTFGR
RNEKIAVHVTVRGPKAEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCRGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR118W, 1258 bp, exon1: 501-565, intron1: 566-885, exon2:
886-1258 (SEQ ID NO 113)
AGCCATGTCGGTCGCACTAGACTTTTCTTCTCACTGTCACTTACCTGTTTGAAATCATGT
CCTTTTTTTTTTTTGCCATTCTTATACATTTTCTTTCTTCTGAAATTAACGTACACCCA
TACCCTATATACACCCATACCCATATTTTTTAAATATAAAAAGTAACTTCATTTTGAAAGA
CCACTCTGCATCAGCAGCGGGCTCTGGAAGGAAGAAATGACGTTTCGGCGGAATACCCCT
TTCAGAAGGTCTGCTCTTGTGGCTGGTTCATGGGAGACACCCAGCGGAGCTCCTCCCGAG
AAAGGCCCTTCATCTCTGCCGATTGCTGACGGAAAGCAGTAGCGGAGGTTTGAGTTCTC
TACGCCGAGAGTACACTGCCGTAATATCACAATGTTTCGACTAACGGTTACAGTACGTTA
AATTAGATACTGCCTATGAATTGACATATTAGATAATGTCAAATTTTACAAAAACCTAAG
ACAACAGGAATAAACAAGATGGGTAAAGGTAAGCCAAGAGGTTTGAACTCTGCTAGAA
AGCTACGTGTCCACAGAAGAAACAAGTATGTTGACTATTTCAAATTAACAAAAAACTATC
AACCCCTATTGTGATATCGTTTTAGGTGAAGGAAATGTTGTGAGCTCTGGAGTGATAAA
TTTATCAAGTAACATATCCTGGCGCAAATCAGTTTGGAGAGGCTTAAATGACACGTCAC
AGTGATAAAAAGTAATGAATAGTGAACGGTCAGCTTCGGCCATTCTTCCCAATCTATAGT
GTGGAAAATAAACCTTTTCTTCCCAAATAACTCAGAAAGTCACAGGAGGCCGTTTTTTA
CAACGGAATCATTTTTTTTACTAACAGTTTTTTTTTTTATTATTATAGCCGTTGGGCCGAAA
CAACTACAAGAAGAGATTGTTGGGTACTGCCTTCAAGTCTTCTCCATTCCGGTGGTTCTTC
TCATGCCAAGGGTATCGTCTTGGAATAATTGGGTATCGAATCCAAGCAACCTAACTCTGC
TATCAGAAAGTGTGTTAGAGTTCAATTAATCAAGAACGGTAAGAAGGTCACTGCTTTCGT
TCCAAACGATGGTTGTTTGAACCTTGTGCGACGAAAATGATGAAGTCTTGCTAGCAGGTTT
CGGTAGAAAGGGTAAAGCTAAGGGTGATATCCAGGTGTTAGATTCAAGGTCGTTAAGGT
CTCTGGTGTCTCCTTGTGCTTGTGGAAGAAAGAAAGGAAAGCCAAGATCATAA

YGR118W, 145 aa (SEQ ID NO 114)
MGKGKPRGLNSARKLRVHRNRRWAENNYKKRLLGTAFKSSPFGGSSHAKGIVLEKLGIE
SKQPNSAIRKCVRVQLIKNGKKVTAFVPNDGCLNFVDENDEVLLAGFGRKGKAKGDIPGV
RFKVVKVSGVSLALWKEKKEKPRS

YGR142W, 1733 bp, CDS: 501-1733 (SEQ ID NO 115)
GGACTACTTTACAGGGTAATGAATATTTGGGCGTTTTTCGCTATTTTAGCATGCTGTAGT
GTATGTACTGTGCATCGTCATGTAGCACTATTTACGCCGTATTTTTCTTTTTTTCTTTTCG
CACCGTCTGTGGTTGTAAAGTTACTGACACTTTTTTTTTCTAGAAAGTTCCGGAAAATTGC
GACACTCGGTGGAGCTCGAGAGTTGTATCCAGTTTTCTTGTTTCGGCGATATTCGGAACCA
GGTCGGGTGGGCTAACAGCCGCCAGGATGGAAGAATTAAGAATTTCATAGAAGCCTTC
AGTTCTTGCGAAGTAAAGTGGCAAAACAAATGGAAGATCTATTGCATTACATATATAAA
AGCATTAGAACAATCTTTTCTCATTGACAGGTATTCTCATTGCTCTATATATATTTTCTT

CTTCTTGAAAGAAATATCAGTATTACAATCATAACAACAACCAAAAGAAAATAACTAATA
GACCCCATTTACAATATAGAAATGTTTTCCATATTCAATTCACCATGTGTTTTTGAACAGC
TGCCATCTTTTAGTCAGCCCCTACATTTCGCGTTATTTTGATTGCAGTTCTCCAGTGAGCT
ATTATCCAGAATGTAAAAGGAGGAAAGCAATAAAAGCTAACCTAAGAGCTCCAAAAAAA
GCGATGCAAATTGTTTCAGAACCTTTGAGGTATGCACCTTGCTGAAACACCAAATGGTTATA
CATTAAGCTTGTCTAAGCGGATTCCATATGAACCTTTTTTCAAAGTACGTTAATGAGAAAT
TAGGTGAGCTAAAGGAGAACCATTACAGACCAACTTACCATGTTGTCCAAGATTTTTTTG
GAAACCAGTATTATGTTGAAGATGAAGCGGATGAAGATGCTCTATTGAGATCTGCATTGA
AAGATCTGGATTTTAGAGCCATAGGAAAGAAAATTGCTAAGGATCTTTTCCAAGACTACG
AAATAGAATTGAATCATAGAGGTGATGAATTGAGCATATTGAGTAAGAAGGATAAAATCT
TTAAGGAATTCTCTCTAGACCAAGTGTGTTGAAGATGTTTTTGTATTGGCTGTGGAGTTG
AAAACATAGATGATGGCTCGAGAGAAAAATATGCACCTTTTAAAGATTGGTTTAGTTAAGC
ATGAGGAAGAAATTTCCGAAGGTGGCATCAACGAACCAAAGATGCCAATAATTGAATCCA
AAATAGACGAGTCTCACGATGATGTTAACATGTCTGAATCTTTGAAGGAGGAAGAAGCGG
AGAAAGCGAAAGAACCACTAACCAAAGAAGACCAAATAAAAAAATGGATAGAGGAAGAAA
GATTGATGCAGGAGGAAAGCAGAAAATCAGAACAGGAAAAAGCTGCCAAGGAAGATGAAG
AAAGGCAAAAGAAAGAGAAGGAAGCCAGATTGAAGGCAAGGAAAGAATCTTTGATAAATA
AGCAAAAACCAAGAGGTCCCAGCAAAAAAATTTGCAAAATTCCAAATCATTGCCTATCT
CTGAGATTGAGGCCAGCAATAAAAAATAATAAGCAATTCTGGTTCAGCAGAAAGTGATA
ATGAAAGTATAAACAGTGATTCTGATACGACTTTGGATTTCTCTGTGTCTGGTAATACAC
TAAAAAACACGCTTCACCCCTATTAGAAGACGTTGAGGATGAGGAAGTTGACAGATACA
ACGAGTCCCTAAGCAGATCTCCAAGGGAACTCTATTATTGAGGAGATATAA

YGR142W, 410 aa (SEQ ID NO 116)

MFSIFNSPCVFEQLPSFSQPLHSRYFDCSSPVSYYPECKRRKAIKANLRAPKKS DANCSE
PLRYALAETPNGYTSLSKRIPYELFSKYVNEKLGELENHYRPTYHVVDFFGNQYYVE
DEADEDALLRSALKDLDFRAIGKKIAKDLFQDYEIELNHRGDELSILSKDKIFKEFSLD
QVFEDV FVIGCGVENID DGSREKYALLKIGLVKHEEEISEGGINEPKMPIIESKIDESH
DVNMSESLKEEEAEKAKEPLTKEDQIKKWIEEERLMQEE SRKSEQEKA AKEDEERQKKEK
EARLKARKESLINKQKTKRSQOKKLQNSKSLPISEIEASNKNNSNSGSAESDNESINSD
SDTTLDFSVSGNTLKKHASPLLEDVEDEEVD RYNESLSRSPKGN SIIIEI

YGR236C, 890 bp, CDS: 501-890 (SEQ ID NO 117)

CAAAAAGTTTTTCGGATGAACCGGATTAATACAAGTAAAATCAGCAAAGATATAGAAGAC
AAAATAAGCGTGAAAACAATCATAAACCACTCACACGGGGGTTTTTCAGCTGTTACTCCT
CCATACATACATTTTGATAAAGATATAATGTTATATTTCTTTTCGTAATTTTGTTTTACT
TCGGTTTGCTCTATAGATTTTCATCAGCCGCACCGAAAAGGGAGATCAATAAGGTACCCTT
TAAAAGGGATAAGAAGCCTACATCACCCCAATAAATGGAGTAATGGCCAGCATTTGGATGA
AGAGAAGAATTACGGGATACTGGGATAACACTGTTAAAAAATGCTTCGCGACGTGAGGGT
CTTCTTCATATAAATTGAACTGCCAAATCTCTTTTACATTATCCAGGATAGTTTGGAATG
TGTGTTACTGAAGGATCAGAATCAATAAATACAATCAATACAAATATTTAGCGCATAAAA
TTCAAACAAAGTTTACTGAAATGAAGTTAGATTTCAGGAATATACTCAGAGGCACAAAGAG
TTGTGAGAACTCCAAAGTTTAGATATATTATGTTAGGGCTGGTGGGCGCTGCTGTGGTAC
CGACCGCATACATGAGGAGAGGCTATACGGTTCCTGCACATAGCTTAGACAACATCAACG
GCGTAGACACAATAAGGCGTCTGTTATGGGTACAGAACAGAGAGCAGCTATGACGAAGG
GTAAGAGTTTACAAGAGATGATGGATGATGATGAAGTAACGTATTTGATGTTCTCTTCA
ATCATGTAAGGGAATTTGTACTTGGTTCCCTGCATTTATGTTCTTTGCATTTTGTTTTCG
CATTTAATCATAGTACGACAAACGGGGAAGGGGATTGTGATTTTACATAA

YGR236C, 129 aa (SEQ ID NO 118)

MKLDSGIYSEAQRVVRTPKFRYIMLGLVGAADVPTAYMRRGYTVPAHSLDNINGVDTTKA
SVMGTEQRAAMTKGKSLOEMDDDEV TYLMFLFNHVREFVLGSLHLCSLHFVFAFNHSTT
NGEGDCDFT

YGR277C, 1418 bp, CDS: 501-1418 (SEQ ID NO 119)

AATCTTTGCGATTGAATTGCTGCACGAACATTAACATTAGTTCTTTTGCTAAAGTTTCTC
CAATATCTGGAATATCAGAATTTAGCAAGGCAATCAAAGCGGATAAAGCAGGGATTAGCC
TGCCATTCTGTTTGTTCAGAGTAAAATCCACAACATTTTACAAATTATGTTGCGGCCAA
TAAGTATATTGACTTGAAATAAGTCTCTGTGCGATTCTGTAAAGTTGTCCATTGTAAAT
TGGATATTATGGGTGAAACGTGTGACCTTATCATTTCAGTTTCTCTCTGAAATTTAA

TGTCCTTCATCCTGTATGGTAGCGGTAGACATGCTGGTTTGTAGCCTTTTTATTCCCTTTTT
AGGTTTCTTACTCACAATGCCAAAATAAATATCAGTGTAATATAATTTTTCAAGAGTACG
TAATGGAAAAAGATAAAAAATAAGGACCGTCATAAAAAGAGACGTGATTAAACCTAAAAAT
CTAAAGTAAAGAAGTGTAAGATGGTTGAGGAAAATTCCAGAGTTTGTATTGTTCTTCCTT
ATACACCGCCTAGTGCTACTTTGCAGAGGATTATAGGGCAAACCTATTCCGTTCTTAAGAG
AATGTCAAAGTCAACTAGACATCGTGATTGTACCTGAATTCAAACCTCATTCCAGTTGG
ATTCTGCGCTAGGGAAGATGTACAGTATTACCAGGGATGTCCTTTTGGGCTATGGAATGA
TCAACAGCGGAATCAACATCATATTCAACAATATTCAATTTCGTCGAGAGTAATTTGCAAT
GGAAAGTGGTTTTATTGCCACAGGAATCCACTTTTGAACTTGAAGCTAGAGTTGGGAC
AAGGACAATACCATAGTATAGAACATTATGCATTACACGATAATATAATGGAAGAGATAG
AAGGTCCCAAAGATGCTAACAAATTTTCATGTACCCGCTTGGGCGGAACGTTCCGACCACA
TTCACGATGGACATAAAATATTGTTGAGCGTCTCTACATTCATCACGTCACAAAGGTTAA
TTTGTGGAATTACGTGCGATGAGCTCTTGCAAAACAAGAAATACAAAGAGTTGATTGAAC
CTTATGATACACGATGCAGGCACGTACATCAATTCATCAAGTTGTTAAACCGGATCTCT
CCGTAGAACTAGTTCCCTTAAGGGACGTGTGCGGCCCCACAGGGAAAGTACCCGAGATAG
AATGTTTAGTTGTGAGTAGAGAAACCGTCAGTGGGGCAGAGACTGTGAATAAGACTAGGA
TTGAAAAAGGCATGAGCCCATTTGGCAGTACATGTGGTTAATGTACTTGGAGGAAGGGAGG
AAGACGGCTGGAGCGAGAAGTTAAGCAGCACGGAATCAGACGCCTACTTAAGTCCTCTG
CTTCGCCAACGTGCACTCCACAAAACCCTTGCGTATAA

YGR277C, 305 aa (SEQ ID NO 120)

MVEENSRVLIVLPYTPPSATLQRIIGQTIPFLRECQSOLDIVIVPEFKTSFQLDSALGKM
YSITRDVLLGYGMINSGINIIIFNNIHFVESNLQWKVLLPQESTFETWKLELGQGQYHSI
EHYALHDNIMEEIEGPKDANKFHV TALGGTFDHIHDGHKILLSVSTFITSQRLICGITCD
ELLQNKKYKELIEPYDTRCRHVHQFIKLLKPDLSVELVPLRDVCGPTGKVPEIECLVVS
ETVSGAETVNKTRIEKGMSP LAVHVNVVLGGREEDGWSEKLSSTEIRRLKSSASPTCTP
QNPCV

YGR284C, 1433 bp, CDS: 501-1433 (SEQ ID NO 121)

AGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGGCCA
CCACGATTGACGAACAAGTTGGTTTGATCGTTGACAGTTTGAATGACGAAGAGTTAGTGT
CCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTGAAGGAATCTG
CAAAGACTATTGTCGATTCTGGCAAACCTACCATCCAGCTTGTGTCTTACTTCGTGTGAA
TACCGTAAGAAATGGAATAGAATATATACGAATGTATACGAATATTATAGAGAACGTTCT
CTTTTATTTCTATAATGAATAGGTTCCGGTAACGGTTCCCTTTTATAGGTATTTCTAGAAG
ATGAGAGAAGAGGGAATAATGAGAAAGGCGAAAAATAAAGGACACCTTTAACGAAAGATC
AAAGGTGTCCTTATTTACTTACAATAGCTGCAATTAGTACGACTCAAAAAAAGTGAAAC
AAAAGTGAAGGATAGATCAATGTCTTACAGAGGACCTATTGGAAATTTTGGCGGTATGC
CAATGTCATCATCGCAAGGACCATACTCTGGCGGTGCACAATTCAGATCAAACCAGAACC
AATCCACTTCTGGCATCTTAAAGCAATGGAAGCATTCTTTTGAAAAGTTTGCCTCCAGAA
TTGAGGGGCTCACTGACAATGCAGTTGTTTATAAATTGAAGCCTTACATTCCAAGTTTGT
CAAGATTTTTCATTGTGGCCACCTTTTATGAAGATTCGTTTAGGATCTTATCACAATGGT
CAGATCAAATTTTATCTGAATAAGTGAAGCATTACCCATACTTCTTTGTCGTTGTGT
TTCTAGTGGTTGTTACCGTTTCCATGTTGATTGGCGCCAGTTTGTAGTTTTAAGAAAGC
AAACCAATTATGCCACCGGTGTGTTATGTGCTTGCCTTATTTCTCAAGCATTAGTTTATG
GGTTGTTTACGGGTTTCATCATTTGTCTTAAGAACTTTAGTGTATTGGTGGGTTGTTAA
TTGCATTACAGCGATTCAATTGTTCAAACAAGACAACATTCGGTATGCTTCCTGAATTAA
ACAGCAAAAACGACAAAGCGAAGGGTTACCTGTTGTTTGCTGGTAGAATTTAATTGTTT
TAATGTTTATCGCTTTCACTTTTCACTAAATCATGGTTTACTGTTGTTTGGACCATTATCG
GCACAATATGTTTCGCCATTGGTTACAAGACAAAATTCGCATCCATTATGTTGGGTTTGA
TACTAACTTTTACAATATCACGCTAAACAATACTGGTTTATAACAATACTAAGAGAG
ATTTCTTGAAGTATGAGTTTACCAGAACTTAAGCATCATTGGTGGGCTTCTATTAGTTA
CTAATACTGGCGCTGGTGAATTATCCGTTGATGAAAAGAAGAAGATTTACTAG

YGR284C, 310 aa (SEQ ID NO 122)

MSYRGPIGNFGGMPMSSSQGPYSGGAQFRSNQNSTSGILKQWKHSFEKFASRIEGLTDN
AVVYKLKPYIPSLSRFFIVATFYEDSFRILSQWSDQIFYLNKWKHYPYFFVVVFLVVVTV
SMLIGASLLVLRKQTNATGVLCAVISQALVYGLFTGSSSFVLRNFSVIGLLIAFSDSI
VQNKTTFGMLPELNSKNDKAKGYLLFAGRILIVLMFIAFTFSKSWFTVVLTIIGTICFAI
GYKTKFASIMLGLILTFYNITLNNYWFYNNTKRDFLKYEFYQNL SIIGLLLVNTGAGE

LSVDEKKKIY

YGR285C, 1802 bp, CDS: 501-1802 (SEQ ID NO 123)

CATTTAGTTCTGATTACAGCAGAAATCGTAGCGCGATGAGACATTTTCATCAAATGGCCTT
TTTTTTTTTGGGCAATTTTTTTTATATCTTGAAATGATAGTTGCCTTGACTTTCAACCGTT
CATTTTCATTAAGAACTTGACTAAATATGAACATTTCTTAAAAAAAAGGTTGACATATAAA
AATAATCGAATATAAACGATGGAATTTTTTATAAAATTAAACACATATATATATATATATT
AACTATAAATATGTCAAAGAAACCATAACAATCATAGATTTATAACTATCTTTTGGATGAC
ATTAATGAACATAACGCTCCTAATACAAATGTCCAAAAAATATTACCCGCAAATACGAAT
CTTTTTTTTTTCTCGATGAAATTTTGCAGAGAGTTTCGAAATTTTTTATTTCAGAGCTGGT
AGAGAAAATTTTCATAAGGTTTTCTTACCGATGCTTTTATAAAATCTTCGTTTTGTCTCAC
ATATACCAACAAGAGTAACGATGTTTTCTTTACCTACCCTAACCTCAGACATCACTGTTG
AAGTCAACAGTTCCGCTACCAAAACCCCATTCGTCCGTCGTCCGGTCGAACCGGTTGGTA
AGTTCTTTTTTGCAACATGCTCAAAGAACTTTGAGAAACCACACCTGGTCTGAATTTGAAA
GAATTGAAGCTGAAAAGAACGTCAAACCGTTGATGAATCCAATGTCGACCCAGATGAGT
TGTTATTCGACACTGAATTTGGCCGATGAAGATTTACTGACTCATGATGCTAGAGACTGGA
AACTGCCGATTTGTATGCTGCTATGGGTTTGTCTAAGTTGCGTTTCAGAGCTACTGAAA
GTCAAATCATCAAGGCTCACAGAAAACAAGTTGTCAAGTACCATCCAGACAAGCAATCTG
CTGCTGGTGGTAGTTTGGACCAAGATGGCTTTTTCAAGATTATTCAAAGGCCTTTGAAA
CTTTGACTGATTCCAACAAGAGAGCTCAGTACGACTCATGTGATTTTGTGCGGATGTTT
CTCCTCCAAAGAAGGGTACCGATTATGACTTTTATGAAGCTTGGGGCCCCGTTTTTCGAAG
CTGAAGCTCGTTTTTCTAAGAAGACTCCTATTCTTCTCTAGGTAACAAAGATTCTTCCA
AGAAGGAAGTTGAACAATTCTATGCTTTCTGGCACAGATTTGACTCCTGGAGAACCTTTG
AGTTCTTGGACGAAGATGTCCAGATGACTCTTCTAACAGAGACCACAAGCGTTACATTG
AAAGAAAGAACAAGGCCGCAAGAGACAAGAAGAAGACTGCTGATAACGCTAGATTGGTCA
AACTTGTTGAAAGAGCTGTCAGTGAAGATCCCCGTATCAAATGTTCAAAGAAGAAGAGA
AGAAGGAAAAGGAAAGAAGAAAATGGGAAAGAGAAGCCGGTGCCAGAGCTGAAGCTGAAG
CTAAGGCCAAGGCCGAAGCTGAAGCGAAGGCTAAAGCTGAATCTGAAGCCAAGGCTAACG
CCTCCGCAAAAGCTGACAAAAAGAAGGCTAAGGAAGCTGCTAAGGCCGCCAAGAAAAAGA
ACAAGAGAGCCATCCGTAACCTCTGCTAAGGAAGCTGACTACTTTGGTGATGCTGACAAGG
CCACCACGATTGACGAACAAGTTGGTTTGTATCGTTGACAGTTTGAATGACGAAGAGTTAG
TGTCCACCGCCGATAAGATCAAGGCCAATGCTGCTGGTGCCAAGGAAGTTTTGAAGGAAT
CTGCAAAGACTATTGTCGATTCTGGCAAACCTACCATCCAGCTTGTTGTCCTACTTCGTGT
GA

YGR285C, 433 aa (SEQ ID NO 124)

MFSLPTLTSDITVEVNSSATKTPFVRRPVEPVGKFFLQHAQRTLNRNHTWSEFERIEAEKN
VKTVDESNVDPDELLFDTELADEDLTHDARDWKTADLYAAMGLSKLRFRATESQIIKAH
RKQVVKYHPDKQSAAGGSLDQDGFVKIIQKAFETLTDSENKRAQYDSCDFVADVPPPKGT
DYDFYEAWGPVFEEAEARFSKKTPIPSLGNKDSSKKEVEQFYAFWHRFDSWRTFEFLDEDV
PDDSSNRDHRKRYIERKNKAARDKKKTADNARLVKLVERAVSEDPRIKMFKEEEKKEKERR
KWEREAGARAEAEAKAKAEAEAKAKAESEAKANASAKADKKKAKEAKAAKKKNKRAIRN
SAKEADYFGDADKATTIDEQVGLIVDSLNDDELVSTADKIKANAAGAKEVLKESAKTIVD
SGKLPSSLLSYFV

YHR010W, 1472 bp, exon1: 501-531, intron1: 532-1092, exon2: 1093-1472 (SEQ ID NO 125)

GACTCGGACGGAACCGTCTCATATTATACGTTTCAGTGAATATTTTTTCACGGAAGAATGGA
AAGGGCCTCGAAAGACGTTAATGCATCCGTACACCTACATCTTTACATTTTTTGCTGTTG
CACCTACACTGTTTTTTTTTTTTTTTTCACCTTATGAGTCCTGTATTTCTTGAAAGAGCCGAT
AACAAATATTCCAGGTGGAGTCCCGAGGCAGAATCAAGGCTGCGGAGAGAAGTTCCTCTCA
AACTAATGGGAGTGATCCGCTCAGTTCTCCCATCACGACAGAACTGTCTGAGACAAAGTC
TTTCCAGCAGAGTCCGCTACGCTCTTGCTGCAGAGATTCGCCCCGAAGGCAGGTTTCCTG
AAATTCTTTTCACTAGTAAAGTGTTCTGTTTCATGTAAACATACTGCCGTAGTTTGTAGCT
AAAATTAAAGATATATTAGATTTTTTAGAATTTCTTAGATAGTCTCAACGTGTTAAAACAA
AAGCATAACCAAAGAAAAAAATGGCTAAGTTCTTGAAAGCTGGTAAAGTTGGTACGTATC
ATTTTCAGTTTTTTGGACATCAACAAAAAACCGTGCAACTGTGGTATTAGAAATCCAAGTT
ATTAGCAGTTGATGTTGTATAATTTGAGTTTGAATTCGAGTATTGTATCTTCATATGGGA
GTAGGGAGGAAAAAGCGTGGAGATGTTAGATCTGGGAAAAAACCTTTAAATTTGAATGAT
AGCTTATTAATAGAAATATTGGACAAAAAGATGAATGATTTAGGAGCGAAACTAACGATT

ATTCATATTCATTGAGCTATACGAGGCAGTGGAAGGGTTATCAAAAAGTTGTAATTTAAA
AGAAAAAGCATCAATAGCCACCAAATAAGATGGTGAAAGTTCCGCGATATATTTGCTAA
GACCATAGGCACATGTACGCAGGCGACCAGGGCCTTTTATTTACTGTAGTTCTTTCCATG
CCCTATTAAAAATTCGTGGGCTATGATAATTTTCTCTCCCTAGTATTGAAGAACAAAA
TTGAGAATTCGCCAACTTTAAGAAGGGTTCACATTTACTAACTATTTCTTTTCTTCCT
TTTTTTACACAGCTGTCGTTGTCCGTGGTCGTTACGCCGGTAAGAAGGTTGTTATCGTTA
AACCACATGATGAAGGTTCCAAGTCTCACCATTGTTGGTCACGCTTTGGTTGCCGGTATTG
AAAGATACCCATTTGAAGGTCACCAAGAAGCACGGTGCCAAGAAGGTTGCTAAGAGAACCA
AGATCAAGCCTTTTCATCAAGGTCGTCAACTACAACCATTTATTGCCAACCAGATACACTT
TAGATGTTGAAGCTTTCAAATCCGTTGTTTCTACTGAACTTTTGAACAACCTTCCCAAC
GTGAAGAAGCTAAGAAAGTCGTCAAGAAGGCTTTTGAAGAAAGACACCAAGCTGGTAAGA
ACCAATGGTTCTTCTCTAAGTTGAGATTTTAA

YHR010W, 136 aa (SEQ ID NO 126)

MAKFLKAGKVAVVVRGRYAGKKVVIVKPHDEGSKSHPFHALVAGIERYPVKVTKKHGAK
KVAKRTKIKPFIKVVNHNLLPTRYTLDEAFKSVVSTETFEQPSQREEAKKVVKAFEE
RHQAGKNQWFFSKLRF

YHR021C, 1299 bp, exon1: 501-503, intron1: 504-1053, exon2:
1054-1299 (SEQ ID NO 127)

TTACTTACGTCTATTATAACCTTCCGCGTAAAAAAGAAATATTGACATCCTTTCTTGAT
TTAGCCCATACATTTTCACCCATGCACCATTGGATTATAAAGAAAAAATTTAATAAAAA
TCTGCCGGGGAAATTTCAGAAGAAAAAAGGAAGGTGTGTTTCGCATTTAACACGGGCCACC
ATAAACTTTTGTGTTGCCACCCATCTAGACGGGATCCGCCCCGCCCAAGGCTCTCTTCCTC
TAGCTAGGCAATGTGGCTCTCGGAAAGGAACTCCCACCAGGACGTGGTGGGAAATGCAG
CAATTCCTCTGCTTCCCGCTGACCTTTCTTGGGCCCAGTTTAGTAAGTATGCTCTCAT
CTTTCATGTGTGCTGTAACCTGCAAGTCATTAACACTATCTATAATTGATATTAGACGTT
AAAAGTTCTATATAGCATTTGCTTTTATTTAGAGAATACGAAAACACACCAGATAATTAG
TGCATATATATTAGATCAATATGGTATGTGAAAGAGATATTAAACATAAGATGTGAAGGA
AACAGAAGAGAACAAATTTTGAAGGAATGAATTCGGATGAAATTCAGTAGAAGAAAAAAG
CCTAAATAAAAAAGAAAGAAAGGAAAAATAAAGCAGTAATCAACCTCTGACATTTGATAGG
AGTATGCGTTTCCGCAAAATCAACAAATCATGCATTAACCTGGTAACGGAGACTTTAAAG
ACGTGCAAAGAAAGCAATTAATTTTATAGATAGGGAATTGAAAGGCTCTGTATAGCAGAAA
ATTTGAGATCTACTGTGGAGATAAGCATATGGTGTGAGTTATGGGTAATCTAACAATAA
TAGAACTTATAGCAGTTGAAGATGGCGGATCATGATGCCGGATACTGCTGGGTAATGAT
TTATCCTTCTTTTTTTGGAGCACAAATGCTCACTTTTCTCTCTCTCTAAGTTTCTG
ATGTATCCTACCCAACCCTACAGTTTCAAATTAACATCAATTTTTTTGTGAAACGA
CTTTCGTTTTCGTTTTCTATTTATTTTATTACAGGTTTTAGTTCAAGATTTGTTGCACCCA
ACTGCTGCTTCTGAAGCCAGAAAGCACAAGTTAAAGACTTTGGTTCAAGGCCCAAGATCC
TACTTCTTGATGTCAAATGCCAGGTTGTTTGAACATCACCAGTGTTTTTTCTCATGCT
CAAAGTGTCACTTGTGAATCATGCTCTACTGTCTTATGTACTCCAACCGGTGGTAAG
GCCAAATTATCTGAAGGTAATCTTTTCAAGAAAGTAA

YHR021C, 82 aa (SEQ ID NO 128)

MVLVQDLLHPTAASEARKHKLKTLVQGPRSYFLDVKCPGCLNITTVFSHAQTAVTCESCS
TVLCTPTGGKAKLSEGTSFRRK

YHR141C, 1262 bp, exon1: 501-504, intron1: 505-945, exon2:
946-1262 (SEQ ID NO 129)

TAAACATGGCATTTTAAATAGTACTGCCAAAATTTAATGCAATGGCAATTAGTTGGCTA
TGTTGCTACATATTATTTTCCATAGCATTTCTCTGTCACAACTTCAAATAAAAGACAGT
GACATCCGAACATCCGATACACCCATACATCATGAAATAAATCCTGACATTGGAAGAAG
TCTTGATACAAAAAAGATCGCTGTCAAAAATGCGGCCAGACTGCCGCTGCATCGTACCA
ACAGTGCGTATGTTTACAGACGGAGAGACGACCTCTAGAGAGACGTCCGTCGGTGCGGCAAC
GCTGACGGTTTAGTTGTTTACGACGGGATGATGGGTTCCGCCAGGGGGAGGGAAGGCTTTCC
ACCAAGAGAGGTAAAATTATTCGTGCAAAATGAACTCAGAGATACATCCATATTGTTGACA
ATGTATATCTTAATTGATGTGGTATTTTCACTGTTTTAACGTAAATTTGAAGGAGATTAG
CAAAAAACAATCAGTAATAATGGGTATGTGACGATTAGGAATAGACAAACCATGTTAT
TTATCTCCATTAGGGCGTGAGAGTGTAATTAGTACACAGGTACTACTAGAATGCTAAAGA
ACTTTTTAAATATCCTGAATCGTAGGGCAAATCCATGTCAAGCAAGAACTAATAGTTA

TTAAACTTCATTTACTTTTGAGCTAGTTAAATATTTTCATCATTTTCCTAAAGTACTGAAC
ACCTGAATGATACTTTTATTGGCCCTTTTAATAAGAACTCTGGTTAGAAAATATATTGAG
GATATCATTAGTAATACTCATTAGATATTTGTGAATTTAGCCGTTTCCCATTTACAGAAA
AAAGATACAACATAATTACATGTGCAGTCAAATTACTTTTTTTTAAAGATCAATTACTAAC
AATCAACTATCATGCTAAATTTGCTGTGATATCATTTTGAACCAGTTAACGTCCCAAAGA
CCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACACAAGGTTACTC
AATACAAAGCTGGTAAGGCTTCCTTGTTCGCTCAAGGTAAGAGACGTTATGACCGTAAAC
AATCTGGTTTTCGGTGGTCAAACCAAGCCTGTTTTCCACAAGAAAGCTAAGACTACCAAGA
AGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACTAGAGCCCAATTAACCTTGAAGA
GATGTAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGCTTTGCAATTCT
GA

YHR141C, 106 aa (SEQ ID NO 130)

MVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGFGGQTKPVFHK
KAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YHR217C, 962 bp, CDS: 501-962 (SEQ ID NO 131)

CATCGCTTGATTTCCGGCCTGCAAAAATAAAGTAGTCGGTACGTACTTTCGTTTTCAATT
TCCATGGTGCACAGTATCTTAATACTATCTGCTTAGTCGAGGAGAACCAGGATTCTGTTCGT
TGCTCAGCCGCTTCGTGGATATTCTCTTGATACCTTAAACATGGACCTACGTTCCGCTC
TCGAAAAGACCAATATAATAAAAAGTTATAAATTACATTTCTTTATTAGGTATACGACCT
CGCGCTTCGAAGTAGAGGAGCCCTTTTTGGCGTACCTACATATGGCGCGTCAGACAGACA
AACTTCCCCCAAAAATGTATTACCCCGCCGAATAAGAAAACAGACCCATTACCCACGAC
GTATCAAGTTACTTCTTGGTGCAATGTCCCACTATAAAAAAATTCCTTGACGCTAGATC
GTTGGACTAAAATCTGCGTCACAATCGCCTAAACAGGAAATATTGCCTATTTTCGTACAA
GGTTACTTCTTAGATGCTATATGTCCCTACGGCCTTGTCTAACACCATCCAGCATGCAAT
ACAGTGACATATATATACACACACCACACCCACACCCACACCCACACCCACACACACCCA
CACACACACACCCACACACACCCACACCCACACCCACACCCACACACACACACACACC
CACACACACACCCACACCCACACCCACACCCACACCCACACACACACACACACCCTATCTA
ACCTGTCTCTTAACCTACCCTCACATTACCCTACCCTCCCCACTCGTTACCCTGCCCCACT
CAACCATAACCACTCCCAACCACCATCCATCTCTCTACTTACTACTACCATCCACCGCCCA
TCATAACCGTTACCCTCCAATTACCCATATCCAACCTCCACTACCATTACCCTGCTATTAC
CCTACCATCCACCATGTCTACTCACTGTACTGTTGTTCTACCCTCCATATTGAAACGTT
AA

YHR217C, 153 aa (SEQ ID NO 132)

MSLRPCLTPSSMQYSDIYIHTPHPHPHPHPTPTHTHPHPTPTPHPHPHPTPHPHPTPTP
TPHHTHTPHTTSLNLSLNLPSHYPTSPVLTLPHSTIPLPTTIHLSTYYYHPPPIITVTLQ
LPISNSTTITLLLPHYHPPCPHCTVVLPSILKR

YIL112W, 3752 bp, CDS: 501-3752 (SEQ ID NO 133)

TTCCATAGGGCTTATTTTCCAGTTGATGGAATGGGAGGTTGCTCTTAACGCGAAGACTAA
CGTGCAAGCCAACAGTTATAGAAAAGTACCGTGAGAGAGAAAAAAGATATAGCA
TTCAATGAGGCTTTATTGAGGGGCACGATGCTCTTTTTTTCTTCTGTACTTTATAAATAA
TTCCGTATTTCTTCGCTTTGTTTCATGCTCTGTTCTGAGCTTTTAGTTTCTCTTATTGAG
AGCCTTTTCCAAATCAAGGCTCAGGAAGTGACTCGTCCTTAGAAGAACAAGGTTTGATT
TGGTAGGGTTCTTGTACGAAGTTCTCAATATAATTTGCGCATTTACTGTACGGTTCATAC
TAGTTTATTCCGGGTAAACAAGTTTTCTTGTGATGCTAAATCAATGTGTATATTGAGAAA
CTATGTAGTAAGTTACACAAAGCAACAAAGGATATTATTATATGTGACAGAGAAGAATTG
CTGTAGAGATTATGACAATATGAATGAGACTACTACAAAACAGCCGCTAAAGAAAAGGT
CCCTGAGCAGCTATCTTTCAAACGTGAGCACGAGACGGGAGGAGCTGGAAAAGATTCTA
AACAAGAAACATCCGAAGAGGAAGATACTGCCGGCAAGCATGAACAAAGGGAAACACTGT
CGGAAGAAGTAAGTGATAAGTTTCCAGAAAATGTTGCATCGTTTCGCTCACAGACTACAA
GCGTTTCAATCAAGCCACCCAAAATAACCTGAATGCAAAGGAATCCGAAGACCTGGCCCAT
AGAATGATGCGAGTTCACACGAAGGAGAGGTTAATGGGGACAGCCGTCCGGACGATGTTT
CTGAAACGAATGAAAAAATAAGCCAAGCAATACGAGCGAAAATTTTCGTCATCATCATCAT
CACCAATGTACGTAATGTTGATATCCAAAACCATCAACCTTTTTTCGAGAGACCAACTTC
GAGCGATGTTGAAAGAACCAGAAAAGGAAAAGTGTGATGATTTATAGAGAAGAGGGTT
TGGGAGCTGTTGAAAGAAGAGGATTTAAGTGATGAGGTACTTGAAAAAATACAACAGAAC
CAGAAAATGTGGAAGAAGATATAGAGTATAGCGACTCAGATAAGGACACAGACGATGTGG

GAAGCGATGATCCACGGCACCCAACTCACCAATAAACTTGGTCGTCGCAAACCTGGTTA
GAGGTGACCAACTTGATGCAACAACAAGTTCCATGTTTAAATAACGAATCAGATTCTGAAT
TATCAGATATCGATGATAGCAAGAATATTGCTTTATCCAGTAGCCTATTTAGAGGCGGTT
CTTCACCTGTGAAAGAGACAAACAACAACCTTTCAAATATGAATTCTTCACCAGCACAAA
ATCCAAAAAGGGGTTCTGTCTCCAGGAGTAATGATAGTAACAAGAGTTCTCATATAGCTG
TTTCCAAGCGCCCCAAACAGAAGAAGGGCATATATAGGGATTCTGGTGGTAGAACAAGAC
TACAGATTGCCTGTGACAAGGGCAAATATGATGTAGTCAAAAAGATGATTGAAGAAGGAG
GTTACGATATTAATGACCAAGACAATGCTGGTAATACAGCATTGCATGAAGCGGCGTTGC
AAGGTCATATTGAGATTGTGGAACCTGTTGATAGAAAATGGTGCAGATGTAAATATCAAGT
CTATTGAAATGTTTCGGCGATACTCCCTTGATCGATGCTTCCGCCAATGGACACTTGGATG
TTGTCAAGTATCTTCTTAAAAACGGTGCGGACCCAACTATACGTAACGCTAAAGGGTTAA
CTGCGTTTGAATCTGTGCGATGATGAATCTGAATTTGATGATGAAGAAGACCAAAAAGATTT
TGCGTGAAATAAAAAAAGGTTGAGTATAGCCGCTAAAAAATGGACTAACAGAGCAGGAA
TTCATAATGACAAATCTAAAAATGGCAATAATGCTCACACAATAGATCAGCCACCTTTTG
ATAATACCACAAAAGCCAAAAACGAAAAGGCCGCTGACTCACCTTCAATGGCTTCCAATA
TTGATGAGAAAGCTCCGGAAGAGGAATTTCTATTGGACAGATGTTACTTCTAGAGCGGGAA
AAGAAAACTGTTTAAAGCTTTCGAAGGAGGGACATTTACCATACGTTGGTACGTATGTAG
AAAATGGTGGTAAGATAGACTTAAGGTCATTTTTCGAAAGCGTTAAGTGTGGCCATGAAG
ATATTACAAGTATCTTTTGGCATTTCGGATTTCCCGTAAATCAAACCTTCAAGGGATAATA
AAACATCCGCTTTAATGGTAGCTGTAGGTCGTGGCCATCTTGGAAGTGTAAACTGCTAT
TAGAGGCAGGTGCAGATCCAACCAAAAGAGATAAAAAGGGTCGTACCGCTTTGTACTATG
CCAAAAACAGCATAATGGGAATAACAAACAGTGAAGAAATTCAATTGATTGAAAATGCTA
TAAATAACTATTTGAAGAAGCACTCTGAAGATAATAATGATGATGATGATGATGATGATA
ATAATAATGAAACATATAAACATGAAAAAAGAGAGAGAAAACGCAATCACCCATATTAG
CAAGCCGAAGAAGTGCCACTCCTAGAATTGAAGACGAAGAGGACGATACGAGGATGCTCA
ATCTGGCAGACGATGACTTTAATAACGATCGTGATGTCAAGGAATCTACAACCTTCGGATT
CGCGCAAGAGATTGGATGACAATGAAAATGTTGGTACTCAATACTCATTGGACTGGAAAA
AACGTAAAACAAATGCCTTGCAAGATGAAGAAAAATTA AAAAGTATCTCACCCTCTCTA
TGGAACCTCATTCTCAAAGAAGGCAAAATCTGTAGAGATAAGTAAAATACATGAAGAAA
CGGCTGCTGAAAGAGAAGCAAGACTCAAGGAAGAGGAAGAATACAGAAAGAAAAGATTAG
AAAAGAAAAGAAAAAAGAACAGGAACCTACTACAAAAGCTGGCCGAAGATGAGAAAAAAA
GGATCGAAGAACAGGAGAAGCAGAAAGTCTTAGAAATGGAAAGATTGGAAAAAGCTACTT
TAGAGAAAGCAAGAAAAATGGAAAGGGAAAAAGAAATGGAAGAAATCTCTTATAGAAGGG
CAGTAAGGGACTTATATCCGTTAGGACTGAAGATTATTAACCTCAACGATAAACTTGATT
ACAAAAGATTTTTCGCGCTATATTATTTTGTAGACGAAAAAACGATAAATTTGTGCTCG
ACTTGCAAGTAATGATATTGTTGAAGGATATCGACTTGCTCTCAAAGGACAACCAACCAA
CTTCTGAGAAGATTCCCGTCGATCCCTCGCACCTGACTCCATTGTGGAATATGTTGAAAT
TCATTTTCCTGTATGGAGGTAGTTATGATGATAAAAAGAACAACATGGAAAATAAAAGAT
ATGTTGTAACTTTGATGGGGTTGATTTGACACAAAGATTGGGTATGAGCTTTTGGAGT
ACAAAAAATTTGTTAGTTTGGCCATGGCGTGGATTAAATGGGATAACGTTGTTATTGAAA
ACCACGCAAAAAGAAAAGAAATTGAAGGAAATATGATTCAAATATCAATAAACGAATTTG
CACGATGGAGAAACGATAAGCTGAACAAAGCGCAGCAGCCGACGCGCAAACAGCGTTCTC
TAAAAATACCTCGAGAGTTACCGGTTAAATTTCAACACCGTATGAGCATATCCTCCGTCC
TCCAGCAGACATCCAAAGAACCATTTTGGTAA

YIL112W, 1083 aa (SEQ ID NO 134)

MNETTTKQPLKKRSLSSYLSNVSTRREELEKISKQETSEEDTAGKHEQRETLSEEVSDK
FPENVASFRSQTTSVHQATQNNLNAKESEDLAHKNDASSHEGEVNGDSRPDDVPETNEKI
SQAIRAKISSSSSPNVRNVDIQNHQPFSDQLRAMLKPKRKTVDDFIEEEGLGAVEEE
DLSDEVLEKNTTEPENVEKDIEYSDSKDITDDVGSDDPTAPNSPIKLGRRLVVRGDLDA
TTSSMFNNESEDSELSIDDDSKNIALSSSLFRGGSSPVKETNNNLSNMNSSPAQNPKRGSV
SRSDSNKSSHIAVSKRPKQKKGIYRDSGGRTRLQIACDKGKYDVVKMIEEGGYDINDQ
DNAGNTALHEAALQGHIEIVELLIENGADVNIKSIEMFGDTPLIDASANGHLDVVKYLLK
NGADPTIRNAKGLTAFESVDDESEFDDEEDQKILREIKKRLSIAAKKWTNRAGIHNDKSK
NGNNAHTIDQPPFDNTTKAKNEKAADSPSMASNIDEKAPEEEFYWTDVTSRAGKEKLFKA
SKEGHLPYVGTYYVENGKIDLRSFESVKCGHEDITSIFLAFGFPVNQTSRDNKTSSALMV
AVGRGHLGTVKLLLEAGADPTKRDKKGRALYYAKNSIMGITNSEEIQLIENAINNYLKK
HSEDNNDDDDDDDNNNETYKHEKKREKTQSPILASRRSATPRIEDEEDDTRMLNLADDDF
NNDRDVKESTTSDSRKRLDDNENVGTQYSLDWKKRKTNALQDEEKLKSSISPLSMEPHSPK
KAKSVEISKIHEETAAREARLKEEEEYRKKRLEKKRKKEQELLQKLAEDEKKRIEEQEK

QKVLEMERLEKATLEKARKMEREKEMEEISYRRVRDLYPLGLKIINFNDKLDYKRFLPL
YYFVDEKNDKFVLDLQVMILLKIDIDLLSKDNQPTSEKIPVDP SHLTPLWNMLKFIFLYGG
SYDDKKNMENKRYVNFVDGVDLDTKIGYELLEYKKFVSLPMAWIKWDNVVIENHAKRKE
IEGNMIQISINEFARWRNDKLNKAQQPTRKQ RSLKIPREL PVKFQHRMSISSVLQQTSKE
PFW

YIL115C, 4883 bp, CDS: 501-4883 (SEQ ID NO 135)

TTTCAATGCGCTACAACTGACTGAACCAGTCCACAAATTTGGCTGGTCTCTATCGTTCTC
GCCCTGAGAGATTTTATTTTCTTATAAATTTTACTAAATAAGGATTTGTACTTTTGATAG
AGTTTTTTTTTTTTCTGACGTTTGTGTTAGTTAATATTATATAATAGTATTTAGGAACTA
GGTGGGAGGGGACATCGCAACTTTTATCGTGACCTACGACCAGTGTTTTTTCAATTGTTT
GATCAAAAGAGAAAAAAGACAAAGGACCGAAGGATAGTTGCACGCATAAACTGGAGAAA
AAATTGTGTTTGACATCGGCGTTTAGGCTTGTTGTTCTGTACACATACGCTGCTTCAC
ACCAATTCATATTTCTCAGGTAAATTTGTCTCCTCTCCAACCTCAATAACGATTTTGCGT
GAAGGTTTAATTTCAATTATTGCAATTTTAGCAGAGAAACGCACATAAATATATATATT
GATTACAGAACCATTATAACATGTCTTCTTTGAAGGATGAAGTACCCACTGAGACTTCCG
AAGACTTCGGTTTTAAGTTTTTAGGTCAAAAACAAATCTACCTTCTTCAATGAAAAAC
TGCCATTTGCATCTCTACAAAATCTCGATATTTCAAACAGTAAGTCTTTATTCGTTGCTG
CCTCTGGTAGTAAGGCGGTGGTCCGCGAATTACAATTACTGAGAGATCATATCACCTCCG
ACTCTACTCCGTAAACGTTCAAGTGGGAGAAAGAAATCCCAGATGTAATATTTGTGTGCT
TTCATGGTGATCAGGTTTTGGTTTTCAACCAGAAATGCATTATATTCGTTAGACTTGGAGG
AATTGAGTGAATTTTGAACGGTCACTTCTTTTGAGAAGCCAGTTTTCCAATTGAAGAACG
TTAATAACACTTTAGTAATTTTAAATTCAGTCAATGATTTATCAGCACTGGATTTAAGAA
CAAAATCGACTAAGCAACTGGCACAAAACGTTACCTCTTTTGATGTACAAATTCGCAGT
TAGCAGTTCTACTAAAAGATAGAAGTTTTCAAAGTTTTGCATGGCGAAATGGCGAAATGG
AAAAACAATTTGAGTTCTCTCTACCGTCAGAAATTAGAAGAGCTTCCAGTAGAAGAATATT
CCCCTTTGAGTGTTACCATTCTCTCTCCACAGGATTTTTTTGGCGGTTTTCCGTAATGTTA
TATCAGAGACCGATGACGAAGTTTCATACGATCAAAAAATGTACATTATAAAGCACATAG
ACGGCAGCGCCTCATTTCAAGAACTTTTGATATTACACCTCCATTCCGGGCAAATAGTAA
GGTTCCCATATATGTACAAAGTTACCTTGCTCTGGTTTTAATTGAACCTGATGCAAACGTAA
ATGTGCTAGCATCATCATGTTCAAGTGAAGTAAGTATATGGGACTCGAAACAAGTTATTG
AACCTTCCCAGGATTCTGAACGAGCAGTATTGCCCATCAGTGAGGAAACAGATAAGGACA
CAAATCCAATAGGTGTGGCAGTTGACGTCGTTACTTCAGGCACCTATTCTAGAACCCTTGTT
CCGGTGTTGATACGATAGAGCGATTGCCGCTCGTTTACATATTGAATAACGAAGGTAGCT
TACAGATAGTCGGGTGTTTCATGTGGCAGCAATCAAAGCGGCCATTATAGCATAAATC
TGGAATCTTTAGAACATGAGAAATCTCTCTCTCTACATCAGAAAAAATTCCTATTGCTG
GACAGGAGCAGGAAGAAAAAAGAAAAATAATGAATCAAGTAAGGCTTTATCAGAGAATC
CTTTCACATCAGCAAATACATCAGGCTTCACTTTTCTTAAACACAACCAGCCGCTGCCA
ATAGCCTGCAGTCTCAAAGTTCTTCAACCTTTGGTGCTCCCTCATTTGGATCATCCGCAT
TTAAATTTGACTTGCCATCAGTCTCATCTACCAGTACTGGTGTAGCGTCCAGTGAACAAG
ACGCAACAGATCCTGCTTCTGCTAAGCCAGTATTCCGGCAAACCCGCGTTCCGAGCTATTG
CCAAAGAACCGTCAACATCAGAAATATGCCCTTTGGCAAGCCATCTTTTGGTGCTCCCTCCT
TTGGCTCTGGAAAGTCATCTGTTGAATCGCCTGCCCTCCGGATCTGCCTTTGGTAAGCCCT
CTTTTGGTACTCCTTCCTTTGGCTCTGGAAATTCATCTGTTGAGCCGCCCTGCCCTCCGGAT
CTGCATTTGGTAAGCCCTCTTTTGGTACTCCTTCCTTTGGCTCTGGAAATTCATCTGCTG
AGCCGCCCTGCTTCCGGATCTGCCTTTGGTAAGCCCTCTTTTGGTACATCTGCATTCGGAA
CTGCATCAAGTAACGAACTAACTCTGGATCCATATTTGGAAAGGCTGCATTTGGTTCAT
CATCTTTTGCACCCGCCAACAATGAACTTTTCGGATCAAACCTTTACTATTTCAAACCTA
CAGTTGACAGCCCAAAGGAGGTAGATTCAACGTCACCTTTCCCATCTTCTGGCGATCAAA
GTGAAGATGAGTCTAAGAGTGATGTAGACTCTTCTTCGACACCTTTTGGTACGAAACCTA
ACACCTCTACGAAACCAAGACCAATGCCCTTTGATTTTGGGAGTTCTTCTTTGGATCTG
GATTTTCAAAGGCTCTGGAATCTGTTGGTTCCGATACAACCTTTTAAATTCGGTACTCAGG
CTTACCTTTCTCTTACAGTTAGGAAACAAATCACCATTAGTTTCTTACAAAAGATG
ATACTGAAAATGGATCTTTAAGTAAGGGCTCTACCAGTGAAATCAATGACGATAATGAAG
AACACGAAAGCAATGGTCCCAACGTAAGCGGTAATGATTTGACAGATTCTACGGTTGAGC
AAACATCTTCTACTAGATTACCGGAAACTCCCTCGGATGAAGATGGTGAAGTTGTGAGG
AGGAAGCGCAAAAATCCCCCATAGGCAAGCTAACTGAACTATAAAAAAAGTGCCAATA
TTGACATGGCTGGTTTAAAAAATCCTGTATTTGGAAATCATGTCAAAGCAAAATCCGAAT
CGCCGTTTTACGATTTGCAACAAATATTACCAAACCAAGCTCTACAACACCTGCTTTTT
CGTTTGGTAACCTCCACAATGAATAAAAGTAATACATCTACGGTTTCACCAATGGAAGAAG

CTGATACTAAAGAACTAGTGAAAAGGGCCCCATAACCTTGAAGAGTGTGGAGAATCCGT
TTCTACCAGCGAAAGAAGAAAGAACTGGAGAAAGTTCTAAAAAGGATCATAACGATGACC
CAAAAGATGGTTATGTATCAGGAAGTGAAATATCTGTAAGGACTTCTGAAAGTGCTTTTG
ATACCACAGCAAACGAAGAAATTCCAAAGTCACAGGACGTGAACAATCATGAAAAAGCG
AAACAGACCCAAAATATAGTCAACATGCTGTGGTTGATCACGATAACAAGTCTAAAGAAA
TGAATGAACTTCGAAGAATAATGAAAGGAGCGGTCAACCAAATCATGGTGTCCAAGGAG
ATGGAATAGCATTGAAAAAGACAATGAAAAAGAGAATTTTGATTCAAATATGGCAATAA
AGCAATTGGAAGACCACCAATCTTCAGAAGAGGACGCGAGCGAAAAAGACAGTAGACAAA
GCAGTGAAGTTAAAGAATCAGATGATAACATGTCACCTCAACAGTGACCGGGATGAAAGTA
TATCTGAGTCCTACGATAAACTGGAAGATATTAATACTGATGAGCTACCTCATGGTGGAG
AAGCTTTTAAAGCACGTGAAGTGAGCGCTTCCGCTGATTTTGATGTACAACTTCATTAG
AAGACAATTATGCTGAATCTGGCATAACAGACAGACCTTTCAGAAAGTTCCAAGGAAAATG
AAGTTCAAACGGATGCCATACCCGTGAAACACAACAGTACACAACTGTTAAGAAGGAAG
CAGTCGACAATGGTCTGCAAACTGAGCCTGTTGAAACATGTAATTTTTCTGTTCAAACAT
TTGAAGGTGACGAAAATTATTTAGCAGAGCAATGCAAACCAAAGCAATTGAAAGAATATT
ACACAAGTGCAAAAGTATCAAATATTCCTTTTCGTTTCACAAAATTCTACGTTAAGGTTGA
TTGAGAGTACATTTTCAGACGGTCAAGCTGAGTTTACTGTTCTGATGGAAAACATCCGGA
ATATGGATACTTTTTTTTACTGATCAATCGAGCATCCCTTTGGTGAAGCGTACAGTGCGGT
CTATCAATAATCTGTATACTTGGAGAATACCAGAGGCTGAAATTCTATTAAATATTCAGA
ATAATATCAAGTGTGAACAAATGCAAATAACAAATGCTAACATTCAAGACCTGAAGGAAA
AAGTTACAGATTATGTCAGGAAAGATATTGCACAAATAACTGAAGATGTAGCCAATGCAA
AAGAGGAGTATCTGTTTTTAATGCATTTTGATGATGCTTCGAGTGGATACGTTAAAGATC
TCAGCACGCATCAATTTAGAATGCAAAAGACATTACGTCAAAAGCTATTCGATGTGTCCG
CCAAAATTAATCATACTGAAGAGTTGCTGAACATTTTAAATTTGTTCACTGTAAAGAATA
AGAGATTGGACGATAATCCATTAGTGGCAAACTAGCTAAAGAATCTCTTGCACGTGACG
GTTTACTAAAAGAAATCAAATTATTGCGTGAGCAAGTGAGTAGGTTACAATTGGAGGAGA
AAGGTAAAAGGCTTCGTCGTTTCGATGCATCCTCTTCAATAACAAAGGACATGAAAGGAT
TTAAAGTAGTAGAAGTTGGGTTGGCCATGAATACGAAAAAGCAAATTGGTGATTTCTTCA
AAAATTTGAACATGGCAAAATAG

YIL115C, 1460 aa (SEQ ID NO 136)

MSSLKDEVPTETSEDFGFKFLGQKQILPSFNEKLPFASLQNLDISNSKSLFVAASGSKAV
VGELQLLRDHITS DSTPLTFKWEKEIPDVIFVCFHGDQVLVSTRNALYSLDLEELSEFRT
VTSFEKPVFQLKVNNTLVILNSVNDLSALDLRTKSTKQLAQNVTSFDVTNSQLAVLLKD
RSFQSFARNGEMEKQFEFSLPSELEELPVEEYSPLSVTILSPQDFLAVFGNVISETDDE
VSYDQKMYIIKHIDGSASFQETFDITPPFGQIVRFPYMYKVTL SGLIEPDANVNVLASSC
SSEVSIWDSKQVIEPSQDSERAVLP ISEETDKDNTNPIGVAVDVVTSGTILEPCSGVDIE
RLPLVYILNNEGSLQIVGLFHVAAIKSGHYSINLESLEHEKSLSP TSEKIPIAGQEQUEEK
KKNNESSKALSENPF TSANTSGFTFLKTQPAANSLQSQSSSTFGAPSFSGSAFKIDLPS
VSSTSTGVASSEQDATDPASAKPVFGKPAFGAIAKEPSTSEYAFGKPSFGAPSFSGSKSS
VESPASGSAFGKPSFGTSPSGSGNSSVEPPASGSAFGKPSFGTSPSGSGNSSAEPPASGS
AFGKPSFGTSAFGTASSNETNSGSI FGKAAGSSSFAPANNELFGSNFTISKPTVDSPE
VDSTSPFPSSGDQSEDESKSDVDSSSTPFGTKPNTSTKPKTNAFDGSSSFSGGFSKALE
SVGSDTTFKFGTQASPFSSQLGNKSPFSSFTKDDTENGSLSKGSTSEINDDNEEHESNGP
NVSGNDLTDSTVEQTSSTRLPETPSDEDEGEVVEEEAQKSPIGKLTETIKKSANIDMAGLK
NPVFGNHVKAKSESPFSAPATNITKPSSTTPAFSFGNSTMNKSNTSTVSPMEEADTKETS
EKGPITLKSVENPFLPAKEERTGESSKKDHNDPKDGYVSGSEISVRTSESADFDTTANEE
IPKSQDVNNHEKSETDPKYSQHAVVDHDKSKEMNETSKNNERSGQPNHGVQGDGIALKK
DNEKENFDSNMAIKQFEDHQSSSEEDASEKDSRQSSEVKESDDNMSLNSDRDESISESYDK
LEDINTDELPHGGEAFKAREVSASADFDVQTSLEDNYAESGIQTDLSESSKENEVQTDI
PVKHNSTQTVKKEAVDNGLQTEPVETCNFSVQTFEGDENYLAEQCKPKQLKEYYTSKVS
NIPFVSQNSTLRLIESTFQTVAEFTVL MENIRNMDTFFTDQSSIPLVKRTVRSINNLYT
WRIPEAEILLNIQNNIKCEQMQITNANIQDLKEKVTDYVRKDIAQITEDVANAKEEYFL
MHFDDASSGYVKDLSTHQFRMQKTLRQKLFVSAKINHTEELNLKLFVKNKRLDDNP
LVAKLAKESLARDGLLKEIKLLREQVSR LQLEEKGKKASSFDASSSITKDMKGFKVVEVG
LAMNTKKQIGDFFKLNLMMAK

YIL148W, 1321 bp, exon1: 501-508, intron1: 509-942, exon2:
943-1321 (SEQ ID NO 137)

TCGATCAACTCTATCCAACAATCTATAATATCCACTGTTCATTAAACGAATATTGGTCTT

TTTCCCTTATGGTGAAGTAAATTTTCCATGCAATATCCGGGTAAGCTATCGACAAGTTTA
TTGACTGCAATTTGAGTTTATTACATCCGTACATTACTAAGATGTATGGTTTTTCTATTT
TTGTGCTCCGTGTCGATATTTTCGTGGAGCAAACCAGAAAAGATGCGGAACCTCTTAGCAC
TCCGCCTGGACATAGGCGGAGCATATTCCTCCTATGGGATGGGTTTTGTTGTACTCTTTT
CTCTCTAGACAGGACCTCCGATTGCCTCCCTGAGGGTGAGATGGTTTCCGGCCTCAGGAC
GGCCTTCTCCAGTTTCTAGCGAGGCATACATTCCAACCAAAGGTGTATCAAGAATATCTG
AAATTAAAGGTAGTTGAATCTCTATTTGTTGTTGTTATTACCGCTTATTATCCCATAGTT
GAGACGACCAAGATTCAAACATGCAATGTATGCACCATATCCATTCTAAACATAGTTTT
TCGAACGTTTCAAGCTTAAAGGGACAATTATTTTAGAACTGAATTTTTTACCCAGTGGAA
TAACATCGTATCTGTAAAGTCTACAAAATTTTTTATCCATCAAAAATTAAACAAAGAAA
ACTGCCAACTGAATATGAGGAACTTTCCTCTCTAGGAATGACTTAGTGAATGTACAGTG
ACTTGTGGAAAATATGATTAGATTTTGTAGCGGGTGATGCGACTTAACAGTCTCATTGCCT
AAGAAATATCCAAATTTGTGGTTCATGCTCTCCCCCAAGATATGACGATGAGAGCTCGTT
TAAAATTTTGTCTTCTTCCGAACAGTTATGAAAAAATTTTACGTGTTTTTATGATATCC
TTACTAACTTGTCAATTTTTTTTATAAAATTATTTTTTTTAAACAGTTTTGTCAAGACTTTGAC
TGGTAAGACCATCACTTTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCAAA
GATTCAAGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCA
ATTGGAAGACGGTAGAACCTTGTCTGACTACAACATTCAAAAAGAATCCACTTTGCACTT
AGTCTTGAGATTGAGAGGTGGTATCATTGAACCATCTTTGAAAGCTTTGGCTTCCAAGTA
CAACTGTGACAAATCTGTTTGCCGTAAGTGTTATGCTAGATTGCCACCAAGAGCTACCAA
CTGTAGAAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTAAATG
A

YIL148W, 128 aa (SEQ ID NO 138)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGIIEPSLKALASKYNCDKSVCRKCYARLP PRATNCRKRKCGHTNQ
LRPKKKLK

YIL150C, 2216 bp, CDS: 501-2216 (SEQ ID NO 139)

AATATTCAACCTGAAGTTGCAGTCAAAGCGGCGATTAACTTTTCCAACGTAACCGATCTA
ACTAACAATAGCACCGATGGAGCAAAAATAACAGAAATTGGAAGTACATCTAAACGGCCA
ATTGAGAGCGGTACATCTTCTGATCCAGACACCAAAAAGGTTAAAGAGAGTCCAGCAAAT
GATCAAGCTTCCAACGAGTGATGTAATATTAAACAATGTAATTATATAAATATGAAACAT
CTACATATTTTAAATGTCACTAATGTCAATTACAGAGGACATAAAGTGATTTATGACACAT
CCGTACTAGTAGTTAAGTATGAACAAATTTTGGGTTTATTTGCCATTTTTTTTTCACGCGG
GTTTCTTGGATGCGCAAACCCACCTTTTCTAACACCACTAAGAAATATCAACTTTATAGG
CCATCGAAGATAAAGGAACGTAAGTTTGTCATTTCAACCTCACATTTTCAACGCACATTA
AGCACTTGTTTCGTGGAGAAATGAATGATCCTCGTGAAATTTTAGCGGTGATCCGTACA
ATAATATTACTTCTGATGAAGAGGATGAGCAAGCCATCGCGAGAGAACTTGAATTTATGG
AACGAAAGAGGCAGGCCTTAGTGGAACGATTAAAAAGAAAGCAAGAATTTAAGAAACCCC
AGGATCCTAATTTTGAAGCCATCGAGGTACCTCAATCTCCTACCAAAAACCGTGTGAAAG
TGGGGTCTCATAATGCTACACAACAAGGCACAAAATTCGAAGGTTTCAATATTAATGAAG
TAAGGTTATCTCAATTACAGCAGCAACCAAAAACCACAGCTAGTACAACCACATACTTTA
TGGAGAAATTTCAAAACGCAAAGAAGAACGAAGATAAACAAATTGCCAAGTTTGAAAGCA
TGATGAATGCAAGAGTACATACGTTTCACTACCGATGAGAAGAAATATGTGCCGATAATCA
CAAACGAATTAGAAAGCTTTTCAAATCTTTGGGTTAAAAAGAGGTACATACCTGAAGATG
ACTTAAAACGGGCTTTGTCATGAGATCAAAATCCTTTCGGTTGGGCAAACCTTTTTGCTAAAA
TTCGCCCACCTAAATTTCAAGAGCCTGAATACGCCAACTGGGCCACCGTAGGCCTCATT
GCCACAAATCGGACATCAAATTTACATCATCTGAAAAGCCAGTCAAATTTCTCATGTTCA
CCATAACGGACTTTCAGCATACACTAGATGTTTATATCTTCGGGAAAAAGGGTGTAGAAA
GATATTATAATCTTCGCCTGGGTGATGTGATAGCAATATTAAACCCAGAAGTACTACCAT
GGAGACCCTCAGGGCGAGGAAATTTTATCAAATCCTTCAACCTTCGAATTAGTCATGACT
TCAAATGTATCCTGGAGATAGGTTCAAGTAGAGATTTAGGTTGGTGTCCCATAGTGAATA
AAAAGACTCACAAAAAATGTGGCTCTCCCATTAACATATCTCTTCATAAGTGTTGCGATT
ACCATAGAGAAGTGCAATTTTCGTGGAACAAGTGCTAAAAGAATTGAATTAATGGTGGGT
ACGCCTTGGGCGCGCCTACGAAAGTGGAATCTCAACCAAGCCTATATAAGGCCAAAGGGG
AAAACGGGTTTAAATATAATCAAAGGTACTCGTAAGCGCCTGTCAGAAGAGGAGGAAAGAC
TTAAAAAGAGCTCTCACAAATTTTACGAATAGTAATTCTGCCAAAGCATTTTTTCGACGAGA
AATTTCAGAATCCAGATATGCTGGCAAACCTTAGACAATAAAAGAAGGAAAATAATAGAAA
CTAAGAAATCGACAGCACTGAGCCGCGAACTAGGCAAAATTATGAGAAGGAGGGAATCCA

GCGGATTAGAAGATAAGAGCGTCCGAGAGCGACAGAAAATGAAACGAACCACAGAAAGTG
CCCTCCAGACAGGGCTTATCCAACGCCTAGGATTTCGATCCCACTCATGGAAAAATTTCCC
AAGTACTCAAGTCTTCTGTATCAGGGAGCGAACCTAAGAACAACCTTACTCGGTAAAAAAA
AACTGTTATAAACGATCTCTTGCATTACAAGAAGGAAAAAGTCATTCTCGCACCTTCAA
AGAACGAATGGTTCAAGAAAAGAAGCCATCGCGAAGAAGTTTGGCAAAAACATTTCCGAT
CCAAGGAACTAAAGAACTTCTGACGGTAGTGCCAGCGATCTTGAGATAATATAA

YIL150C, 571 aa (SEQ ID NO 140)

MNDPREILAVDPYNNITSDEEDEQAIARELEFMERKRQALVERLKRKQEFKKPQDPNFEA
IEVPQSPTKNRVKVGSHNATQQGTFEGSNINEVRLSQLQQPKPPASTTTYFMEKFQNA
KKNEDKQIAKFESMMNARVHTFSTDEKKYVPIITNELESFNLWVKRYIPEDDLKRALH
EIKILRLGKLFAKIRPPKFQEPEYANWATVGLISHKSDIKFTSSEKPVKFFMFTITDFQH
TLDVYIFGKKGVERYYNLRLGDVIAILNPEVLPWRPSGRGNFIKSFNLRI SHDFKCILEI
GSSRDLGWCPIVNKKTHKKCGSPINISLHKCCDYHREVQFRGTS AKRIELNGGYALGAPT
KVDSQPSLYKAKGENGFNIIKGTRKRLSEEEERLKKSSHNFNTNSNSAKAFFDEKFQNPDM
LANLDNKRRIIETKKSTALSRELKIMRRRESSGLEDKSVGERQKMKRTTESALQTGLI
QRLGFDPTHGKISQVLKSSVSGSEPKNLLGKKKTIVINDLLHYKKEKVILAPSKNEWFKK
RSHREEVWQKHFGSKETKETS DGSASDLEII

YIL167W, 1133 bp, CDS: 501-1133 (SEQ ID NO 141)

GACATTTTGAAAAAATTACATTTATAGAAGTTTATTATAACGTAACAGTTAACAACAAAG
GCTCATAGTCCGAGATCAATATAATAAATTATTCAAGGTTTAAGGAAGAAGTTACCATGG
AAATGACTTACTATGAAAAGACACCTTTGATTCGTCAATTTTGAACAATGGTAAGACAA
ATTCGTGGTTTTACGTTAAGCATGAGATGTTACAACCAGGTGGAAGTTTCAAATCGAGAG
GAATCGGGCATTGATAAGGAAGAGTAATGAAGAAGCGCTAAGCGAGGGTTCTGGGAAGC
TTGCTGTATTTCTAGCTCTGGGGGAAATGCTGGTTTAGCAGCAGCAACTGCCTGCAGAT
CGATGGCACTTAATTGCAGTGTAGTGGTTCCTAAACTACAAAACCTAGAATGGTAAAGA
AAATTCAAAGTGCAGGAGCCAAAGTCATTATCCATGGTGATCATTGGGGGGAAGCAGATG
AATACTTGAGGCACGAATGAATGGCGCAAGAAAGCCAACATGGTTCGAAGACACTATATG
TGCACCCGTTTGATAACGAGACAATTTGGGAAGGTCATTCTACGATTGTGGATGAAATCA
TAGAACAATTGAAGGAAAATGATATATCCTTACCTAGGGTGAAAGCTTTGGTTTGTAGTG
TTGGTGTTGGTGTTGGGCTATTTAGTGGCATAATTAAAGGCCTAGATAGGAATCAGCTTGCTG
AAAAAATTCGGTCGTTGCTGTAGAACTGCCGGTTGTGACGTATTGAATAAGTCTCTCA
AAAAAGGTAGTCCAGTTACTCTTGAAAAATTGACAAGTGTTGCAACTTCTTTGGCCTCCC
CATACATAGCATCATTCGCGTTTGAGAGTTTTAACAAGTATGGATGTAAGTCTGTAGTTT
TATCAGATCAAGACGTTCTGGCAACATGCTTGAGATATGCCGATGACTACAATTTTATAG
TGGAACCAGCCTGTGGAGCATCCTTACATTTATGTTATCATCCAGAGATTCTTGAAGACA
TTCTGGAACAAAAAATATATGAGGATGATATCGTTATTATAATCGCATGCGGTGGATCAT
GTATGACGTATGAAGACTTGGTGAAAGCGTCGAGCACATTAAACGTATCATAA

YIL167W, 210 aa (SEQ ID NO 142)

MAQESQHGSKTLYVHPFDNETIWEHSTIVDEIIIEQLKENDISLPRVKALVCSVGGGGLF
SGIIKGLDRNQLAEKIPVVAVETAGCDVLNKSLLKKGSPVTLEKLT SVATSLASPYIASFA
FESFNKYGCKSVVLSQDVLATCLRYADDYNFIVEPACGASLHLCYHPEILEDILEQKIY
EDDIVIIIACGGSCMTYEDLVKASSTLNVS

YJL034W, 2549 bp, CDS: 501-2549 (SEQ ID NO 143)

CCATGAACTCAGCATGTGCTACTCCAGTTAATGACTTGTTCTGTATCGTTCATGCCATAAG
CCATCACCTGGCCAGTTGGCGTATGTACAAAGATGCAAGCTACCGGTGTCTCATCGTGGT
CAAGAGCGTATCTAGCCAAACGGACAGCTGTCCTCATATGTTTAATATGCTGCATAGTGT
GAGTCCTCTAGTTTTTACCGCAGCCACCAGCCGCTTCTCGAGCAAAGTG TAGATCCCATT
AGGACTCATCATTCATCTAATTTTGCTATGTTAGCTGCAACTTTCTATTTTAAATAGAACC
TTCTGGAAATTTACCCGGCGCGGCACCCGAGGAAGTGGACAGCGTGTGAAAAAGTTGC
TTTTTTATATAAAGGACACGAAAAGGGTTCTCTGGAAGATATAAATATGGCTATGTAATT
CTAAAGATTAACGTGTTACTGTTTTACTTTTTTAAAGTCCCCAAGAGTAGTCTCAAGGGA
AAAAGCGTATCAAACATACCATGTTTTTCAACAGACTAAGCGCTGGCAAGCTGCTGGTAC
CACTCTCCGTGGTCTGTACGCCCTTTTCGTGGTAATATTACCTTTACAGAATTCTTTCC
ACTCCTCCAATGTTTTAGTTAGAGGTGCCGATGATGTAGAAAACCTACGGAAGTGTATCG
GTATTGACTTAGGTACTACTTATTCCTGTGTTGCTGTGATGAAAAATGGTAAGACTGAAA
TTCTTGCTAATGAGCAAGGTAACAGAATCACCCCATCTTACGTGGCATTACCGGATGATG

AAAGATTGATTGGTGATGCTGCAAAGAACCAAGTTGCTGCCAATCCTCAAAACACCATCT
TCGACATTAAGAGATTGATCGGTTTGAATATAACGACAGATCTGTTTCAGAAGGATATCA
AGCACTTGCCATTTAATGTGGTTAATAAAGATGGGAAGCCCGCTGTAGAAGTAAGTGTCA
AAGGAGAAAAGAAGGTTTTTACTCCAGAAGAAATTTCTGGTATGATCTTGGGTAAGATGA
AACAAATTGCCGAAGATTATTTAGGCACTAAGGTTACCCATGCTGTCGTTACTGTTCTTG
CTTATTTCAATGACGCGCAAAGACAAGCCACCAAGGATGCTGGTACCATCGCTGGTTTGA
ACGTTTTGAGAATTGTTAATGAACCAACCGCAGCCGCCATTGCCTACGGTTTGGATAAAT
CTGATAAGGAACATCAAATTATTTGTTTATGATTTGGGTGGTGGTACTTTTCGATGTCTCTC
TATTGTCTATTGAAAACGGTGTTTTTCGAAGTCCAAGCCACTTCTGGTGATACTCATTTAG
GTGGTGAAGATTTTGACTATAAGATCGTTCGTCAATTGATAAAAGCTTTCAAGAAGAAGC
ATGGTATTGATGTGTCTGACAACAACAAGGCCCTAGCTAAATTGAAGAGAGAAGCTGAAA
AGGCTAAACGTGCCTTGTCCAGCCAAATGTCCACCCGTATTGAAATTGACTCCTTCGTTG
ATGGTATCGACTTAAGTGAAACCTTGACCAGAGCTAAGTTTGAGGAATTAAACCTAGATC
TATTCAAGAAGACCTTGAAGCCTGTGCGAGAAGGTTTTGCAAGATTCTGGTTTGGAAAAGA
AGGATGTTGATGATATCGTTTTTGGTTGGTGGTTCTACTAGAATTCCAAAGGTCCAACAAT
TGTTAGAATCATACTTTGATGGTAAGAAGGCCTCCAAGGGTATTAACCCAGATGAAGCTG
TTGCATACGGTGCAGCCGTTCAAGCTGGTGTCTTATCCGGTGAAGAAGGTGTCGAAGATA
TTGTTTTATTGGATGTCAACGCTTTGACTCTTGGTATTGAAACCACTGGTGGTGTCTATGA
CTCCATTAATTAAGAGAAATACTGCTATTCCTACAAAGAAATCCCAAATTTTCTCTACTG
CCGTTGACAACCAACCAACCGTTATGATCAAGGTATACGAGGGTGAAAGAGCCATGTCTA
AGGACAACAATCTATTAGGTAAGTTTGAATTAACCGGCATTCCACCAGCACCAAGAGGTG
TACCTCAAATTGAAGTCACATTTGCACTTGACGCTAATGGTATTCTGAAGGTGTCTGCCA
CAGATAAGGGAAGTGGTAAATCCGAATCTATCACCATCACTAACGATAAAGGTAGATTAA
CCCAAGAAGAGATTGATAGAATGGTTGAAGAGGCTGAAAAATTCGCTTCTGAAGACGCTT
CTATCAAGGCCAAGGTGAATCTAGAAACAAATTAGAAAACCTACGCTCACTCTTTGAAAA
ACCAAGTTAATGGTGACCTAGGTGAAAAATTGGAAGAAGAAGACAAGGAAACCTTATTAG
ATGCTGCTAACGATGTTTTAGAAATGGTTAGATGATAACTTTGAAACCGCCATTGCTGAAG
ACTTTGATGAAAAGTTCGAATCTTTGTCCAAGGTGCGCTTATCCAATTACTTCTAAGTTGT
ACGGAGGTGCTGATGGTTCTGGTGCCGCTGATTATGACGACGAAGATGAAGATGACGATG
GTGATTATTTGGAACACGACGAATTGTAG

YJL034W, 682 aa (SEQ ID NO 144)

MFFNRLSAGKLLVPLSVVLYALFVVILPLQNSFHSSNVLVRGADDVENYGTVIGIDLGT
YSCVAVMKNGKTEILANEQGNRITPSYVAFDDELRIGDAKNQVAANPONTIFDIKRLI
GLKYNDRSVQKDIKHLFPNVVNKDGKPAVEVSVKGEKKVFTPEEISGMILGKMKQIAEDY
LGTKVTHAVVTVPAYFNDAQRQATKDAGTIAGLNLVRIVNEPTAAAIAYGLDKSDKEHQI
IVYDLGGGTFDVSLLSIENGVEVQATSGDTHLGGEDFDYKIVRQLIKAFKKKHGIDVSD
NNKALAKLKREAEKAKRALSSQMSTRIEIDSFVDGIDLSETLTRAKFEELNLDLFFKTKL
PVEKVLQDSGLEKDVDDIVLVGGSTRIPKVQQLLESYFDGKKASKGINPDEAVAYGA
QAGVLSGEEGVEDIVLLDVNALTGLIETGGVMTPLIKRNTAIPTKKSQIFSTAVDNQPT
VMIKVYEGERAMSKDNNLLGKFELTGIPAPRGVPQIEVTFALDANGILKVSATDKGTGK
SESITITNDKGRLTQEEIDRMVEEAKEFASSEDASIKAKVESRNKLENYAHSKLNQVNGDL
GEKLEEDKETLLDAANDVLEWLDNDFETAIAEDFDEKFESLSKVAYPITSKLYGGADGS
GAADYDDEDEDDDDGDYFEHDEL

YJL035C, 1253 bp, CDS: 501-1253 (SEQ ID NO 145)

TACCTAAGTCAATACCGATAACAGTTCCTAGTTTTCTACATCATCGGCACCTCTAACTA
AAACATTGGAGGAGTGGAAGAATTCTGTAAAGGTAATATTACCACGAAAAGGGCGTACA
GGACCACGGAGAGTGGTACCAGCAGCTTGCCAGCGCTTAGTCTGTTGAAAAACATGGTAT
GTTTGATACGCTTTTTCCCTTGAGACTACTCTTGGGGACTTTAAAAAAGTAAAACAGTAA
CACGTTAATCTTTAGAATTACATAGCCATATTTATATCTTCCAGAGAACCCTTTTCGTGT
CCTTTATATAAAAAAGCAACTTTTTCGACACGCTGTCCAGTTCCTCGGGTGCCGCGCCGG
GTGAAATTTCCAGAAGGTTCTATTAATAAGAAAGTTGCAGCTAACATAGCAAAATTAGA
TGAATGATGAGTCCTAATGGGATCTACACTTTGCTCGAGAAGCGGCTGGTGGCTGCGGTA
AAAACCTAGAGGACTCACACTATGCAGCATATTAACATATGAGGACAGCTGTCCGTTTGG
CTAGATACGCTCTTGACCACGATGAGACACCGGTAGCTTGCATCTTTGTACATACGCCAA
CTGGCCAGGTGATGGCTTATGGCATGAACGATACGAACAAGTCATTAACCTGGAGTAGCAC
ATGCTGAGTTCATGGGGATCGATCAGATCAAGGCGATGTTGGGCTCCCGAGGAGTTGTTG
ACGTGTTCAAAGACATTACTCTATATGTTACTGTAGAACCGTGTATAATGTGTGCATCTG
CTCTCAAGCAATTAGACATTGGAAGGTGGTGTTCGGTTGTGGCAACGAGAGATTTGGAG

GCAACGGTACTGTCTTGTCAGTAAATCATGATACGTGTACATTAGTGCCCAAGAACAATA
GTGCGGCAGGGTACGAGAGTATACCGGGGATCTTGAGGAAAGAAGCAATAATGCTGCTGA
GATACTTTTATGTAAGACAAAATGAAAGGGCGCCAAAGCCACGGTCCAAGAGTGACAGAG
TGTTGGATAAAAACACGTTTCCGCTATGGAATGGTCAAAGTATCTTAATGAAGAAGCAT
TCATTGAGACTTTTGGTGATGATTACAGGACTTGTTTTGCGAATAAAGTTGACTTGTTCCA
GTAATAGCGTCGATTGGGATTTGATTGACTCCCAAGATAATATAATCCAAGAAGTGG
AAGAACAATGCAAAATGTTTAAGTTTAATGTACATAAGAAATCTAAGGTTTGA

YJL035C, 250 aa (SEQ ID NO 146)

MQHIKHMRTAVRLARYALDHDETPVACIFVHTPTGQVMAYGMNDTNKSLTGVAHAEFMGI
DQIKAMLGSRGVVDVFKDITLYVTVEPCIMCASALKQLDIGKVVFCCGNERFGNGTVLS
VNHDTCTLVPKNNSAAGYESIPGILRKEAIMLLRYFYVRQNERAPKPRSKSDRVLDKNTF
PPMEWSKYLNEEAFIETFGDDYRTECFANKVDLSSNSVDWDLIDSHQDNIIQEELEEQCKMF
KFNVHKKSKV

YJL070C, 3167 bp, CDS: 501-3167 (SEQ ID NO 147)

TCCCCTGATGGTCAAATACTGTGCATGGCATCCCGTGCAGTCAAGGATGCTTTGAGACTA
GTTTCATCTGCCTTCTTGTCAGTGTTCAGCAACTGGCCTACCAGCGGGACGCCTTTGGGT
AAAGTTACCAGTGTTCGCATTTTCGCCATCTGGTGGGCTACTGGCCGTGGGTAACGAACAA
GGTAAAGTGAGGCTCTGGAAATTAAACCACTACTAAATTTCCATTTATAGACAAACTTAG
ATATTAAAAGCAATGTACAAATACATACACAAAATATCACTGTAAAAAATTGCGAAGAA
ACTTGAAATTGAATATGATTCTGCCCACTTTTTTCTTGCTGTCAATTTATAGTCAGAAATG
AAAAATTGTCCGAGAAATTAAATATAATATATGGAAAAAAGGGGACATTGAGTTTAAAG
AATTTGATTAAAAATGTCCTCTCAATATCCTCTGTAAGAGTTATCTAAATCTCACTTTACT
TATTCATCTCGCTGGGAATTATGCAGGCGGTAGAGAGAAGGCCCTCGTTACTCTTTGACG
AATATCAAATTTCTGTTACTAAGCCTAATGAGACGAAGAATAAAGAAGCCAGGGTCTTGT
CAGAGAATGACGGTGATGTCTCCCATCTGTTTTGAAACAGAAGGAAATATCAGTCGATG
ATATGGATATGATTTCTTTGCCACGGAATTTGACAGGCAAATGGTTTTAGGTTACCTA
TGTTTTTCGATCTTGAAGACGAAGAAACAAAATTGATCCACTTCCTTCAGTTTCCCATC
ATTATGGAAATGGAGAAAGTGACAGCTTTGTCTCATCGTACACGCCCTCAAATCTGAAAA
CGGGTGAAGAACTAAAGATCTTTTCATTAATCCGTTTGAATTGCTTTCTCAAATGAGAA
AAAGATACATTGCTGCTTCCAAACAAGATGGCATTTCAAACATAAAAAATGACACTGAAA
AGTGGTTTTTATACCCAAAACCACTGCCAAAGTTTTGGAGATTTGAAGACGATAAACGAT
TCCAAGATCCCTCTGACTCTGACTTAAATGACGATGGAGACAGTACTGGGACCGGAGCCG
CTACACCGCACCGCCATGGCTACTATTACCCAAGTTACTTTACCGATCACTACTACTACT
ACACAAAATCTGGTTTGAAAGGAAAAGGAAATATAAAAGTACCATACACCGGTGAATATT
TCGATTTAGAGGATTACAAAAACAATACATTTACCATTAAAGTAATCAGGAAAATACGC
AAAACCCACTTTCACCTTATTCTAGTAAGGAGGAGTCACTAGAGGAAGAATTTTAAACAG
ATGTGCCCTACGTTTCAAGAATTTAGGGATGATTTTGCATACATAATAGAGTTAATCCAAT
CTCATAAATTTCAACGAGGTTTCACGAAAGCGATTATCTTATTTATTAGATAAATTTGAAT
TGTTTCAGTACCTAAACTCTAAGAAAGAAATTTTAGCTAATAAAAAATGTTCCCTACAGAG
ATTTTTATAATTCTCGTAAGGTAGATCGAGACTTGTCTTTAAGTGGTTGTATTTCTCAAC
GTCAATTGAGTGAATATATATGGGAGAAAATAAATTTAGAACCTGAAAGGATAGTTTATC
AAGACCCGGAAACGTCAAGGAACTCAGTTTGAGAGACATTTTTCAGTTTGGTTGTTCTT
CTAATGACCAACCCATTGCGATTGGGTGAAATTGATTGATGATGAATCTTGGATTGGT
ATAGAAATATTTACCTAATAGATTACCATCTAACTCCTAACAAGTAGCAAAGTTGGTCG
GCAAAGAAATGAGGTTTACCTATTAGCCAAAGTGTTTCTGGAGTTTGATAATTTCAATTG
AAGGTGAGTACCTAGCAGAAATTTTCATAAAATACGTTATTTCATATCCTCGAAAAATCAA
AGTACCAATTGGCCCAAGTATCAGTTAATTTTCAATTCTATTCCAGTGGTGAAGACTGGT
ACAAGAAATTTTCTCAATGGTTGCTACGATGGAAGCTAGTATCGTATAATATCCGCTGGA
ATATACAAATTGCCAGGATTTTCCCAAATATTCAAGGAAAATGTCGTGTCAAATTTCC
AGGAGTTTTTGGATCTTATCTTCAATCCTTTATTCACTCTGGAAAAGGAGCAGTTACCAA
TAGATTCATCTGTAAATACTGATATCATTTGGTCTGCAGTTTTTTTTTATCAAATGTGTGTT
CTATGGATCTGGTCATTAAAGAGTCGGATGAATATTACTGGAAAGAATTTACTGATATGA
ATTGTAAGCCAAAATTTTGGACAGCACAGGGTGACAATCCAAGTGTGCGCATTACATGT
ATTATATTTATAAAAGTTTAGCGAAAGTTAATTTTCTGCGGTCACAAAATCTTCAAATA
CAATCACCTAAGAAATTATTGTTCTCCACTATCCAGCAGAACTTCCCAATTTGGAGTGG
ATTTATATTTTACAGATCAAGTTGAATCGTTAGTGTGCAACTTACTGCTTTGTAATGGTG
GTCTGCTACAGGTAGAACCGCTTTGGGATACTGCAACAATGATTCAATATTTATTTATC
TCTTTCAAATACCCATTTTAGCTGCGCCATTATCATCTGTTTCATTACTGAATTCGCAA

AATCGACCTTTTTGAAGAATAAAAACGTGCTTCTAGAACATGATTATTTGAAAGACCAGG
AAACAGCCAAAATCAATCCTTCTAGAGATATCACTGTGGGCGAACAAAGATCATATGAGA
CAAATCCTTTTCATGAAAATGTTTAAGATGGGACTAAAAATTTCTTTATCATCAAAATCGA
TTCTTTACAATAGTTCATACACGCTAGAACCTCTCATTGAAGAATACAGTGTAGCAGCAA
GTATTTACTTGCTGAACCCAACAGATTTGTGCGAGTTGTTCGAGAACAAGTGTGCTATCTA
GTGGCTATGAAGGTTGGTACAAGGCTCATTGGATTGGCGTTGGAGTTAAAAAGGCGCCTT
ACTTTGAGGAGAACGTGGGTGGGATAGATAATTGGTACGATACAGCGAAAGATACCTCGA
TAAAGCACACGTTCCGATGATTAGAAGAAGATATAGAAAGGAGACATTGGATCAAGAGT
GGAACCTCGTTCGGGATCACTTTGGAGTAATTAACCTCCATTTGGTAG

YJL070C, 888 aa (SEQ ID NO 148)

MQAVERRPSLLFDEYQNSVTKPNETKNKEARVLSNDGDVSPSVLKQKEISVDDMDMISL
PTEFDRQMVLGSPMFFDLEDEENKIDPLPSVSHHYNGESDSFVSSYTPSNLKTGEETKD
LFINPFELVSQMRKRYIAASKQDGISNIKNDEKWFLYPKPLPKFWRFEEDKRFQDPSDS
DLNDDGDSTGTGAATPHRHGYYPYFTHDYHYTKSGLKKGKGNIKVPYTGEYFDLEDYK
KQYIYHLSNQENTQNPLSPYSSKEESLEEEFLTDVPTFQEFRDDFAYIIELIQSHKFNEV
SRKRLSYLLDKFELFQYLNKKEILANKNVPYRDFYNSRKVDRDLSLSGCISQRQLSEYI
WEKINLEPERIVYQDPETSRKLSLRDIFQFGCSSNDQPIAIGLKLIDDEFDLDWYRNIYLI
DYHLTPNKVAKLVGKEMRFYLLAKVFLEFDNFIEGEYLAEIFIKYVIHILEKSKYQLAQV
SVNFQFYSSGEDWYKKFSQWLLRWKLVSYNIRWNIQIARIFPKLFKENVVSNFQEFDLI
FNPLFTLEKEQLPIDSSVNTDIIGLQFFLSNVCSMDLVIKESDEYYWKEFTDMNCKPKFW
TAQGDNPVVAHYMYIYKSLAKVNFLRSQNLQNTITLRNYCSPLSSRTSQFGVDLYFTDQ
VESLVCNLLLCNGGLLQVEPLWDATMIQYLFYLFQIPILAAPLSSVSLNLSQKSTFLKN
KNVLEHDYLDQETAKINPSRDITVGEQRSYETNPFMKFMGLKISLSSKSILYNSSY
TLEPLIEEYSVAASIYLLNPTDLCELSRTSVLSSGYEGWYKAHWIGVGKAPYFEENVG
GIDNWDYDTAKDTSIKHNVPIMIRRRYRKETLDQEWNFVRDHFGVINSIW

YJL078C, 3146 bp, CDS: 501-3146 (SEQ ID NO 149)

TTTTTCTTCGCACATGGCTGGTCTGCTGGAGGCGGCTGGGTGTTTATAGTTACCGCAAT
GCAGGTCGCTTCGTTTACTTTTCTCTGCGTGCTCGAGAAGTGAATAACTGGTTTAGGA
AAACCGTCCACTTATGGATTTAACAAGGAGGTGAAAGGTAGGTACCATGGCAATATAGCT
AGCAACGCTACGCACTAGCTGTGTGTGCTTGCTCTCTTGTGTTCGTCTTTCGTATATTGC
GGGTTCGCGCGTTAATTCAACAACAAATATGGTATCTAGGCAGGGACCCAGCAACGGAA
GGATGTAATTGCTATATAGGGCCGATGAAACAGTTCTCATGTTTCAACTCGGTCTGAAGAA
TTCTCTAAACATATTCTATACTTCAAAGTTTCTAGCTTCTTGCTTTTCGGTAGTTGCCA
AACCAATATCGGCATAAAATTATAATTGCTGCACCCCTGCAACTCCAAACAACCTTAAAC
AACTTAAACGAAAACGCTTATGCTGGAGTTTCCAATATCAGTTCTGCTAGGATGCCTAG
TAGCCGTCAAGGCACAAACCAGTTTCCAAACTTCGAGAGCGATGTGCTGAACGAGCATA
ACAAGTTCAGAGCGCTACATGTTGACACAGCGCCGCTCACCTGGTCCGACACTCTGGCCA
CCTATGCGCAGAACTACGCCGACCAATATGATTGTTCCGGGTGCTTAAACGCATTCCGATG
GCCCATATGGTGAGAACCTTGCCCTTGGTTACACAGACACGGGAGCGGTGGACGCCTGGT
ACGGGGAGATAAGCAAGTATAATTATTCAAATCCCGGATTTTCTGAATCCACGGGTCACT
TCACACAGGTGGTTTGGAAGTCAACCGCCGAGATTGGATGTGGTTATAAATATTGTGGTA
CGACATGGAACAATTATATTGTGTGCTCCTACAACCCTCCTGGAACTACCTGGGTGAGT
TTGCAGAGGAAGTGGAACCACTTATAAGCACTGTTTCTCCTCGTCTCATCCTCGTCTCTT
CTACCTCAACTACATCAGACACAGTCTCCACCATCTCATCCAGTATTATGCCCGCTGTAG
CGCAAGGGTATACAACAACGGTATCGTCTGCGGCTAGCAGCAGTTCTTTAAATCGACGA
CCATAAACCTGCCAAGACCGCTACCCTCACTGCGTCTCTTCTACCGTAATTACTAGTA
GCACAGAATCAGTTGGATCCTCCACTGTCTCATCAGCCTCAAGCTCTTCTGTCACTACTT
CCTATGCTACCTCCTCGAGTACCGTCTGCTCTAGTGATGCTACTTCATCCACTACCACCA
CCTCATCGGTGCTACATCGTCCAGTACCCTTCTTCCGACCCTACCTCGAGCACTGCTG
CTGCTTCTTCTTCTGATCCTGCCTCAAGTTCCGCTGCCGCTTCTCCAGCGCGAGTACCG
AGAACGCCGCTTCTTCTAGCAGCGCCATCTCGAGCTCTTCATCAATGGTTTCTGCTCCTT
TGAGTAGTACTCTTACTACTTCCACCGCAAGCTCCAGAAGTGTAACCTCCAATTCAGTTA
ATTCTGTAAAGTTTGCAAACACAACCTGTGTTTCTGCTCAAACAACCTCTTCTGTAAGCG
CCTCATATATCATCATCTGTAGCTGCTGACGATATTCAGGGTAGCACTTCCAAGGAGGCCA
CAAGCTCAGTTTCCGAACATACTAGTATAGTAAGTGAAGTCAACTAATGCTGCCCAATATG
CAACGAGACTTGGGTCTCTTCCAGAAGTTCTTCCGGGGCCGCTCTTCTCCTCAGCTGTGT
CGCAATCTGTTCTGAATTCCGTTATAGCCGTCAACACCGACGTATCTGTAACCTCAGTTA
GTAGCACAGCCCATAACCACAAAGGACACCGCCACCCTTCAGTAACCGCCTCAGAAAGTA

TCACTTCGGAAACTGCTCAGGCTTCAAGTTCAACAGAGAAGAATATTAGTAACAGTGCCG
CCACATCGAGTAGCATTTACTCCAACAGTGCTTCTGTGTCAGGACACGGTGTAACATACG
CTGCCGAATACGCCATTACATCCGAGCAATCCTCTGCGCTTGCCACATCTGTGCCTGCTA
CAAATTGCTCTAGTATCGTGAAGACCACAACCTTTAGAAAATTTCGAGTACCACAACCATCA
CAGCCATTACTAAGAGTACTACAACCTTGGCCACTACTGCTAACAACTCCACAAGGGCAG
CTACCGCAGTAACCATAGATCCACATTGGACCCTACCGACAACCTCAGCTAGTCCAACCG
ACAATGCTAAACACACCTCTACATATGGATCTTCTTCCACAGGCGCATCTTTAGATAGCT
TACGCACAACCACCAGTATTAGTGTCTCAAGCAACACCACACAGTTAGTCTCTACCTGCA
CTTCCGAGAGCGATTATTCCGATAGTCTTAGCTTCGCCATCTCCACTGCCACCACCCTG
AAAGCAATCTGATCACAACACCATCACAGCTTCTTGTAGTACGGATAGTAATTTCCCTA
CCTCCGCTGCTTCTTCTACAGATGAGACGGCCTTCACTAGAACAATCTCGACATCTTGTA
GCACTTTGAACGGCGCCTCAACCCAAACCAGTGAGCTAACACATCGCCTATGAAAACCA
ACACGGTGGTTCCAGCTTCTTCTTCCCTTCAACTACAACCCTTGTCTAGAAAATGATG
ACACTGCCTTTTCTAGTATCTACACTGAAGTCAACGCCGCAACTATCATTAACCCCGGAG
AAACATCTTCTCTCGCTAGCGATTTCGCCACATCTGAAAAGCCAAACGAGCCCACTTCTG
TCAAATCCACCTCAAACGAAGGCACCTCTTCCACAACAACCTACCAACAGACTGTTG
CTACACTGTATGCCAAGCCCTCCAGCACAAGCCTAGGTGCAAGAACAACCTACTGGTAGCA
ACGGTCGTTCAACTACCAGCCAACAAGACGGGTCTGCCATGCATCAGCCAACCTCCTCGA
TCTACACTCAACTAAAAGAAGGCACATCAACCACCGCAAAACTTTCTGCATACGAAGGTG
CTGCAACACCTCTTTCCATTTTCCAGTGCAATAGTCTAGCTGGAACGATTGCCGCTTTTG
TCGTAGCTGTTCTGTTCGCCTTCTAG

YJL078C, 881 aa (SEQ ID NO 150)

MLEFPISVLLGCLVAVKAQTTFPNFESDVLNEHNKFRALHVDTPPLTWSDTLATYAQNYA
DQYDCSGVLTHSDGPYGENLALGYDTGAVDAWYGEISKYNSNPGFSESTGHFTQVWWK
STAEIGCGYKYCGTTWNNYIVCSYNPPGNYLGEFAEEVEPLISTVSSSSSSSSSTSTSD
TVSTISSIMPAVAQGYTTTVSSAASSSSSLKSTTINPAKTATLTASSSTVITSSSTESVGS
STVSSASSSSVTTSYATSSSTVSSDATSSTTTTSSVATSSSTTSSDPTSSSTAAASSSDP
ASSSAAASSSASTENAASSSSSAISSSSSMVSAPLSSTLTSTASSRSVTSNSVNSVKFAN
TTVFSAQTTSSVSASLSSSVAADDIQGSTSKEATSSVSEHTSIVTSATNAAQYATRLGSS
SRSSSGAVSSSAVSQSVLNSVIAVNTDVSVTSVSSSTAHTTKDTATTSVTASESITSETAQ
ASSSTEKNISNSAATSSSIYSNSASVSGHGVTYAAEYAITSEQSSALATSVPATNCSSIV
KTTTLENSSTTTITAITKSTTTLATTANNSTRAATAVTIDPTLDPTDNSASPTDNAKHTS
TYGSSSTGASLDSLRTTTSISVSSNTTQLVSTCTSESDYSDSPFAISTATTTESNLITN
TITASCSTDSNFPSTSAASSTDETAFTRTISTSCSTLNGASTQTSELTTSPMKTNTVVPAS
SFPSTTTTCLENDDTAFSSIIYEVNAATIINPGETSSLASDFATSEKPNEPTSVKSTSNE
GTSSTTTTYQQTVATLYAKPSSTSLGARTTGTSGNGRSTTSQQDGSAMHQPTSSIIYTQLKE
GTSTTAKLSAYEGAATPLSIFQCNSLAGTIAAFVVAVLFAF

YJL179W, 830 bp, CDS: 501-830 (SEQ ID NO 151)

TTGCATTATCAACTATAATTCCATTTCCCTAGAGGAGTTTTTATAGTCCTGCCATCTAATT
GTAGAGCAATCTTTCCTTTCTCAACATCCCTATTTAGTGACACCTTTTCCCAAACTTCT
GTGAAGTTTTGCTCAATCTATTTGTTTCCGTAGGAGTGTTATTCTCAATCGTGTGCTG
TCCCCAGTGGCTGGGCATTTAATGAGTAGAATCGGGGCAGTTTCAATCTTATGGAATTCA
CAATGAAGCATCCCTTCCCTAATGATGGCAGCATTCGGTATTCTCTTTTGTAGGGTTTCG
TTTGCCTTCAAGTGTTTTGTTCTTATTTAGCCTTTTCCCTTACCTTAATTTTTTCTTTT
CTCTGAAGAAAATGAATGAGTTTAAAGATATAGCAATTAAGAAAGTAACAGTGAAGAAATT
TCTCAGATGAGCAGATGGGAATTAAAGAACTATCTACAGAGCTCTTTACTAAATTGAATC
AATAATACATACTTACAAACATGTCACAGATAGCACAAGAAATGACAGTGAGCTTAAGAA
ACGCCAGGACACAATTGGATATGGTCAATCAGCAGCTAGCATATTTGGACAGACAAGAAA
AGCTTGCTGAATTGACAAAGAAAGAACTAGAGTCTTATCCAACGGACAAAGTATGGAGAT
CTTGCGGTAAATCGTTTATCTTACAGGATAAATCCAAATACGTTAATGATTTATCACATG
CCGAAACTGTTCTTCTGGATCAAAGAAAAACATTAAAGATAAAGAAAGAACTATTTAGAAA
CTACTGTTGAAAAACAATAGACAATCTAAAGGCATTGATGAAGAATTAA

YJL179W, 109 aa (SEQ ID NO 152)

MSQIAQEMTVSLRNARTQLDMVNQQLAYLDRQEKLAELTKKELESYPTDKVWRSCGKSFI
LQDKSKYVNDLSHAETVLLDQRKTLKIKKNYLETTVEKTIDNLKALMKN

YJL180C, 1478 bp, CDS: 501-1478 (SEQ ID NO 153)

AATAGTTCTTCTTTATCTTTAATGTTTTCTTTGATCCAGAAGAACAGTTTCGGCATGTG
ATAAATCATTAAACGTATTTGGATTTATCCTGTAAGATAAACGATTTACCGCAAGATCTCC
ATACTTTGTCCGTTGGATAAGACTCTAGTTCTTTCTTTGTCAATTCAGCAAGCTTTTCTT
GTCTGTCCAAATATGCTAGCTGCTGATTGACCATATCCAATTGTGTCCTGGCGTTTCTTA
AGCTCACTGTCAATTTCTTGTGCTATCTGTGACATGTTTGTAAGTATGTATTATTGATTCA
ATTTAGTAAAGAGCTCTGTAGATAGTTCTTTAATTCCCATCTGCTCATCTGAGAAATTC
TTCACGTGTTACTTTTTTAATTGCTATATCTTTAAACTCATTCATTTTCTTCAGAGAAAAGA
AAAAAATTAAGGTAAAGGAAAAGGCTAAATAAGAACAAAACACTTGAAGGCAAACGAAAC
CCTACAAAAGAGAATACGGAATGCTGCCATCATTAAGGAAGGGATGCTTCATTGTGAATT
CCATAAGATTGAAACTGCCCCGATTCTACTCATTAATGCCAGCCACTGGGGACAGACA
ACACGATTGAGAATAACACTCCTACGGAAACAAATAGATTGAGCAAAACTTCACAGAAGT
TTTGGGAAAAGGTGTCACTAAATAGGGATGTTGAGAAAGGAAAGATTGCTCTACAATTAG
ATGGCAGGACTATAAAAACCTCTTAGGAAATGGAATTATAGTTGATAATGCAAAGTCTC
TCTTAGCATACCTATTAAAACCTGGAGTGGTTCCTTATCCAGTCTTCCATCAAAACTC
ACTCTTTGCCACTAACTTCATTAGTGGAAGATGCATAGATTTACAAATGACAAATGAGC
CTGGCTGTGACCCCTCAATTAGTTGCAAAGATTGGAGGCAACAGTGATGTTATAAAAAATC
AGTTGTTAAGATATTTAGATACCGATACTTTATTTGGTCTTTTCCCCTATGAATGAGTTTG
AAGGAAGATTACGCAATGCGCAAAATGAGTTATATATACCCATCATCAAAGGAATGGAAG
AGTTTTTACGCAACTTTTCATCCGAGTCTAATATTCGACTACAAATTTTAGATGCCGACA
TCCATGGGTACGAGGCAATCAGCAGTCGGATATCGTTAAGAATGCAGCAAAAAAATATA
TGAGCAGCTTATCACCATGGGATCTTGCAATTCTTGAAAAAACTGTATTAACCACAAAGT
CCTTCATTTGCGGCGTGCTATTATTAGAAAATAAAAAAGATACTGCGAACTTAATTCCCG
CCTTGAAAACCTGATATGGATAATATTGTACGTGCCGCCACCTTAGAAACAATCTTCCAAG
TTGAAAAGTGGGGAGAGGTTGAAGATACTCATGACGTTGACAAAAGAGACATCAGAAGAA
AAATTCATACTGCTGCGATTGCTGCTTTTAAGCAATAA

YJL180C, 325 aa (SEQ ID NO 154)

MLPSLRKGC FIVNSIRLKLPRFYS LNAQPLGTDNTIENNTPTETNRLSKTSQKFWKVS L
NRDVEKGKIALQLDGRITIKTPLNGIIVDNAKSL LAYLLKLEWSSLSSLSIKTHSLPLTS
LVARCIDLQMTNEPGCDPQLVAKIGGNSDVIKNQLLRYLDTDTLLVFS PMNEFEGR LRNA
QNELYIPIIKGMEEFLRNFSSES NIRLQILDADIHGLRGNQQSDIVKNA AKKYMSSLSPW
DLAILEKTVLTTKSFICGVLLLENKKDTANLIPALKTDMDNIVRAATLETIFQVEKWGEV
EDTHDVKRDIRRKIHTAAIAAFKQ

YJL181W, 2336 bp, CDS: 501-2336 (SEQ ID NO 155)

GCAAGTCAGTACGATGCATCCTTGGATCAAGAAGGTGAGTCTGGAAACGGTGCTTCTAAT
GGCGATGTTTACCATTATAATGAAGGGGACTTGGCTGCCTCCTTCAAGGGATGTAGATCA
AGAGGTACGTGTGCTAGTGAAATAGGTCACATGTACCAGAAAATCAAGAAATCTTAGATG
TGTGTAATCTTGCAATTTAGTTTCAAACAAGATCCTTGTATTTATATAAACAAAGATATA
ATTTTTTAAAAAAAATTAGAAAAAGCAAATATAATTCAGGTCCCACTTGGAATAATGGCA
CTGTATTGATGCATTTTCCCTTATGCTTAGTGACGCGTTTTTCGCGCGTCAGTTTCAAGTTT
TTCTTGGCTTTTTTTTTTTTCATTTTCGTAAAGGGTCTTAAAGGATTAAAAAATGCAGTA
TTGAAATAAAGAACAATTACGAACGGTGAAGCTGCTATTTTGGTTATTATACCCTTCCAG
GACAGTACGCGCAAACCTATTATGGAGATATTCAAGGAAGAAGAAGAAGCTTTTTTCGG
CGATAGAAGGTATAATATATGCCTGTGAGGTGTATGACCCTGTACCCCGTCATTTACATA
AAAGCAAAACAAAGATCATCAATGCTGCTAAATTAATTATAGAAACGCATCTTTCATATT
ATACAATACTCAATAACATTTTCAGATATAACAAGCCTATCTTTCTACTTGGCTTAGGGATC
TTGGAACGACAGGTCCATACCAACAATTCCTTTCAGAAAGTATTTCTCTCATGTTTGACC
GCACTGTATCTATCTTCAGGAAATGTACGATAGAGGGAGGTTTTCCACATTTGATCGCAC
GTCTTTATCTCAGATTGAAAAGCTACCAGAAGCTCTTAAACGATGCAGGATTAAAGAATT
TTTTTTCAAGCTACGATTATGCTTTTCGGGGTTGCATACAACCTTGTAATTTGCTCTGAAT
ACAGGTATGACGAAGTTCATTACATATCGAACGGCACTTACTCATTAGTTGCATCGATGA
AGATAGATCCTGCTGAAGTCATTAAGGGAACATTTTAGGCTTACAATTCCGAAATTTA
ACATATCTAATATATTAATTGAAATTTTTCATTTGCTCGATGGATTAGCATTTTTTAAGG
TGAACCTTGATAGTTTATCTATATCTACAGCTTCAGCAGAAACAATCTTTCGCAGTATCT
CCGAAGGTAATCATCAGGTCCTAGAATTGGGGAGAAGTTTAATGTTTCCATTGTTGAGGA
CTGGAGATTTTGAAATCTGTCGTATTGACGACGCGGGAGCTGTCATAACATTTACAGAAG
CGAAGGATGTAAACTAGAAATAATCAGTCTGGATGAAGTTTCTGCGGTAATGCAGTGGA
AATCTTGTCTTCAAAATTATGAGAGAAGGGCAGCAAATGACAGTTCATTTATCAAAACAC
ACCTACAATTTAAGAAGGCCAACAAATTTCAATGAAGATAATAATGGGCTAGGACTAATTG

TAGACAGAAATATTCCAACAGATGATTTTACGCTAGCTTCTACAAACCGTCAAAGTCCCC
CGCCTTCAAATACTGGTTGTTTCATTACACAGGTCTAAACCCTTGCATATCCCTTTATCAT
CTGTTATTCGTGAAGACTTTTATGATAGCTCTCTAAATGAGCGTATATCTAAAGACGGAG
ATAGCAGTTGTGAATCCTTCAGTGGCGCCGAAAGTATCTTATCAGACTACGATTTTCATG
ATAATGAATTTTTTAACAACCAGTCACCTCATTATTTTTTCAGAACACATAGACAATAACT
CGAGAGAGGTGGTAATAACAGATGAAAAATACGATAATATCTTTGGAAAAATACCCAAGTAA
GTCGGTGGTCAAATTACTCATGGCAAAAAATTTACCGCATCAATTACAGGTCTCTATTA
TCCAACCTGCGCATGGGAACTTCATTGTGGCTTATGATTCTGATTATAACCTTCATCAGT
TCAAAATTCGTTTGTGTGACGATATAAAATGTATACAATCCACAGAGCAAGACATACAAA
TACGTGTCCCGCTCGGCGCAATAATGTGCAGCGTCACTGGTATCTTGAATATTAGGACGA
AGGACGCTGACAAGTTGCTTCGGGTATTAAGCTTTTATACCACTGACCACACGGAAGCTG
TATCGCACTCAAACAATCAAGATGCTACTGCAAGTCCACTTTCGTCACTTCATCAGCAA
TGGATCTCAAGCATTTCATTACAGAAATGTTCTCTACAATAATGCCCAAGAGTTGACGC
AGGACGTCATCGGTTCAAATCAGACCTAATCAGTAATATTCGTCAAAAAATATAA

YJL181W, 611 aa (SEQ ID NO 156)

MEIFKEEEEEAFSAIEGIIYACEVYDPVPRHLHKSSTKIINAAKLIIETHLSYYTILNNI
SDIQAYLSTWLRDLGTTGPYQTLSEISLMFDRTVSIFRKCTIEGGFPHLIARLYLRLK
SYQKLLNDAGLKNFFSSYDYAFGVAYNLVNCSEYRYDEVHYISNGTYSLVASMKIDPAEV
IKREHFRLTIPKFNISNILIEIFHLLDGLAFFKVNPDSLSISTASAETIFRSISEGNHGV
LELGRSLMFPLLRTGDFEICRIDDAGAVITFTEAKDVKLEIISLDEVSWVMQWKSCLQNY
ERRAANDSSFIKTHLQFKKANNFNEDNNGLLIVDRNIPTDDFTLASTNRQSPPPSNTGC
SLHRSKPLHIPLSSVIREDFYDSSLNERISKDGDSSCESFSGAESILSDYDFHDNEFFNN
QSPHYFSEHIDNNSREVITDENTIIISLENTQVSRWSNYSWQKISPHQLQVSIQLRMGN
FIVAYDSYDNLHQFKIRLCDDIKCIQSTEQDIQIRVPLGAIMCSVTGILNIRTKDADKLL
RVLSFYTTDHTAVSHSNNQDATASPLSSVSAMDLKHSLOKCSSTIMPQELTQDVIGSK
SDLISNIRQKI

YJL187C, 2960 bp, CDS: 501-2960 (SEQ ID NO 157)

TCTTGCAACCATCGTCCTCTAAGGAAAGAAATGTGGCACCTTTAAATAGGTTCCACCTCA
CAGATGCCAACATGTGGGAGATAGGGGGCTATTTCGAATTTATTAACGTCTCTAGTACTG
GTAAGCCTTTCTAACATTCTTGTGGTCACGTGATGTGTATGTTTCTTTTTTTTATTCCTC
CGGGTGATAACGACGCGAAAAATATTTTTTCATTTTTCTTTTAACCATCACAAATTTGCGA
CGCGACGCGAAAAAATGCAGAGAAGTAAAGAATGCTGGATAAGAAATCAACAACACAG
TTGAACATTGGCGTGCCCTGTGTATTAAGTAAAGGTTGTCCAAGAGGCTCTTTTTTGTA
TGTATGCGTGTGTAACTATCCTGCACATCATCTTGCGCAGTTAGTCCAATAAAAAAGGA
TTACTACTGAACAGGTCTTACTATTTTTGATTGCGTAGTGCTGGGGAAAAGTAAACACAC
ACAGGCGCACACGAGAACAGATGAGTTCTTTGGACGAGGATGAAGAGGACTTCGAAATGC
TGGACACGGAGAACCTCCAGTTTATGGGGAAGAAGATGTTTGGCAAACAGGCCGGCGAAG
ACGAGAGTGATGATTTTGCTATAGGGGGTAGCACCCCGACCAATAAACTGAAATTTTATC
CATATTCGAACAACAAATTGACAAGAAGTACGGGGACCTTGAACCTGTCATTAAGTAATA
CAGCTTTGTCAGAGGCTAACTCCAAATTTCTTGGGAAAATTGAAGAAGAGGAAGAAGAGG
AGGAAGAAGGCAAGGATGAGGAAAGCGTGGATTCTCGTATTAAAAGGTGGTCTCCGTTC
ATGAAAATGAAAGTGTTACTACTCTTATTAACAAAAGATCTGCGGAAAAAACGAACAGTC
CTATTTCTCTCAAACAATGGAACCAGCGATGGTTTCCGAAAAATGATGCTCGCACTGAAA
ATACATCCTCATCCTCTTCATATAGCGTCGCTAAACCTAACCAATCAGCCTTTACGTCTT
CGGGCCTCGTATCTAAAATGTCTATGGACACTTCGTTATACCCTGCGAAATTGAGGATAC
CAGAAACACCAGTGAAAAATCACCTTAGTGAGGGAAGAGACCATAAGCATGTCCACC
TTTCGAGTTTCGAAAAATGCATCGTCTTCTCTAAGTGTTCCTTTTAAATTTTGTTGAAG
ACAATAATTTACAAGAAGACCTTTTATTTTCAGATTCTCCGTCTTCGAAAGCTTTACCTT
CCATCCATGTACCAACCATAGACTCATCCCCACTGAGCGAGGCAAAATATCATGCACATG
ATCGTCACAATAACCAGACAAACATCCTGTCTCCCACTAATAGCTTGGTTACCAACAGCT
CTCCACAAACATTGCATTCTAACAAGTTCAAAAAATCAAAAGAGCAAGGAATTCGGTTA
TTTTGAAAAATAGAGAGCTAACAAACAGTTTACAACAATTCAAAGATGATTTATACGGCA
CGGACGAGAATTTCCACCTCCAATCATAATATCAAGTCATCATTTCAACTAGAAAGAACC
CTCAACCTTATCAATTTCTGTGGACGCTATGACAATGACACTGACGAAGAGATCTCCACTC
CAACAAGACGAAAATCTATTATTGGGGCAACATCTCAAAACACATAGAGAAAGCAGACCAT
TGTCACCTCTCTCTGCCATCGTGACAAACACAACAAGTGCAGAGACGCATTCCATATCTT
CCACCGATTCTTCGCCGTAAATTTCAAAAGGCGTCTAATCTCTTCAAATAAGTTATCAG
CAAATCCAGATTCCCATCTTTTCGAAAAATTTACGAATGTGCATTCCATTGGTAAAGGCC

AGTTTTCCACGGTCTACCAGGTTACGTTTGCCCAAACAAACAAAAAGTATGCAATCAAAG
CCATTAAACCAAACAAATATAATTCCTTGAAACGCATATTACTGGAAATTAAAATACTAA
ACGAGGTAACAAACCAAATTACAATGGATCAAGAAGGGAAGGAATACATCATCGATTACA
TCAGTTCCTGGAAGTTTCAAATTCATACTATATTATGACAGAATTGTGCGAAAATGGTA
ATTTGGATGGATTTTACAAGAGCAAGTTATCGCAAAGAAAAAAGGTTGGAAGATTGGA
GAATTTGGAATCATCGTGAATTAAGCCTGGCTTTACGATTCATCCATGATTCTTGTC
ACATTGTGCATCTGGACTTGAAACCCGCAAACGTCATGATCACATTTGAAGGTAACCTAA
AACTAGGTGACTTTGGAATGGCTACTCATTTACCGTTGGAGGATAAAAGTTTGAATG
AAGGTGACAGAGAATATATTGCACCAGAAATCATTTCTGATTGTACGTACGATTACAAGG
CAGATATTTTCCCTGGGTCTGATGATTGTTGAAATTGCAGCGAACGTTGTGTTACCTG
ACAATGGCAACGCATGGCATAAGTTGAGATCGGGTGATTTATCGGATGCAGGAAGATTAA
GTTCCACAGATATTCATTCTGAATCATTATTTTCAGACATTACGAAAGTAGATACAAATG
ATTTATTTGATTTTGAAGAGACAATATCAGTGGTAATAGTAACAACGCTGGCACCTCCA
CTGTTTATAACAATAGTAATATCAACAACCCTAATATGAATAATGGCAACGATAATAATA
ATGTCAATACTGCCGCTACCAAGAATCGTCTTATTTTGCATAAAAGTTCTAAAATTCCCG
CATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACGATGGATGA
TAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGAGGAATGCC
TGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTTTGGACCTA
AGCCAAAATTTTTTATATGA

YJL187C, 819 aa (SEQ ID NO 158)

MSSLDEDEEDFEMLDTENLQFMGKKMFGKQAGEDESDDFAIGGSTPTNKLKFPYPYSNNKL
TRSTGTLNLSLNTALSEANSKFLGKIEEEEEEEEEEGKDEESVDSRIKRWSPFHENESVT
TPITKRSAEKTNSPISLKQWNQRFWPKNDARTENTSSSSYSVAKPNQSAFTSSGLVSKM
SMDTSLYPAKLRIPEPVPKKSPLVEGRDHKHVHLSSSKNASSLSVSPNLFVEDNNLQED
LLFSDSPSSKALPSIHVPTIDSSPLSEAKYHAHRHNNQTNILSPTNSLVTNSSPQTLHS
NKFKKIKRARNSVILKNRELTNLQKFDDLYGTDENFPPIIISSHHSTRKNPQPYQFR
GRYDNDTDEEISTPTRRSIIIGATSQTHRESRPLSLSSAIVTNTTSAETHSISSTDSSPL
NSKRRLISSNKL SANPDSHLFEKFTNVHSIGKGQFSTVYQVTFQTNKKYAIKAIKPNKY
NSLKRILLEIKILNEVTNQITMDQEGKEYIIDYISSWKFNQSYIIMTELCENGNDGFLQ
EQVIAKKRLEDWRIWKIIVELSLALRFIHD SCHIVHLDLKPANVMITFEGNLKLGDFGM
ATHLPLEDKSFENEGDREYIAPEIISDCTYDYKADIFSLGLMIVEIAANVVLDPNGNAWH
KLRSGLSDAGRLSSTDIHSESLFSDITKVDTNLDFDFERNISGNSNNAAGTSTVHNNSN
INNPNNMNGNDNNNVNTAATKNRLILHKSSKIPAWVPKFLIDGESLERIVRWMIEPNYER
RPTANQILQTEECLYVEMTRNAGAI IQEDDFGPKPKFFI

YJL188C, 809 bp, CDS: 501-809 (SEQ ID NO 159)

AATTCCTCGCATGGGTACCGAAATTTCTTATTGATGGTGAATCACTTGAGAGAATAGTACG
ATGGATGATAGAGCCCAATTATGAGAGAAGGCCACGGCAAATCAAATCTTACAACTGA
GGAATGCCCTGTATGTAGAAATGACACGCAATGCAGGTGCTATTATCCAGGAAGACGACTT
TGGACCTAAGCCAAAATTTTTTATATGATAAATGGAACAAAAACCTTGTTTTATTACA
TACTTTTTTCCCACACGTGCTTATGGGCCGCTTGTATAAATAATCCAATAACGAAAAAG
AGTGTAATTGCAGTCCGGTAGTAATACCATGTAAAACCTTAGATGAGTTTATTTTAAGTA
CAGCCGCTTCAAGCATTTTTTATTTTTATTTTACAGATGTAGCAGATAACAACCGTTAAAT
TATATTATATATATATATATATATATATCAAAATACGACGTATTACATATATATTGAGAAT
AAGGGAAGGATGGAAGACAAATGACAAAAAGTTTGAAGCATAAATATGTTCTTCGCTTAG
ATGTTTCATCTTGTTCTTCTCCAGTTTCTTCTCTTAGCGTTGTAACGGATAGTGTTGTTG
GTTCTCAATCTGATCCATTGTGGCAATGGTCTGTTTGTCTTCTTAGCCTTAGCCATTTTT
TGCTTGATTCTGAAAGACTTTTGAGCCTAATTAAGGGAACATATCGTGCACATACGA
AGTGTAACAATTGTAAAAATGTTAGTAACAATGTTCAAACATCAATATGATGCATTCA
CGGATCCAAGGCAATACCACCTGACATAA

YJL188C, 102 aa (SEQ ID NO 160)

MTKSLKHKYVLRDLVHLGSSPVSSLSVVTDSVVGSDPLWQWSVLLLSLSHFLLDSERL
LSLIKRETYRAHTKCTIVKNVSNNVQTHQYDAFTDPRQYHLT

YJL189W, 1042 bp, exon1: 501-506, intron1: 507-892, exon2:
893-1042 (SEQ ID NO 161)

TATTCAAGAATTATTTACATCTTCCAGCGAGTAAACATGCCGCTGGTAATCGCGCGTCC
TCAATATTTGAGTTTTTCAAATAGTGAGGTGTGGATGTATAGAGGAATTACACACTTTTA

AGTATGTGATGTATGGGCGCACAGTACCAATTTAACTTTTTTTTTTTTCATTTTTTAGC
TTGATTTTCAAAAAACTTATGGGCGTTTTAGGCTCCGGCTCAAACCTACCACCACCACGCG
GCAGGCCGAGGCAAACAGTACGCCTTGGCGGGGACGCCGAAGCGACTCCTTCTGTTCCTAA
GCTCAATGGTCCTTGCCTTTACGCTCGCGCGTGGGCTAACTAACGCAATTCGGCTTTTGG
GCTGTCGAGAACCGAGAATTATCTTCGCCTTGATAGATACTTTAAACTTCTACTTAAT
ATACTTTCTACAATTTTTGGTACATTCATATTATACTGAAAATTCGAAAAAGACAAGCAA
ATAAACACAGATAGATCAACATGGCTGTATGTTAGAAAGATATTATAAATCCCAGTTAGA
TGCTGAACTGATCAATAGCAAATTATAAACACATCCATCTAAATGACCTTACCACCTAC
AATTTGGATTTGAAATAGAAGCAATGTGTAAATATAGGGAAAGGATTAGGAGTGTAAAC
CATACTAAAATTTTTCTTATCCGAAACAGAAATCTAAAGTCGCCACTACGCAGATTAAAA
TATGGTCATAAACTGCTTATTCTGAGAACTTTTGGTGGTCCAGCGTGGTTTATGTCAGGT
GGTATTGCCTTGGATCCGTGAATGCATCATATTGATGAGTTTGAACATTGTTACTAACAT
TTTTTACAATTGTACACTTCGTATGTGCACGATATGTTTCCCTTTTAATTAGGCTCAAAA
GTCTTTCAGAATCAAGCAAAAAATGGCTAAGGCTAAGAAGCAAAACAGACCATTGCCACA
ATGGATCAGATTGAGAACCAACAACACTATCCGTTACAACGCTAAGAGAAGAACTGGAG
AAGAACCAAGATGAACATCTAA

YJL189W, 51 aa (SEQ ID NO 162)

MAAQKSFRIKQKMAKAKKQNRPLPQWIRLRTNNTIRYNAKRRNWRRTKMNI

YJL190C, 893 bp, CDS: 501-893 (SEQ ID NO 163)

TCTCGACAGCCCAAAGCCGAATTGCGTTAGTTAGCCACGCGGAGCGTAAACGCAAGG
ACCATTGAGCTTGGAACAGAAGGAGTCGCTTCGGCGTCCCCGCCAAGGCGTACTGTTGC
CTCGGCCTGCCGCGTGGTGGTGGTAGTTTGGAGCCGGAGCCTAAAACGCCCATAGTTT
TGAAAATCAAGCTAAAAAATGAAAAAAGTTAAATTGGTACTGTGCGCCCATAC
ATCACATACTTAAAAGTGTGTAATTCCTCTATACATCCACACCTCACTATTTGAAAACT
CAAATATTGAGGACGCGCGATTACCAGCGGCATGTTTACTCGCTGGAAGATGTGAAATAA
TTCTTGAATATGGGTTTGCAGTTAGTCAATTTCAATCTAAATAATCTTAATCGACTATTC
AATTCTTAAATTGTAAGGTTTTTAAATGGCCTTTTCAAGTTCTAGTATTTTTTATAAAACA
GACCAACATACATATCCAAGATGACCAGATCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAACAACGCTGAAAAGACCGGTAAGCGTCAAGTTTAAATCAGACCATCCTCCAAGGTCA
TTATCAAGTTTTTGCAAGTTATGCAAAAGCACGGTTACATTGGTGAATTTGAATACATCG
ATGACCACAGATCTGGTAAGATTGTTGTTCAATTGAACGGTAGATTGAACAAGTGTGGTG
TTATTTCCCAAGATTCAACGTTAAGATTGGTGACATTGAAAAATGGACTGCCAACTTGT
TGCCAGCCAGACAATTCGGTTACGTCATCTTGACCACCTCTGCTGGTATCATGGACCATG
AAGAAGCCAGAAGAAAGCACGTTTTCTGGTAAGATTTTGGGTTTCGTTTACTAA

YJL190C, 130 aa (SEQ ID NO 164)

MTRSSVLADALNAINNAEKTGKRQVLIRPSSKVIIFLQVMQKHGYIGEFYIDDHRSKG
IVVQLNGRLNKCGLVISPRFNVKIGDIEKWTANLLPARQFGYVILTTSAGIMDHEEARRH
VSGKILGFVY

YJL197W, 4265 bp, CDS: 501-4265 (SEQ ID NO 165)

CTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAGTAGATAGAAAGGGCGATCGCT
ATTTAAGTGTGATGACTTTCTTAACGAGAGGTGTTCCAGCTTCTATTTTGGCTTTCCTAT
GTGTCATTACTCTAGGTTATGGTATCATGGCATCTGTTGTCAAGGGTAACGCAACCTCTG
CGTAAGAGATACGTCTACGATAGCATGTAACAGCGTATATATAATCTATATGTATTTCGAT
TAATCCAACACTTCTGTTGTGTAGTCTAATGTTGAAAAAAGGTACGCTTCCCTGTTAT
AATCAGGTATATTTCTGTTATTCTTATAAGCTAAAAGATTAAAAATTTTTCCACTTTCCTT
GAAATTTGGTCGGTTCGTGGAAAAATATTATTACGTATTGAAGAAGTGCATGAAGATAAA
AGATGGGATTACTGGAAAAATAAGGGAGGAAAAATCCTGCAGAACGTTGTTGTTTCAATC
GAAGGTTTCTTCATTTCGAAAATGGGTTCTTCAGATGTTTCAAGTCGTGAATGTTCAATTGG
TTTATAATGAAGATCCCGATTTACCGATGGCACAACACCATGTGATCGGTTGGGAGTGG
ACTTGATGAATGTTCTAGATGACAAGGATGAAATAAAGCAAGAGTCTGTCCCAGTCTCAG
ATCGTGAAATTGAGGATACGGAATCCGATGCTTCCGCTGTTTCTTCATTTGCTAGCGCTA
ATGAGTTAATAGCTGAGCCACACGCTGCAAGTGAACTAATCTTGGAATAATGGTCAAG
ATGGAAGAAATGTCTTAGAACAACAAGAGACGTGGTTGCTAGACTAATAGAAGAAAACA
AGGAAACGCAAAAAGAGGGTGATAAAGTCTGTATTGTCCCCAAGGTTTGGTACGATAAAT
TTTTCGACCCCGATGTTACCGATCCTGAAGATATAGGCCCTATTAATACACGCATGATTT
GCAGAGACTTTGAAAATTTTGTGCTTGAGGATTACAATAGATGTCCGTATCTGTCTATTG

CAGAGCCTGTTTTCAATTTTCTATCAGAAATTTACGGCATGACAAGTGGCTCTTACCCAG
TGGTAACTAATTTGGTTATCAACCAAACACAGGGGAGTTAGAGACAGAATACAATAAAT
GGTTTTTCAGACTACATTACCTGACCGAAAAACAAGACGGGAGGAAAAGGAGGCATGGCC
AGGACGATTCAATAATGTACCTCTCGATGTCTGCGTTGAATTTAGTACGTGATTTGGTTG
AAAAGAGTATGAATCTGTTTTTTGAGAAAGCTGATCATCTAGACGTGAATGCGGTGGATT
TTAAAATTTGGTTTGTGTCAGAGGGATCTGATATTGCCACAGATAGCAATGTAGTACTT
TTTTGAATTTCTTCATATGAAATAACTCCGCTTCAATTTCTCGAACTACCGATAAAGAAAC
TACTAATACCAGACATGTTTGAAAACCGTTTAGACAAGATAACTTCAAATCCGAGTGACC
TTGTCATAGAAATTAAACCTATAGAAGGGAATCACCATTGGCCTTCAAACATTTTTGCTT
ATAATAAACTCGAACCAGCATCAGGTACTACTGGTTTGGTCAATTTGGGAAATACATGTT
ACATGAATTTCTGCGTTGCAATGCCTGGTACACATTCCGCAGTTGCGTGATTATTTCTTT
ATGATGGTTATGAAGACGAAATCAATGAAGAAAATCCTCTTGGGTACCACGGCTATGTGG
CTAGGGCATTTAGTGACTTGGTTCAGAAGTTGTTTTCAAACAGGATGAGCATAATGCAAA
GAAATGCTGCTTTCCCCCTTCAATGTTCAAATCCACTATCGGGCACTTTAATTCGATGT
TTTCTGGTTATATGCAACAGGATTCTCAAGAATTTTATAGCCTTCTGTTAGACAGTTTAC
ATGAAGATTTGAACAGGATAATAAAGAAAGAAATACACAGAAAAACCATCATTATCTCCTG
GTGATGACGTGAATGATTGGAATGTAGTCAAGAACTGGCAGACGATACTTGGGAGATGC
ATTTAAAGAGAAATTGTTCCGTTATAACGGATTTATTTGTCGGGATGTACAAATCAACGC
TATATTGTCCCGAATGTCAAATGTTTCTATAACGTTTGACCCGTATAATGATGTTACAT
TGCCGCTTCCGGTTGATACAGTGTGGGATAAACTATAAAAATTTTTCCCATGAACTCTC
CACCCTTCTTCTTGAAGTTGAGTTAAGCAAATCGTCCACTTATATGGACTTGAAGAATT
ATGTTGGTAAATGTCGGGCCTAGATCCAAATACACTATTTGGCTGTGAGATTTTCAGTA
ATCAAATCTATGTTAACTATGAGTCAACAGAGTCGAATGCTCAATTTTAACTTGCAGG
AATTGATCAAACCTGCTGATGACGTTATTTTTTATGAATTACCAGTAACAAATGACAATG
AAGTAATTGTTCCCGTATTGAATACTAGAATTGAAAAAGGCTACAAAAATGCAATGTTAT
TTGGAGTCCCTTTCTTTATTACGTTAAAGAAGATGAATTGAATAATCCAGGTGCAATAA
GAATGAATTTGCAAAACAGGTTTGTCCATTTAAGTGGTGGGTATATCCCATTTCTTGAAC
CTGTAGGAAATCGAACCGATTTTGTGATGCTTTTCCATTATTAGTAGAAAAATATCCAG
ATGTTGAATTTGAACAATATAAAGATATACTACAGTATACGTCTATTAAGGTGACTGACA
AGGATAAATCCTTTTTTTTCCATCAAGATTCTGTCTGTAGAAAAAGAGCAGCAATTTGCTA
GTAATAACCGAACAGGGCCTAATTTCTGGACCCCTATCTCCAGTTAAACCTTGACAAAG
CTACAGATATAGACGATAAACTTGAAGATGTGGTGAAGGATATCTACAATTATTCATCCT
TAGTAGATTGTGCTGAAGGGGTCTTATGCAAGTGGATGATGAGGGAGATACCGAGGGTA
GTGAAGCAAAGAATTTTCCAAGCCCTTCCAATCGGGAGATGATGAAGAAAATAAGAAA
CTGTAACAAATAATGAAAATGTAAATAATACTAATGATCGGGATGAAGATATGGAATAA
CAGATGATGTTGAAGAAGATGCAAGTACAGAGCCAGAATTAACAGATAAGCCAGAGGCGT
TAGATAAAATTAAGGATAGCTTGACTTCCACTCCGTTTTCGATTTCTTCTATGAATGATA
TTATTGTTTGTGAGTGGAGCGAATTGGGTTCAAATGAGGCATTTTCCGATGATAAAATAT
ATAACTGGGAAAATCCAGCTACTTTGCCTAACAAAGAGTTGGAGAACGCTAAGTTGGAAA
GATCTAACGCTAAGGAAAGAACATAACCTTGGACGATTGTCTCCAATTATTTTCCAAAC
CAGAAATACTAGGATTAACCGATTTCGTGGTACTGCCCTACATGCAAGGAACATCGTCAGG
CTACCAAACAAATACAACCTTTGGAATACACCAGATATTCTGCTAATTCACCTTAAAAGGT
TTGAAAGTCAAAGGTCTTTTAGCGATAAAATTGATGCCACGGTTAATTTCCCATTTACAG
ATTTGGATCTGTGAGGTACGTTGTCTATAAAGATGATCCCAGAGGTTAATCTATGACC
TGTATGCAGTAGATAACCACTATGGTGGTTTGGGTGGTGGGCACTATACCGCGTACGTAA
AGAATTTTGGCGACAATAAATGGTACTATTTTGTGATGATTCTCGAGTAACTGAACTGCGC
CAGAAAATAGTATAGCTGGATCGGCTTATTTGCTATTTTACATTCGCCGTCATAAAGATG
GCAATGGATTAGGCAGCTCTAAACTACAGGAAATAATCCAAAAGTCACGCCACGGATATG
ATGAGCGTATCAAAAAGATATACGATGAACAGATGAAGTTGTATGAATTTAATAAGACTG
ACGAGGAGGAAGATGTTTCTGATGATATGATAGAATGTAATGAAGATGTGCAGGCCCTG
AATATAGTAATCGTAGTTTGGAGGTTGGGCATATTGAACTCAGGACTGCAACGACGAAG
ATGACAATGATGATGGTGAGAGGACAAATTCAGGTAGGAGAAAGTTAAGATTGTTGAAAA
AAGTCTACAAGAATAATTCAGGCTTGGGTTTCATCGAGTACGTCTGAAATATCTGAGGGAT
GCCAGAAAACGAAGTCGCTGATTTGAATTTAAAAAATGGTGTGACACTAGAATCGCCAG
AATAA

YJL197W, 1254 aa (SEQ ID NO 166)

MGSSDVSSRECSLVNEDPDFDGTTPCDRLGVLDLMNVLDKDEIKQESVPVSDREIEDT
ESDASAVSSFASANELIAEPHAASETNLGTNGQDGRNVLEQQRDVVARLIEENKETQKEG
DKVCIVPKVWYDKFFDPDVTDPEDIGPINTRMICRDFENFVLEDYNRCPYLSIAEPVFNF

LSEIYGMTSGSYPVVTNLVINQTTGELETEYNKWFFRLHYLTERKQDGRKRRHGQDDSIMY
LSMSALNLVRDLVEKSMNLFFEKADHLVDNAVDFKIWFVSEGSDIATDSNVSTFLNSSYE
ITPLQFLELPIKKLLIPDMFENRLDKITSNPSDLVIEIKPIEGNHHWPSNYFAYNKLEPA
SGTTGLVNLGNTCYMNSALQCLVHIPQLRDYFLYDGYEDEINEENPLGYHGYVARAFSDL
VQKLFQNRMSIMQRNAAFPPSMFKSTIGHFNSMFSGYMQQDSQEFLAFLLDLHEDLNRI
IKKEYTEKPSLSPGDDVNDWNVVKKLADDTWEMHLKRNC SVITDLFVGMKYKSTLYCPECQ
NVSITFDPYNDVTLPLPVDTVWDKTIKIFPMNSPPLLEVELSKSSTYMDLKNYVGKMSG
LDPNTLFGCEIFSNQIYVNYESTESNAQFLTLQELIKPADDDVIFYELPVTNDNEVIVPVL
NTRIEKGYKNAMLFGVPFFITLKEDELNNPGAIRMKLQNRVHLSGGYIPFPEPVGNRTD
FADAFPLLVEKYPDVEFEQYKDILQYTSIKVTDKDKSFFSIKILSVEKEQQFASNNRTGP
NFWTPISQLNLDKATDIDDKLEDVVKDIYNYSSLVDCAEGVLMQVDDEGDTEGSEAKNFS
KPFQSGDDEENKETVTNNENVNNTNDRDEDMELTDDVEEDASTEPELTDKPEALDKIKDS
LTSTPFAILSMNDIIVCEWSELGSNEAFSDDKIYNWENPATLPNKELENAKLERSNAKER
TITLDDCLQLFSKPEILGLTDSWYCPTCKEHRQATKQIQWLWNTPDILLIHLKRFESQRSF
SDKIDATVNFPIITDLDSRYVVYKDDPRGLIYDLYAVDNHYGGLGGGHYTAYVKNFADNK
WYYFDDSRVTETAPENSIAGSAYLLFYIRRHKDGNLGLSSSKLQEI IQKSRHGYDERIKKI
YDEQMKLYEFNKTDDEEDVSDDMIECNEDVQAPEYSNRSLEVGHIE TQDCNDEDDNDDGE
RTNSGRRKLRLLLKKVYKNNSGLGSSSTSEISEGCPENEVADLNLKNGVTLESPE

YJL198W, 3149 bp, CDS: 501-3149 (SEQ ID NO 167)

TGTCGTATTTCCACTGATTTGGATGTATGTTGCATGGTGCTAGATTGTGAATAAATCATT
TCCACTGGTTTCTAGCAGAGGTAAGAAAATCAGTAGTAGCGGCAGCAGCCAAGAAAAATG
GCAGCCTGGCAAGCAGCGAAGGCCATCTGTGCTGCATTTCCACACTCCTTGTATGACTGC
ATACGCATAAAGAGGTGCCTTGCTGTAGGCGTATATGATCCTAAGCAACAGAGAAACCAC
GGTTCTCTTCTCTTCTTATTTCGTTATTGTCTTCCCTTTTTTACTATGGGTAAAGTCGCCC
TAAAGCGGGGCGCTCACAATATCGCCGCAGCTACAGCCGTTTTTTTTTTTTTTGTTTTTT
TTTGCGCTGCTTCTCGAAGAATGAATGGCTCACTGAAAAATTTTGATTCATCGATATAAA
GAACACTGTTCACTTCGATGTCATCCGGCCAATAAAGTTGTTTTTAGGATAAACGAGTAA
GTGGTAGCTGGTACAGGATCATGAGATTTTACACTTCTTGAAGTACAATGCTGTCCCAG
AATGGCAAAACCATTATATGGACTACAGCGAGCTGAAAAATCTTATTTACACGCTACAAA
CAGATGAACCTTCAGGTTGGTGATAACGAAGAAGGATTTGGCGCAGGAAAGAGCTCTAACA
TTACAGATAGGTTCAAAAACAAGTTTCTTTTAAAAATGCGAAGGAAGATACGTCTTCCG
GTATGAACAAAGATGCAGGCATCGTTGAGGAAACCATCGAGTTGCGAGAGTTGCCTACTG
CTCAGACGGTCGCTGCCAAACCTTCTCCTTTCAGAAGAATGAAGGAAAAGATATTTTACA
AAAGAAGGTCGTCTTCCGCATCGTCCGTCTCCTCCACGGCCAACGAAAATCTGCAATTAG
ACACTTATGATACGTTTGTGGTGATTTAACAGCTGAAAAACAGAAAGTAGATGATTTTT
ATAAGAGGACAGAAGCGAAGTTCTACGACAAATTTGACGCGCTGGTGAAGGACCTGAAGA
AAATCGGAGTTATAGAATACGATATCGACGATGATACTCTGTTTAAACGAACCGATTGCCA
GCACAAATGACGAAGTTCCCCCACTAGACTTGGATGATGACGAAGACGACGACGAATTTT
ACGATGATCAATCTAATATTGAAGATAATACTGCTTTGCTGCATCATTCGCAGTATAACA
TTAAGTCTCAGAAAAAATCGCTGTTGAAGAAGTCGATCGTAAACCTATATATCGATCTTT
GCCAGTTGAAGTCGTTTCATCGAATTGAACCGCATTGGGTTTGCAAAAATTACAAAGAAAT
CAGACAAAGTTCTTCACTTGAATACAAGAACCGAACTGATCGAATCGGAGCAGTTTTTCA
AAGACACATATGCATTCCAGGCAGAAACGATCGAATTGCTAAATTCCAAAATTTCCCAGC
TAGTCACATTTTATGCGCGCATCACTGACCGGCCTCATAATATCTCGCATAGCAAGCAAG
AGTTGAAATCCTACCTGCATGACCACATTGTTTGGGAAAGAAGTAACACTTGGAAGACA
TGTTGGGACTGCTATCGCAAGCTGACGAGTTGACACCAAAGGAAACAGAATATAATGCAA
ATAAGCTGGTAGGCAAGTTAGATTTGGAATACTACAGATGGCCACTACCCAGACCGATAA
ACTTAAAATTCAGTAGTATAAACAACGTTGCACTACCGAAATTATTTTTTACCAAGAAAG
CATACAAGATTTACTTTATTATTCTAGTCACTGGACTCTTGTTAGGAATAAAGACCTTCA
ACGACGCTGCTCAGCACCGCTGCATGGCCCTTGTCGAGTGTGTCGCCCTTTTTGTGGGCTA
GTGAGGCCATCCCATTACACATTACAGCATTCCCTGTACCACTACTTGTAGTCCTTTTCA
AAGTCCTAAAAACCTCCGACGGGGCTATAATGAGTGCTGCAAGCGCTTCATCAGAAATTT
TGGCCGCCATGTGGTCTTCTACAATTATGATTCTGCTGGCAGGTTTTACTTTGGGTGAAG
TACTTGCACAATATAACATCGCCAAAGTTCTTGCCCTCGTGGTTGTTGGCCTTCGCTGGTT
GTAAACCCAGAAACGTTCTTTTAAATGGCAATGTGTGTCGTGTTCTTCTATCAATGTGGA
TTTCCAATGTGCGCAGCACCTGTTCTAACATATTGTTGTTATCTCCCCTATTGGATGCCA
TGGATGCAGATAGCCCATTTGCGCAAGCATTGGTGTTAGGTGTAGCGTTGGCTGCAAATA
TCGGTGGTATGTCCTTACCAATCTCTTACCTCAAAACATCATTTCCATGTCGTACTTGA
AACCCTATGGTATTGGCTGGGGCCAATTCTTTGCTGTTGCATTGCCATCTGGTATCCTGG

CCATGCTTTTGGTTTGGATTTTATTGTTCACTACTTTCAAGATGAATAAGACCAAATTGG
AAAAATTTAAGCCTATTAAGACGAAATTCACAGTTAAGCAGTATTATATCATTACTGTCA
CTGTGGCCACTATTTTGTGTGGTGTGTGGAAAGCCAGATTGAAGGTGCTTTTGGGTCAT
CAGGTCAAATTGCAATCATTTCCCATCGTTTTTGTTTTTTGGTACCGGATTACTATCAACAC
AAGATTTAAATGCCTTTCCGTGGTCAATCGTTATTTTGGCAATGGGAGGTATTGCTTTGG
GGAAGGCCGTCTCATCCTCGGGTTTGCTATCAACCATTGCAAAAGCATTACAAAAGAAAA
TTGAGAATGATGGTGTTTTTTGGCATTCTATGTATTTTCGGTATCCTGATGTTGGTTGTGG
GTACTTTTCGTCTCGCATAACAGTATCCGCTATTATCATCATTTCCCTTGGTGCAAGAAGTTG
GTGACAAGCTTGGCAACCCCAAAGCTGCTCCTATCCTTGTTCGGTGTGCATTATTGT
CATCCTGTGGTATGGGACTAGCTTCTTCGGGGTTCCCAATGTCACTGCCATCTCTAAAG
TAGATAGAAAGGGCGATCGCTATTTAAGTGTATGACTTTCTTAACGAGAGGTGTTCCAG
CTTCTATTTTGGCTTTCTATGTGTCACTACTTAGGTTATGGTATCATGGCATCTGTTG
TCAAGGGTAACGCAACCTCTGCGTAA

YJL198W, 881 aa (SEQ ID NO 168)

MRFSHFLKYNAVPEWQNHMYDSELKNLIYTLQTDDELQVGDNEEGFGAGKSSNITDRFKN
KFSFKNAKEDTSSGMNKDAGIVEETIELRELPTAQTVAAKPSPFRRMKEKIFYKRRSSSA
SSVSSTANENLQLDITYDTFVGDLTAEKQKVDDFYKRTEAKFYDKFDALVKDLKKIGVIEY
DIDDDTLFNEPIASTNDEVPLDLDDDEDDDEFYDDQSNIEDNTALLHHSQYNIKSQKKS
LLKKSIVNLYIDLCLQKSFIELNRIGFAKITKKSQKVLHLNTRTELIESEQFFKDTYAFQ
AETIELLSKISQLVTFYARITDRPHNISHSKQELKSYLHDHIVWERSNTWKDMLGLLSQ
ADELTPKETEYNANKLVGKLDLEYRWPPLRPINLKFTSINNVALPKLFFTKKAYKIYFI
ILVTGLLLGIKTFNDAAQHRMALVECVAFWASEAIPLHITAFVLVPLLVFLFKVLKTS
GAIMSAASASSEILAAMWSSTIMILLAGFTLGEVLAQYNIKVLASWLLAFAGCKPRNV
LMAMCVVFFLSMWISNVAAPVLTYSLSPLLDAMDADSPFAQALVLGVALAANIGGMSSP
ISSPQNIISMSYLPYIGIGWGQFFAVALPSGILAMLLVWILLFTTFKMNKTKLEKFKPIK
TKFTVKQYYIITVTIVATILLWCVESQIEGAFGSSGQIAIPIVLFFGTGLLSTQDLNAPF
WSIVILAMGGIALGKAVSSSGLLSTIAKALQKKIENDGVFAILCIFGILMLVVGTFSHT
VSAIIIIPLVQEVGDKLGNPKAAPILVFGCALLSSCGMGLASSGFPNVTASIKVDRKGDR
YLSVMTFLTRGVPASILAFLCVITLGYGIMASVVKGNATSA

YJR049C, 2093 bp, CDS: 501-2093 (SEQ ID NO 169)

ACTGCCATCTCTTCCATTCTTTGAAAAGATTATTAAGTTCGTCGTTAAGTTCGCAATCT
GCATTTCAATTTAAAGACGGATCATATATCTTGTGCTTTTTTGTTTTATCTCTTTACTTA
CTTGTGCTTCCATTTCGTTGGCCTCTTTTATGGATTTTACCTTAGACACGTTCTTGGGCC
TCTGGTAACGTGAATAATCCTTGTATCCACCTGCCGACTCTGCTTGCTGCTCTTGAAATC
GTACCAGAACTGAGTTGGCCTTATCTACATTTCTACTCATTTTGAATGCACAGGTATCTG
ATTACTGATGTGGTGCCTTGGCATATAACGGTGTGTCACTTTTATTTGCTCTTTCATG
CATCCTGAAATTATTTACCCGCACTACGCAAAGAGAACGGAGAAAAAGGTATAATAGGGC
AAATGATCATTGACATCGTGATCGTAAGCCAAAAAATAACAATAGGCTCCCTAAATAA
GTAGAGTAAAAGCTCTTGAGATGAAGGAGAATGACATGAATAATGGCGTAGATAAATGGG
TAAATGAGGAAGATGGTCGAAATGATCATCATAACAACAATAAATACTTGATGAAGAAGG
CCATGATGAACAATGAGCAAATTGATAGAACTCAGGATATCGACAACGCCAAAGAAATGT
TGAGGAAAATATCAAGTGAAAGCAGCTCGCGCAGAAGCTCCCTGTTGAATAAAGATTTCAT
CTCTCGTGAACGGCAATGCAAACAGTGGCGGTGGTACGAGCATTAAACGGAACAAGAGGAA
GTTCTAAGAGTAGTAATACACACTTTTCACTATGCCTCCACGGCGTATGGTGTAAAGATGT
TGAGTAAAGATATATCTAATACCAAAGTGGAAGTGGATGTGGAAAATTTGATGATTGTTA
CGAAACTCAACGATGTCTCACTGTATTTCTTAACAAGAGAGTTGGTAGAATGGGTTTTTG
TACATTTTCCACGTGTGACTGTTTATGTGGATTCCGAATTGAAAAACAGCAAAAAATTTG
CCGCTGGCGAGTTATGTGAAGATAGTAAATGTAGAGAATCAAGGATCAAGTATTGGACAA
AGGATTTTCATCAGGGAACATGATGTTTTCTTCGATTTGGTAGTGACTTTGGGTGGCGACG
GTAATGTTCTTTTGTAAAGTTCCATTTTTCAGAGACATGTACCACCCGTTATGTCGTTTT
CATTAGGGTCTCTAGGATTTTTTAACAAATTTTAAGTTTGAACATTTTCAGGGAGGATTTAC
CTCGGATTATGAATCATAAAATCAAGACAAATTTACGGTTGAGGTTGGAGTGCACAATTT
ATCGTAGACACCGCCCTGAAGTAGACCCAAACACGGGGAAGAAAATATGTGTGGTGGAAA
AACTAAGCACACACCACATTTTGAACGAAGTGACCATCGATCGTGGTCCAAGTCCTTTTC
TATCCATGTTAGAATTGTATGGTGACGGCTCATTAATGACCGTTGCGCAGGCGGACGGAC
TGATTGCTGCTACTCCGACTGGGTCCACGGCCTATTCTTTGAGTGCAGGTGGGTGATTGG
TATGCCCAACCGTCAATGCAATCGCTTTAACACCCATTTGTCCACATGCATTGAGTTTCA
GACCCATCATCTTACCAGAAAGTATAAATTTAAAAGTGAAAGTCTCGATGAAGTCAAGGG

CTCCAGCATGGGCGGCTTTTGATGGGAAAGATAGAATTGAATTGCAAAAAGGTGATTTTA
TAACCATATGCGCCAGCCCATATGCTTTTCCAACCGTGGAAGCCTCGCCCGATGAGTTTA
TTAACAGTATCAGTCGACAACCTAACTGGAATGTGAGGGAACAACAAAAGTCCTTTACGC
ATATTTTGTCCCAAAGAACCAAGAAAAATATGCACATGAGGCGAACAAAGTCAGAAATC
AAGCAGAACCTTTAGAGGTAATAAGAGATAAATACTCTCTGGAAGCAGACGCTACTAAGG
AAAACAACAACGGAAGCGATGATGAGAGCGACGATGAGAGTGTAAGTGCAGAGCTTGCA
AATTAAAGCCTTCGAGCGTCCCAAACCTTCTCAAGCAAGGTTTTTCAGTATAA

YJR049C, 530 aa (SEQ ID NO 170)

MKENDMNNGVDKWVNEEDGRNDHNNNNNLMKKAMMNEQIDRTQDIDNAKEMLRKISSE
SSSRSSLLNKDSSLVNGNANSGGGTSINGTRGSSKSSNTHFQYASTAYGVRMLSKDISN
TKVELDVENLMIVTKLNDVSLYFLTRELVEWVLVHFPRVTVYVDSELKNSKKFAAGELCE
DSKRESRIKYWTKDFIREHDVFFDLVVTLGGDGTVLVSSIFQRHVPPVMSFSLGSLGF
LTNFKFEHFREDLPRIMNHKIKTNLRLRLECTIYRRHRPEVDPNTGKKICVVEKLSTHHI
LNEVTIDRGPSFPLSMLELYGDGSLMTVAQADGLIAATPTGSTAYSLSAGGSLVCPTVNA
IALTPICPHALSFRPIILPESINLKVKVSMKSRAPAWAAFDGKDRIELQKGDFTICASP
YAFPTVEASPDEFINSISRQLNWNVREQQKSFTILSQKNQEKYAHEANKVRNQAEPLEV
IRDKYSLEADATKENNNGSDDESDDSVNCEACKLKPSSVVPKPSQARFSV

YKR094C, 1255 bp, exon1: 501-508, intron1: 509-876, exon2:
877-1255 (SEQ ID NO 171)

AGGTTGTGTTCTTCAATGATGGGCAATGCAATTTGGCGTTAAGCGCCTGAGCAATAAGGT
AACAGCGAAATTTATGACATATTATTTTCAACCTTTTACAACTAGTAGATTTAGTGATT
TATTACCTATTGGCATTCAATTTGTGTTCTATATGTGGATGAGGATAGCCGCCTTTCTTCT
CATCGGAGGCCATATCATCTTTTCGACAATCCTTTTAAATACTATTTCCATCCGTGCCTC
TAATAGATTTGTGTAGTTGTCTGGGTGCAATCTTTCCATTTTGTCTGAACTTTTTTTTTT
TTTTTCATGTTTTTCAGATTCTGAAGTACCGCAATAGGATATGGCGGATAATCCGCCATAT
GATCCGCCTCATACTAGCCATTACCCATCTATCCCAGGCATTATGGGTATGCAACTCATA
ATCTCAAATACACAAATAAGAGCAACCTTATATATCACTTTTTCCCGTTCAGCAAGAGGT
AAAGCCACCAAAGGTTCAAATGCAAATGTATGTTACGGCGAATACAGAATACTATGTTC
GAAATAATATGAGGATTATACGATAGCAAAAAAGCCATAAACGAAAGACATAAATGGAAA
ATGATTGACAAGCTCACAATTTATTAACAAGTAGCAATTGAGAAAACTATTACTCGCG
GCAAGCTTCTGAGTTTACATTAAATCTGTAGAGCAAATTGAAAATGTCGCATATGTGCTG
AAGGGTTTGTGTTCCATCTTATTTTGCATAACATAGTTATATTTACTTTGGTCGCATAA
AAAATATTTTTTACTAACGTGAAGTTTCTTTCTTTATGATGTACGCACGCACGTCTGTGC
TTACTCCATAAATGAACTTATTTCCAATTTTGTACAGCTTCGTTAAGACTTTGACTGGTAA
GACCATCACTTTGGAAGTTGAATCTTCTGACACCATTGACAATGTCAAGTCCAAGATCCA
AGACAAGGAAGGTATCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGA
AGACGGTAGAACTCTATCTGACTACAACATCCAAAAGGAATCCACTTTACATTTGGTCTT
GAGATTAAGAGGTGGTATCATTTGAACCATCTTTGAAAGCCTTGGCTTCCAAATACAACG
TGACAAATCTGTTTGTCTGTAATGTTACGCCAGATTACCACCAAGAGCTACCAACTGTAG
AAAGAGAAAGTGTGGTCACACCAACCAATTGCGTCCAAAGAAGAAGTTGAAATAA

YKR094C, 128 aa (SEQ ID NO 172)

MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQQLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGIIEPSLKALASKYNCDSVCRKCYARLPPRATNCRKRKCGHTNQ
LRPKKKLK

YLR040C, 1175 bp, CDS: 501-1175 (SEQ ID NO 173)

AGCTCTCAAACAATACTATAAGTTCAAGTACAAGCACAGGAGGTGTAGGTTTCAGTC
AAGCCATGTCTTTACTTCGTTTTAATGTTAGAAACAATCGCTTATTTGTTTTCTTAAACA
AATATATTAGGTTCAAGGTCTTCGCAGGTGTAAGAAAACCCGTGGTCTCCATATTCCTAA
GTATGATAAATAAAAAAAACTTAATAAATTATTAATTGCTTCAAACCTTTTTCTTTTTT
TAGTTTTTAATATTTCAAACGTTATCTTCATTGAACGCCCAAATAGGGAAAAATCCTGGC
AAATTTTTTATTGCTGTCAATCAAGGCTATGCTAGAAAATTCAAGAGCTTGGATGATTTA
AAAAGACACTCTCAATCGAGAAAGTTTATTCCTTTGTTATTCTGCTTTACCTGATCATATT
CCGGCGTATTGTTTCTAATCAAGTGATTTTCGATATCCAGTTACGAACCATTTACAACATT
CCTGAAAATATTGCGTATCAATGATATTTGCTCCTTCTTTCTCCCTCATTAATAAATATTC
TCCTGGTAAGCTTTCTAATCAGCCACAGTTTTGCTGCCAAAACCTTTAACGTCTAGTTCCA
ATGACGATACACTTGCCAGGTCCGCAGCTGCAGATGCAGACATGGCATTCTTCATGGAGT

TTTAAACGATTTCGACACCGCTTTTCCACAGTATACCTCATACATGATGCAAAACCATTT
TAACCCTACCTCAACCTGTTGCTGACTACTACTATCACATGGTTGATTTGGCCTCAACAG
CAGATTTACAATCTGATATTGCTCAGAGTTTTCGGTTCCTCAATTCCAAACATTCATTA
CGGCCTTTCCATGGTATACCTCTTTGCTAAACAAAGCCTCCGCCACCACCATATACCTTC
CCCAACACTTCATAACAGGTGAGACAGAAGCTACCATGACTAACTCATCTTATGCCAGCC
AAAAAACTCCGTTTCCAATTCTGTTCTTTCTCGACAGCGAACGCAGGCCAGTCCATGA
TTTCCATGGCTAATGAAGAAAACAGTACAACAGCACTTATATCCGCATCAAACCTTTCTT
CAACATCCAGAACTAGTCAATCACAGAATGGTGCCCATGCCAAAAGCTTATATTTCCCA
TGGCGTTGTTCCGAATCTTTGCAGTTGCCCTTTAA

YLR040C, 224 aa (SEQ ID NO 174)
MIFAPSFSLIKNILLVSFLISHSFAAKTLTSSSNDDTLARSAAADADMAFFMEFLNDFDT
AFPQYTSYMMQNHLLTPQPVADYYYHMDLASTADLQSDIAQSFPFTQFQTFITAFPWYT
SLLNKASATTIYLPQHFIETETATMTNSSYASQKNSVNSVPFSTANAGQSMISMANEE
NSTTALISASNSSSTSRTSQSQNGAHAKSLYFPMALFGIFAVAL

YLR048W, 1618 bp, exon1: 501-590, intron1: 591-949, exon2:
950-1618 (SEQ ID NO 175)

GCACCCTTTTCTTTTCAATAACAAAAAGAGCTTGGGCATTACGTTTCAACACTTTT
AATATTTCCCTTTTACATCCGTACATATAAAATGTAAACCCATGCATTCATGACAATTT
TACCTATTTCTTAAAGGCCTTTGTCACTTCTTTATGGGAATGGCGCTACTTTAATTTTCC
GCCTACTTTGAAAAATTTACCAAGGCGAAATTGAGTGCGCTAGGCGGAAGTTCCAGGGCA
CGGTCACCGAACCTTTGTGCTGTTTCGAACGAGGGTCCCGCTGGAGGTTGACGGACGCGG
GAGGAGCTGGAAAGATGGAATGGAAGGACTGCAACACTCAGTAAGAAGGTTCTGTGGTAGG
GAACATCACCTTCTCTAGTTCCTGTAAAAATAATATGATCAAGTTTGAATCCTCGTATTG
AAAAATCGCGAGTTATTAAGTGTGTAATTTAGAATACCGAAATAGCACAAGAAGAGATAA
GATAAGATACTGATAGGATAATGTCTTTACCAGCTACTTTTGATTTGACTCCAGAGGATG
CCCAACTTTTGTGGCCGCTAACACCCATTTAGGTGCTAGAAACGTTCAAGTATGTACAC
ATATCCCATACGATTATGTTCTATAGATGATAATAGGTCTCGAAAAGAATATGTCCCCGA
TTTAATCATATTTGGAGGTCAGAGGACCAAAGGTAATTTAGAGGAATTTTGAACACGCC
GGGTTTAGAAGAGTTAGAATTTCACTTCTTAGTGAGGGTAAGGAGAAGAACTCAATAAG
AATATACATCCTCGACTGTGTCAAAGATTATGAACTCCGATGAAACAGTAAACGTCAAA
AAATTCACGGGATATAATTCGGTACTTTATTGGATATGGAAGAAAACATTATATATGCA
CAATGAACGCTCTTACTAACATAATTTATCTTTCTCTCTTTTTTTAGGTCCACCAAGA
ACCATACGTTTTCAATGCTAGACCAGATGGTGTTCACGTTATCAATGTTGGTAAGACCTG
GGAAAAGTTGGTTTTGGCTGCTAGAATTATTGCTGCCATTCCAAACCCAGAAGATGTTGT
TGCCATCTCTTCCAGAACCTACGGTCAAAGAGCTGTCTTGAAATTTGCTGCTCACACTGG
TGCTACTCCAATCGCCGGTAGATTCACTCCAGGTTCTTTCACTAATTACATCACCCGTTT
TTTCAAGGAACCAAGATTGGTTATTGTTACCGACCCAAGATTAGACGCTCAGGCCATTAA
GGAAGCTTCTTACGTTAACATTCCAGTCATTGCTTTGACTGATTTGGACTCCCCATCTGA
ATTTGTTGATGTCGCCATCCCATGTAACAACAGAGGTAAGCACTCCATCGGTTTAACTCTG
GTACTTGTGGCTAGAGAAGTTTGGAGCTAAGAGGTGCTTTGGTCGACAGAACTCAACC
ATGGTCCATCATGCCAGATTTGTACTTCTACAGAAACCCAGAAGAAGTTGAGCAAGTTGC
TGAAGAAGCTGCTGCCGCTGAAGAAGGTGAAGAAGAAGAAGTTAAGGAAGAAGTCACTGA
AGGTCAAGCTGAAGCTACTGAATGGCTGAAGAAAATGCAGACAACGTTGAATGGTAA

YLR048W, 252 aa (SEQ ID NO 176)
MSLPATFDLTPEDAQLLLAANTHLGARNVQVHQEPYVFNARPDGVHVINVGKTWEKLVLA
ARIIAAIPNPEDVVAISSRTYGQRAVLKFAAHTGATPIAGRFTPGSFTNYITRSFKEPRL
VIVTDPRDLDAQAIKEASYVNIPVIALTDLDSPSEFVDVAIPCNNRGKHSIGLIWYLLARE
VLRLRGALVDRTQPWSIMPDLYFYRNPEEVEQVAEEAAAAEEGEEEEVKEEVTEGQAEAT
EWAEENADNVEW

YLR088W, 2345 bp, CDS: 501-2345 (SEQ ID NO 177)
CTTCCCATGTAGAATATCATTGTCAAACATACTACTACCGTGAGAATCCAATCTACTAAA
AAGACCCAGCTAAAGTCCTTTTGGTGTGTCAATGGAACACCACGTAATTGTGAAATAGCT
TCCATGCTTGCTAACTTATTACCGTCAATAGAAGACTTGAGTCAGGTGGCTTTAATGAGT
ACTATTCTTTTTTTTTTTTCCAAAGAGCACTATGTTGATAATACCGCAGTAATTTTTTTTG
AGTATCCTGTAGCCTAGAAAGGTTGAAGCTTATAAAACCGTGCCAACAGCTTTATAGTGG

GGAGTTTGGCTTCCCTCTATTTGTATATTGATCGCCATCCCTACGAAGTTATTGGGAACG
CATCGTGAACCTCTCACTTTAATGCCAGCGGTAGAAAAAAGTCATAAACAATACACGC
CGGCTACACTTAGAAAGAAATGACATTTGCTGTCTTATAAAAGGACTTGACAGACCAAAG
ACGCGTATAATACACCAAGAATGGCCTTATTGGAGAAGTTGCATCGAAGGATTGTTGATA
TGGGGCTTGTCCCGCGTATAATCGCCTTATTACCAGTTATTTCCATGCTATGCGCTCTAT
TTGGGTTTATTTCTATAGCTATTCTGCCTATGGATGGACAGTACAGAAGAACATACATTT
CTGAGAATGCATTGATGCCTTCACAAGCGTATAGTTACTTTAGAGAATCTGAATGGAACA
TTTTGAGGGGCTATCGATCTCAAATTAAGAAATGGTAAACATGACTTCTATGGAAAGAA
ACAATTTGATGGGTTCTTGGTTACAAGAATTTGGTACTAAGACTGCTATTTACGAAAATG
AACAATATGGAGAAACATTGTACGGTGTAAATGCACGCTCCTAGGGGTGATGGAACAGAAG
CGATGGTGCTTGCCGTTCCATGGTTTAATTCAGATGATGAATTCATATTTGGCGGCGCAG
CTTTGGGTGTATCTTTAGCAAGATTTTCTCACGTTGGCCAGTATGGTCCAAGAATATAA
TTGTTGTCTTCAGCGAAAATCCTCGTGCAGCATTAAAGATCATGGGTTGAGGCATACCATA
CTTCCTTAGATTTGACTGGTGGTTCCATTGAAGCTGCTGTTGTGTTGGATTATTCGAGTA
CGGAAGATTTCTTCGAGTATGTAGAAATCTCATAACGACGGTCTGAATGGTGAGCTGCCCA
ATTTGGATCTTGTCAACATCGCTATATCCATTACGGAACATGAAGGTATGAAAGTTTCTT
TGCACGGTCTACCCAGTGATCAGTTAACTAATAATAATTTCTGGTCAAGATTAAAAATAT
TATGCCTGGGAATAAGGGATTGGGCGTTGTCCGGTGTAAAAAGCCCCATGGTAACGAGG
CATTTAGCGGCTGGAGGATTCAATCTGTAACATTGAAAGCACATGGAACAGTGGTCATG
ATATTACTACATTTGGACGTATACCCGAAGCAATGTTTCGCTCTATTAATAACCTTTTGG
AAAAATTTACCAATCGTTCTTCTTTTATTTGTTATTAGCACCACGTCAGTTCGTATCCA
TTAGTAGTTATTTGCCAAGCGCTGTGGCTTTATCTATAGCATTGCCATAAGTTCATTAA
ATGCATTTATAAACAATGCTTATGCAAATATATCCTTATTTTCCGAGTATAATTTGGTAG
CGTTGTTGGTTTGGTTCGTGTCAATTGGTGATATCATTTGTTGTTTCACAAGCGTTTCTTC
TAATACCTTCATCGGGATTATTGATGACAATTAGCATGGCATCTTGTTTPTTACCTTTGA
TACTTTCCAGAAAAATTCACATCTCAGAACCACATCATAACAGGTTGAAAAATGTTGCTT
TTTTATATTTTCAGTTTGGTTTCAACATCTTTGCTAATGATAAACTTTGCAATGGCTTTAC
TGATCGGCACATTGGCATTTCCTATGACATTTGTGAAGACCATTGTTGAAAGTTCTAGCG
AACATGAGGTGACAACTCAATCCTCTAACCCAATAAAAACTGAGCCGAAAGATGAGATAG
AGCTCGTCGAGAATCACATGGATACAACGCCAGCAACCCCCAACACAGAAACAAAAAC
TAAAAAATTTAGTACTATTAATTTTGACAAATCCATTTATTTCAATAACCTTATTCGGAC
TATTTTTTTGATGATGAATTTTCATGGATTTGATATAATAAACAACAACTGGTTTCAGCATGGT
TGGATTTGAAATGTTGGAGTTGGTTTGTACTTTGTATAGGTTGGCTTCCATGTTGGCTAT
TGATATTAGCGTCATCGTTTGAATCTAAATCTGTCGTAGTAAGGTGAAAGAAAAGCAAA
GTTAG

YLR088W, 614 aa (SEQ ID NO 178)

MALLEKLHRRIVDMGLVPRIIALLPVISMLCALFGFISIAILPMDGQYRRTYISENALMP
SQAYSYFRESEWNILRGYRSQIKEMVNMTSMERNNLMGSWLQEFGTKTAIYENEQYGETL
YGVMHAPRGDTEAMVLAVPWFNSDDEFNIGGAALGVSLARFFSRWPVWSKNIIVVFSN
PRAALRSWVEAYHTSLDLTGGSIEAAVVDYSSSTEDFFEYVEISYDGLNGELPNLDLVNI
AISITEHEGMKVS LHGLPSDQLTNNNFW SRLKILCLGIRDWALSGVKKPHGNEAFSGWRI
QSVTLKAHGN SGHDITTFGRIP EAMFRSINN LLEKFHQSF FFYLLAPRQFVSISSYLPS
AVALSIAFAISS LNAFINNAYANISLFSEYNLVALLVWFVSLVISFVVSQAFL LIPSSGL
LMTISMASCFLPLILSRKIHISEPLSYRLKNVAFLYFSLVSTSLLMINFAMALLIGTLAF
PMTFVK TIVESSSEHEVTTQSSNPIKTEPKDEIELVENHMDTTPATPQQQKQKLKNLVLL
ILTNPFISITLFLGLFFDDEFHGFDIINKLVSAWLDLKCWSWFLVCIGWLPCWLLILASSF
ESKSVVRSKEKQS

YLR159W, 845 bp, CDS: 501-845 (SEQ ID NO 179)

TCCGTCCCAAAGATAGCTTGATCATCCTAAGCGGGTTCGCATTTTACTATCCCCAGTTCCG
AAGAATAACAAGGCTCAATGCATATGCTGTTTATCGTGTCTCACAAGGCGGTATGACGTTT
TTAGCAATGTAATTATATTA AAAAGATCTTCAGTCACTATGAGTGGTTGATTGCCCCATA
GAGAGCTATAAGCCGACGTGAAAGCTGCTGGTTCCAGCTTGGCTCATGTCGTCACCAGTC
ACTAGTCACTTGGTCGCATTCATTGCTACTCATCTGCGAGTGAGCATATTTGAGATCTGA
CTTGCCAAGGGATTAGAATCACGTAAGACTCTTGATCCTTAGAAGATATTTCTGACAAAG
AACCACCTAAGCCATGCAAGTTTTTTTTTTTTCATTTGGTGGCGAAACAAAGGTGATGAAAG
TTTCTTCTTGTACAAACGCCAAGCCCGATAGGTGAGACAATTCTTGAAGTAATGGACCTC
TGAGTAAGCATATCAGTCGAATGAAGTTCCAATATGCGTTGGCCAAGGAACAGCTAGGCA
GCAACTCGCGCAGTGGCGTCAAAAACTAATAAGTAAACACCACTGGCTTCCGGAATACT

ATTTCTCTGATCTCTCATTCTTCTGTTGTACAGCAGTGGGACAGTAGAGCCATTGAAAAAA
CTACAATCATATCTTGTATGCGGCCCGCAAACCAAGAGATTATCCTTTGAGACATTGTG
AGACCCTCCGTTTCGCAACCGTGCTCTCTGTTTTCATCACTATATGCACGCTCTTTCCAAA
GCTCCTGCACTTTGCACGTGGCGGAGCCATCGCCCGGCTTCCATATGTACGGCTGCCACA
CCTAA

YLR159W, 114 aa (SEQ ID NO 180)
MKFQYALAKEQLGSNSRSGVKLISKHHLPEYYFSDLFSVQWDSRAIEKTTIISCM
RPNQEIYPLRHCETLRSQPCSLFSSLYARSFQSSCTLHVAEPSPGFHMYGCHT

YLR167W, 959 bp, CDS: 501-959 (SEQ ID NO 181)
ATCAAAAGAGTGTTTCAAGTAAGTAAAAACATTTGAGCCTCCCCATTTGTTGAAAGGAGA
GAAATTAAACTTGGTTGGGGTTAATTATTTGATGGGTATATTAATTTGCAACCGCAAGGT
ATCGATAATAAATATTCTACAAAACCTTTATCAATAGTGGTGAAGTCTTTAGTGCGATCT
ACCTGGGGTTAATGAACGAGAAGTTCTTGAGATATCTTTCTGTTTACCTCCGTGCATCC
TGTAAGGAATTGGGTTTATCATTTATCATTTATTTTAGTACAAACTTTTTTTTTTGGCCC
GGCGCACTTTTTCAAGCGGTGGGAACATCAAAATGAAAACTAGATACTTTTAGACT
TATTAATGGTTTAAATATTTTGAGATGTTTCGTTATATCAGAACTTCCTTACTTCTATC
TTTTATTCCAATACAAAGAAGTCACAAGATTACTTGGTAAGAAAGAAGCAGTTAATTTTT
AATTTTGCCGACAAGCCAAGATGCAAATTTTCGTCAAGACTTTAACCGGTAAGACTATTA
CCCTGGAAGTTGAATCTTCTGACACTATTGACAATGTCAAGTCCAAGATCCAAGACAAGG
AAGGTATTCCACCTGACCAACAAAGATTGATCTTTGCTGGTAAGCAATTGGAAGATGGTA
GAACCTTGTCCGACTACAACATCCAAAAGGAATCTACTCTACACTTGGTCTTGAGATTGA
GAGGTGGTGGTAAGAAGAGAAAGAAGAGGTCTACACCACCCCAAAGAAGATCAAGCACA
AGCACAAGAAGGTCAAGTTGGCTGTCTTGTCTACTACAAGGTGCTGAAGGTAAGG
TTACCAAATTGAGAAGAGAATGTAGCAACCCAACTTGTGGTGCTGGTGTCTTCTTGGCTA
ACCACAAGGACAGATTGTACTGTGGTAAGTGTCAATCCGTCTACAAGGTTAACGCTTAA

YLR167W, 152 aa (SEQ ID NO 182)
MQIFVKTLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYN
IQKESTLHLVLRRLRGGGKKRKKKVYTPPKIKHKHKVKLAVLSYKVD AEGKVTKLRRE
CSNPTCGAGVFLANHKDRLYCGKCHSVYKVNA

YLR232W, 848 bp, CDS: 501-848 (SEQ ID NO 183)
AGCCACCAATTCCACCAGGCCCGGCATTCAAGTACTTGTAAAGAACACCAACAGGCAAAGT
CAACACCCCAATCATGAAGTTGCAATGGGACGTTCCCTACAGCGTGTGCTAAATCCCATC
CAACCAATATGTCGGGGAATTGGTGGGCAAATGAGGTGATTTCGGCCAATATCGAAATATT
GCCCCGTGTAATACTGAACACCTGACAAACAGACCAGCGCCAATTCATCTTGATTTACCT
CTATGGTATCCAGGATATCTTGAGTTCTGATATAAGTCTCTCCCTCGCGTGGCTCGATCT
GAATAAAAACATTCTCAGGTTCCGAAATTCATGAATTTTGCACCTGGTTGTAGAAAGCAT
AATAGTCTGATGGAAGGAGCCCTTTTCAAAAAGGATCTTGAATCTTTTCTCAGTAGGTT
TATAAAACGTAATTAACAATGAATTCAAATTTGCAGTGAGACTATTCATTACTGCAACTT
CATTTTCTTGAGCACCCACGATGGGGGCTAGTAGTGAAGAATAGGTAAGTCAATGCTGA
CCCAAGGCACCTTTCCTCTGGCTTCTTCAGGATGTTTGAAATGCGATTCCACAGCACAAT
CGCTCCACGCATCTAGCTCAGCATTAATTGAATTCCTAGTTGACTTCGGCATCAAACCTA
AAGAATTCCCGCATAAGTACGTCACAGGCTTATCGTCCGACGATAGTCCCATGGATTAA
ATGTAGGGATGTTGAATTCATCCCTCAGAGATTCCGGATATTCTCCGTCTAATTCCAAAG
CTTTCTCCATAATTACCAGTTTGTCTTTTTTTCCACAGAATATTAGGCTTAATATGTA
CGTATTGA

YLR232W, 115 aa (SEQ ID NO 184)
MGASSGRIGKSMILTQGTFLASSGCLKCDSTAQSLHASSSALIEFLVDFGIKPKEFP HKY
VTGLSSDDSPMDLNVGMLNSSLRDSGYSPSNSKAFSIITSLFLFSTEYLG LICTY

YLR233C, 2600 bp, CDS: 501-2600 (SEQ ID NO 185)
GCGCATTTTCCCCACCCATGCGAATCATGGCTGAAATCAATGCCTGTTAGGTGCCCTGCA
ACACTAGTCATGGTAACTTCGCAGTTAGCCCCATTTCTGGCAAACGGGAACCCACTAAAC
ATGAAATCATAGTTCTTTACATACATGTAGCCGGAATCCCTTGAAGTTGATCTGCCTCCT
CCTAGGATCTGTGAACTGCCTTCGCTATAGAATTTTTCTCTGCGACACATAGCACTTTC
ATTATTGTCTATAATACACCTTTACGTAGCTGAAGCGAGCGCACAGACGAAGGTGCTTTC

AAAAGCGATGCCCTCTTTATTGACAGTTACTAATTCGCCAAACTGCTTTTTTTTATCAAT
GTGATTTTCGCGTTCACGCCATTATCCAATGTCAAAAAGGATAATGGAAATGTTAACATG
CCTGTATGATCCGACCGTTTTTAGCAAACCTTATCAGGGGAAAAAGTATATTCATTAAAT
GACACATGCCACCATAGATAATGGATAATGAAGAAGTTAACGAAGAATGTATGAGATTAT
TTTTCAAGAACGCTCGTGCGCATCTGGATAAACATCTAACATCAAGGTTGACATGCGATG
AAAATGCATATATCACGTTTCAGATGCTTCCTGGATGGAATACATCGCAAATCTACTAGGT
TTCTCGAAGAGCTACTTTTGAAACAAGAAAATATGTACCATAATAACAATTACGAACGCA
TAAATGATTCCGTGATACCATTTGGTTCTGAAACTTTTATGGCTTCAAATTCACGAACCTA
CACTCCAATGGTTTGAGCACTGGTTCCATGATATCATGCGACTAAGTAACAGAAGAAAGT
TCAGAGTTTTTAGAATTTTTCAAAAAAAATGATTCAATTTTTCAAAATTACACACAGGT
ATTACTATGACATCATCGAACACCTATGCGCAAAGTACGATATGAATTCCGTTATTTCAA
ATGCTCTCTTCGCGAAGTTGAATTTAATGCAATACACAGATGGACTTTCAACTCATGAGA
AAATTATCTTAAACACGAGTAATCCACTGACGTTTTCCATTGTAATCTCACTACAAAGAT
GCGTGATTAATCTAGGTTCCACACATTTTTATAAAACACTACTAAACAAGCCGTCTAACA
AACCCAAGAGTGTGGAAGGTTTTGAGAAGTCTATTAGGTACTTGAATATTGCCTCACTCT
ATCTCCCAGCCGTTGGAGATACTTATTTTTCAACGAGCGAAAATTTACTTGATCACTGGGA
AATTCTCACTGTATTTCTTTGAATTAGTAAGAGGAGCATTTGGTAAGGATTCCGTCTAAAT
GTGCGTTAAACAATTTGAAAGATTTCAATTTTGACTCCTGATTTTCCGGAAAGAAGACGTC
TGATGAAAAAATTGGCAATTCTTGTTGTCAAAAGATCTCAAAGGTGAGAAATCATTCTTTG
AAGGTCAAATTGTTTTGCAATTTCTATCGATAGTAGAACACACTTTGGTTCCACAGTCAT
GGAACGCATCACGTGCTTCTAATTGTTGGTTATTGAAAGAGCATTTACAAATGGCTGCAT
TAAAGTATCATTACAGGTAATATTAATGTTATACTTGAAAACCTGGCTGCCACAATGGGAA
GTTTCGATCTTATGTTTACAACTCGAAAAAGTAAGGAACAAAAGAACAACCTCAAATATG
CAGATTTGAGTGAGCGCCAGGTTTTTTTTTTTAGACTTGAGCTTTGATTTTATTGCTAATA
TCATAGACGTCGTCATCAAACCTCCTGGCAAAAAAACATGGAAGACTTTCGATATCTAG
CCATTATTCGTTTGCTTATGTGCTGGATTAAAGTCATATAGATCTATTTTGCAGTACACTC
ACAGACACAGGAAGTTTTGCACTTTCATTCGCCTTGTTGCTGAACGACTTGATAAATAGTC
CACTGAATTGTTTCAGGAAATATATATAGCCACAGGCCGAAAAGAAGCTATCTTTTAGAG
AAGATATTATTTTCAGGGAATTTCTTGCAATTAACCTTTGCACTAACAGATTTTAATGACG
ATTATGTGTATGATTCTCCCGACATGATTAATAATATAAATTGGATGCCCTACATTGACTA
AAGTGCTTTCTCCAAAAGAAGAATGTGTTCTGCGAATTAGATCAATAATATTTTCTGGCA
TGAAATTTTGTAGAGAAAAATGACACCGGCGTCATATGGAATGCCAGCAAATATAAGTTTG
ATTTAATAAGCCCAAATATTAATAAAACGCCAAATAGCATTATCGGAAATTTCTCTCA
AAATAAATGTAAAAACACAACAGGAAAGAGTAGTCTCTTCGAGAAAAGTTGAGGCCAAAA
GAGATGAACAACAGCGCAAAAGAGCCGGGAAAATAGCTGTGACAGAACTGGAAAAACAAT
TTGCAAATGTCCGGAGAACAAAAAATTTGTCTCCGCTCCAGAAAAGATGGCGTTTCTT
CTGAGTTGGTAAACATGCTGCTTCACGAGGGAGAAAACTATCACTGGCCCACTATCCT
CTGATTTTCTCTCATATCCAGACGAAGCAATTGATGCTGATGAGGACATCACCGTCCAAG
TGCCAGATACTCCTACTTGA

YLR233C, 699 aa (SEQ ID NO 186)

MDNEEVNEECMRLFFKNARAHLDKHLTSRLTCDENAYITFRCLDGIHRKSTRFLEELL
KQENMYHNNNYERINDSVIPLVLKLWLQIHEPTLQWFEHWFHDIMRLSNRRKFRVFRIF
QKKMIQFFKITHRYYYDIIHLCAKYDMNSVISNALFAKLNLMQYTDGLSTHEKIIILNTS
NPLTFISIVISLQRCVINLGSTHFYKTLNPKSPKPSVEGFEKSIRYLNIAASLYLPAVGD
TYFQRAKIYELITGKFSLYFFELVRGALVRIPSKCALNNLKDFILTPDFPERRRLMKKLAI
LVSKDLKGEKSFFEGQIVLQFLSIVEHTLVPSQSWNASRASNCWLLKEHLQMAALKYHSGN
INVILENLAATMGSFDFLMFTTRKSKEQKNKLKYADLSERQVFFLDLSFDFIANIIDVVIK
PSWQKNMEDFRYLAIIRLLMCWIKSYRSILOQYTHRRHKFCTSFALLLNDLINSPLNCSGN
IYSHRPKRSYLFREDIIFREFSCINFALTDFNDDYVYDSPDMINNIIGCPTLTKVLSPE
ECVLRIRSIIFSGMKFLEKNDTGVIWNASKYKFDLISPNIKIKRQIALSEISSKINVKTQ
QERVVSSRKVEAKRDEQQRKRAGKIAVTELEKQFANVRRTKKLSPLPEKDGVSSSELVKHA
ASRGRKTITGPLSSDFLSYPDEAIDADEDITVQVPDPTPT

YLR234W, 2471 bp, CDS: 501-2471 (SEQ ID NO 187)

AATGGTATCACGGAATCATTTATGCGTTCGTAATTGTTATTATGGTACATATTTTCTTGT
TTCAAAAGTAGCTCTTCGAGAAACCTAGTAGATTTGCGATGTATTCCATCCAGGAAGCAT
CTGAACGTGATATATGCATTTTCATCGCATGTCAACCTTGATGTTAGATGTTTATCCAGA
TGCGCACGAGCGTTCTTGAAAAATAATCTCATACATTCTTCGTTAACTTCTTCATTATCC
ATTATCTATGGTGGCATGTGTCATTTAATGGAATATACTTTTTCCCCTGATAAGTTTGCT

AAAAACGGTCGGATCATAACAGGCATGTTAACATTTCCATTATCCTTTTTGACATTGGATA
ATGGCGTGAACGCGAAAATCACATTGATAAAAAAAGCAGTTTGGCGAATTAGTAACTGT
CAATAAAGAGGGCATCGCTTTTGAAAGCACCTTCGTCTGTGCGCTCGCTTCAGCTACGTA
AAGGTGTATTATAGACAATAATGAAAGTGCTATGTGTGCGCAGAGAAAAATTCTATAGCGA
AGGCAGTTTCACAGATCCTAGGAGGAGGCAGATCAACTTCAAGGGATTCCGGCTACATGT
ATGTAAAGAACTATGATTTTCATGTTTAGTGGGTTCCTGTTTGCCAGAAATGGGGCTAACT
GCGAAGTTACCATGACTAGTGTGTCAGGGCACCTAACAGGCATTGATTTTCAGCCATGATT
CGCATGGGTGGGGAAAATGCGCCATCCAAGAGTTATTTGATGCGCCACTGAACGAGATTA
TGAATAACAACCAAAAAAAGATAGCAAGCAACATCAAGCGAGAAGCGAGGAATGCAGACT
ATCTGATGATATGGACAGATTGCGACCGGGAAGGAGAGTACATCGGTTGGGAGATATGGC
AGGAGGCCAAGAGAGGCAACAGGCTCATAAAAATGATCAAGTATACCGGGCAGTCTTTT
CGCATCTCGAAAGACAACACATATTAAATGCAGCACGAAACCCAAGTCGATTGGATATGA
AGAGTGTGCACGCTGTAGGCACGCGGATTGAAATCGATCTTCGAGCAGGTGTTACATTCA
CCAGACTCTTAACAGAAACGCTACGAAATAAACTGAGAAACCAAGCCACCATGACCAAGG
ATGGTGCAAAACACCGCGGTGGTAACAAGAACGACTCACAAGTCGTATCGTATGGTACAT
GCCAGTTTCCAACGCTCGGCTTTGTAGTAGACAGGTTTGAAAGAATACGAAATTTTGTTC
CCGAAGAGTTCTGGTATATCCAATTGGTAGTCGAAAACAAAGACAACGGCGGAACAACAA
CGTTCAGTGGGACAGGGGCCACTTGTTCGACCGGCTGAGCGTGTTAACGTTTACGAGA
CATGCATCGAAACCGCCGCAATGTTGCTCAAGTAGTAGACTTGAAATCAAAGCCAACAA
CGAAATACAGACCTTTACCTCTGACCACAGTGGAGCTACAAAAAACTGCGCCCGGTACC
TGCGTCTGAACGCCAAACAATCACTAGACGCAGCAGAAAAGCTATACCAAAGGGGTTCA
TATCGTATCCAAGAACAGAGACTGATACTTTCCACACGCAATGGACCTAAAATCCTTGG
TCGAAAAGCAAGCTCAATTGGACCAACTCGCTGCAGGCGGCAGAACCGCCTGGGCATCGT
ACGCGGCATCGCTGCTCCAACCCGAAAACACAAGTAACAATAACAAGTTCAAGTTCCAC
GAAGCGGCTCCCATGACGACAAAGCGCATCCACCAATCCACCCCATCGTAAGTCTGGGGC
CTGAAGCAAATGTTTCGCCAGTGGAAAGAAGAGTATACGAGTACGTGGCCAGGCACTTT
TGGCATGCTGCTCAGAGGACGCCAAGGGCCAATCGATGACCTTGTGTTGGACTGGGCCG
TTGAACGTTTCTCAGCTTCAGGTCTCGTAGTCCTAGAGAGAAATTTCTCGATGTTTACC
CTTGGGCCCGATGGGAACCAAGCAGTTACCGCGGCTTGAAATGAATGCCCTCGTAG
ACATCGCGAAGGCCGAAATGAAGGCGGGCACTACGGCGCGCCCAAGCCGATGACTGAGA
GTGAACTCATTTCTCCTCATGGATACAAACGGCATTGGCACAGACGCCACCATTGCGGAGC
ACATAGACAAGATCCAAGTACGTAATTACGTTAGGAGCGAGAAAGTAGGCAAGGAAACCT
ACTTACAACCCACGACCCTGGGTGTCTCACTAGTGCACGGCTTCGAGGCCATCGGCCTCG
AAGACTCCTTTGCAAAGCCCTTCCAGCGCAGAGAAATGGAGCAAGACCTCAAGAAAATCT
GCGAAGGTCATGCCTCCAAGACTGATGTTGTAAAGGACATAGTCGAGAAGTATAGGAAGT
ACTGGCACAAGACGAATGCCTGCAAGAATACTCTCTTGCAAGTTTATGACCGTGTCAAGG
CATCCATGTAA

YLR234W, 656 aa (SEQ ID NO 188)

MKVLCAEKNLSIAKAVSQILGGGRSTSRDSGYMYVKNYDFMFSGFPFARNGANCEVTMTS
VAGHLTGIDFSHDSHWGKCAIQELFDAPLNEIMNNNQKKIASNIKREARNADYLMIWTD
CDREGEYIGWEIWQEAQRGNRLIQNDQVYRAVFSHLERQHILNAARNPSRLDMKSVHVG
TRIEIDLRAVTFTRLLTETLRNKLNRQATMTKDGAKHRGGNKNDQVVSYGTCQFPTLG
FVVDREFIRNFVPEEFWYIQLVVENKDNGGTTTFQWDRGHLFDRLSVLTFYETCIETAG
NVAQVVDLKSPTTKYRPLPLTTVELQKNCARYLRLNAKQSLDAAEKLYQKGFISYPRTE
TDTFPHAMDLKSLVEKQAQLDQLAAGGRTAWASYAASLLQPENTSNNNKFKFPRSGSHDD
KAHPPIHPIVSLGPEANVSPVERRVYEVVARHFLACCESEDAKGQSMTLVLDWAVERFSAS
GLVVLERNFLDVYPWARWETTKQLPRLEMNALVDIAKAEMKAGTTAPPKPMTSESELILLM
DTNGIGTDATIAEHIDKIQVRNYVRSEKVGKETYLQPTTLGVSLVHGFEAIGLEDSFAKP
FORREMEQDLKKICEGHASKTDVVKDIVEKYRKYWHKTNACKNTLLQVYDRVKASM

YLR238W, 1937 bp, CDS: 501-1937 (SEQ ID NO 189)

CTTCGTTACACTTAATATTAAATAACAGCTCTTTCCTAATAATAACATATACACTAGAT
ATATAATACCAAATAAATTAATAAAAAAAGAAAAACAAAAATAACGTAGCTTTGTTACAG
TCGTAAAAAAGAACAATAAACCAATCTTATTGCCAGCGTCTAACTAGTCCTATTATAT
TCCAATATATTAAAGGGGTAAGGACTACTATTATTCGCCCTGAATTGAAATCTTTTAGAAA
GCACCTGTTCTCTCTCTGGTGTCTTTTTTTCTCATCTATTATCTAATTTCTTCAACCTT
CGTTATTTGTTGTTATTCCGTAATCGTGGTGCTCAACTTTTGAAATTTCACTTGTTTACC
ATAACGGAACATAATTAATAATTTGTTCTTGAAAGTCACAAGCACTACGTGAACACAAAA
TTAAGGCAAGAGTGACAAAGTAACCCTCACAAGGAGCCTGTCGTTGGTTATATTGGAAGC

TATAGATATAATCGAATCCAATGACTGGTCCTGGACCTGAAATAAATAAGGAGGAGCACC
CCAGTTCTCCGGGCAAGAAACAGATAACATATAATAGTATACCCAAGAATGCAAATCTAA
TTGATGGATCTACGAATTCATCGAAGAGGCCAATTGAAAAGTATGACAAGAGAATAGCCG
ACCCAACAAAAAGCTATTTTCCACATAGCATATCAAGAACACCAAGGAGAAAATATACTT
ACATTCTAGTCCTCACATCACTAAATGGAACCTTTGAGAGCAAACATGTGGTGATACCAT
TTAAACCAGATGGTTTGAAATTGGGAAGGCCTGTTGCTAATAGTAATAGCAGCTCCAGTT
CATCGCTCAGGGGCGGTAAAAGAGTGGATTACACACTTTTTCCCAAGTAAGGTCCGATA
ATGGTAATTTTCGATTCAAGAGTACTCTCCAGGAATCATGCATTGTTAAGTTGCGACCCGC
TCACGGGTAAGGTATATATACGAGACTTAAAATCCAGTAATGGTACGTTTATTAACGGTC
AAAGAATTGGCTCAAATGACGTAGAAATCAAAGTTGGCGATGTGATAGACTTGGAACAG
ATATAGATACGAAAATTGAGCATCGAAAAATAAGTGCCACAGTTGAAGAACTATTTGTAC
AACCTTTATTAGAATCACCGATTTTGAAGATAAGTAGTGATGATTGCCATACAATTA
CAGAAAAAGAGGAGGCTGCTGCCATAACAAGTCACATATATGGTGATTCCAACAACCTAG
AATTGGAAGAAGTTATCCTGGGCTCTGATACAGAAATACTGAGTGGAATTTTATTAATA
ATTGTATTGGTACGAGCCCGACTTTATCTAATATCATCAAAACCCTGGCAATGGAAATTC
CATTTTCCAAATGCGATAATTTAAATTACAGTCGATGGAGAATTTCTTAATTAATTATA
CGACACATCTAGAATACACGAACAACTTTTAGTGGAAGAAAATGATCAGCAACTGGTAA
AGCTGCAAAATGGATTAAGAAGGAACTGTCTGGGGAAATACGAAAAGATTATCGAACAAA
ACAGAAATCAAGTAAAACAGTTGGAAAGGGACCATATGTTTTTCAAAAAGTCATTTGAAG
TGAAGAAAAGAAGAAATAATGAAAAGCAAAAAGCATGGAAAGGGAAATAGAAGACTTGA
AACTAGGTTAGAAGTGGAAACGATATAAGAATTCACAAATGATGAAGAAGAACAACAGA
AAGAACAAGAACTCTCAACTGCATCTAAAAAAAAGACTACCGAACATGACACTAGAGGCG
TCCCGGGCATGAATCCTAAGGGTACTGACAAATTTAGCATCAAGAACACGCTATGTAATC
ATTTACACTATTAACATTTGGAACATTTCCATCGGGATTATAGCTATTGTCTTCAAGA
TCCTTTCCCCCAACTAG

YLR238W, 478 aa (SEQ ID NO 190)

MTGPGPEINKEEHPSSPGKKQITYNSIPKNANLIDGSTNSSKRPIEKYDKRIADPTKSYF
PHSISRTPRRKYTYILVLTSLNGTFESKHVVIPEKPDGLKLGRPVANSNSSSSSLRGGK
RVDSTFSQVRSDNGNFDNRVLSRNHALLSCDPLTGKVIYIRDLKSSNGTFINGQRIGSND
VEIKVGDVIDLGTIDTKIEHRKISATVEELFVQPLLESPIFENEDSDDCHTITEKEEAA
AITSHIYGDSNNLEEVILGSDTEILSGIFINNCIGTSPTLSNIIKTLAMEIPFSKCDN
FKLQSMENFLINYTTTHLEYTNKLLVEKNDQQLVKLQNLRRKLSGKYEKIIEQNRNQVKQ
LERDHMFVKKSFEVKKRRNNEKQKSMEREIEDLKTRLEVERYKNSQMMKKNKQKEQELST
ASKKKTTEHDTRGVPGMNPKGTDKFSIKNTLCNHFTLLTFGTISIGIIAIVFKILSPN

YLR241W, 2849 bp, CDS: 501-2849 (SEQ ID NO 191)

CGAACATACCTGATATCAGAATAGATCCCAATGGTGCTATATTACGTGTAAGAGAGAGAT
TTAATTTGAATATGTCCGAAGAAGATGCCACAGTGCAATTTTCAGAATCTAATCAATGATA
GTGTAAATGCTTTGCTGCCTATCGTGATTGATCATTTACATAATCTGGCACAATACTGGC
GGACCTGATTGGTTGATAATTGGTGCTTCAAATTTAAATTTTCGTCACTCTAATTATACT
TAACATATAAATGGTACCTTCAATATATCTTCTTAGTAAAAAGTAGCATGATTTTGTGTT
AATTTGCACTTTTTTTTATTTAAAAATAAAAATCACAGTTAATTTTTCATGATCTTGCAA
GACACGCCTCCCCCTAATGTGGCATATATAACAATTGTGAATCAGAAAACTCAACACTT
TAACATAATGGCGGGCACGAAGGCTAAACAAACAAGATTAGCATTGAATGCCTTTTTTGG
GTACAATAGAACAGTACTGAATGACATCATATATCGAAAGGCTCAAGTCGGCAGCATCGT
ATCTTGATACAGTTCCAGATGAGCATCATGATTTTCAGAAAACCCACCGCCAAGGTTGTAA
CGACGCAACTGACTATTGCTACTTCACTAGGTATTTTTTGCTTTGCTTTTCGTTCTCAATTC
TACTAAAAAAGTGGCCTAGATTATACGCAAGCAGACGATATAAAGATGACGGGAACCTTC
GCTTACCGTCTTGAATCAGTCAAGTTTATTCGGCTGGTTAACAGTGTTGTATAAGATAC
GGGACGAACAGATTCTGGAATATGCAGGTTTAGATGCGTATGTGTTTTTGAGTTTTTTCA
AAATGTGCATCAAATTACTTTCTATTTTTTGTCTTCTCTGTGTGCGTTATATCTCCAG
TAAGATATCATTTTACTGGAAAAATTGATGACGGCAACGATGATGATGACAGTGAAAGTT
CTTTAATACATCTGGTAAAAAGAATTGTGGAGGGAAGTGGCGATGGTGACAATCATTCAG
CTCCCGAACGTACAAATGTGTACCTCTGGATGTATGTTCTCTTCACATATTTCTTCACCT
TCATAGCAATTAAATGGCAGTTGCGGAAACAAAGCACGTCGTAAGTACTAGGCAAGCTT
ATCTTGGGAAGCAAAATACGATTACTGATAGAACGATAAGGCTCTCAGGCATCCCGATAG
AGCTTCGTGATTTCGGAAGCCTTAAAGACCAGAATTGAACAATTAAAAATCGGCACCGTTT
CATCAATCACTATTTGTGCGAGAGTGGGGTCTTTGAACAAGCTATTTTATTGTTCGGAAGA
AAATACTCAAAAACCTGGAATTAAATATTTCAAGATGTCCAAGGGAGCTCCGTACTCGAC

AACCATATTTCGGAGAACTATCATTTATTGGGAAACGAGCAATCAGGCGCAGTTACACATG
GAGAAAATGTTCCATCAAGCAATAATAATGACGAGGATACTATACTATATTCTCAAATTT
CTCTTGGAGAGAGACCAAAAATGAAAATTGGATATCGTGGTATCTTTGGGAAGGAAGTAG
ATGCCATAGAGTACCTGGAGCAGCAATTAAAATTTATTGATGCTGAAATTATTGAAGCGA
GGAAACAACACTACTCCGCAACACCTACGGCATTCGTTACGATGGATTCTGTTGCTAATG
CGCAAATGGCAGCTCAGGCGGTATTAGATCCTAGAGTACATTACTTCATAACCAGATTGG
CTCCTGCACCTCACGATATCAAGTGGGATCATGTTTGTCTTTCTAGAAAGGACCGGTAA
CAAAAGTTTATTCTACTACCGTATTTATAGGCCCTTTCAAGTTTGTTTTATGTCATTCTTG
TATCATACTTAGCCACATTGCTAAATTTGAAAACACTTTTCGAAATTCTGGCCAAGCGTAG
GGCAGCTACTAAAAGATCACCAGTGGGCGCTAACATTGTAACGGGGCTATTACCAACCT
ATCTCTTCACATTGCTTAACTTTGGAATCCCTATTTTACGAGTATTGACTTCTTATC
AAGGATTGGTATCATAACAGCGAAGAGGAAATCTCACTTGTTCAAAAAATTTCTTTTATA
TTTTTGTCAACCTTTTCTTAGTTTTACATTGGCAGGTACAGCATCTAATTACTGGGCGT
ACCTCAGCGATACCACCAAATTGCTTATCAACTTGCTACATCTGTGAAGGAGTTCTCCT
TATTCTATGTCGATTTGATTATATTGCAAGGTATTGGTATGTTCCCGTTTAAGTTGTTAT
TAGTTGGTAGTTTGATCGGCTTTCCTCTAGTGAAAATCAAGGCTAAGACACCTAGGCAAC
GGAATGAACTTTACAATCCACCGATATTTAACTTTGGACTACAATTACCACAGCCAATTC
TGATTTTGATTATAACGTTGATCTACAGTGAATGAGCACGAAAATTTGACTTCAGGGC
TGGCGTACTTTATTATTGGGTTTTACGTCTATAAATATCAATTGATTTTGGCCACAGATC
ATTTGCCCCATTCTACAGGAAAAGTATGGCCATTAATTTTGAAGAATCATCGTTGGAT
TGCTATTGTTTCAATTAACAATGACAGGAACACTGGCAGGATTCGAAGGAGGATGGGTTT
TGTCATCTTGCCTTTTCCCGCTTCCAGTAGTGACATTATGTTTCTATATGATTTTCGAGA
AGAATATTTGCCGTTGTCAAAATATATCGCATTGAGTTCAATTCCGAGTACGAAAGAG
ACAATTCTACGGTGAATTCTGCCAATGAGGAAGAGTCGTATGCATACCCTTACGCTGTGA
GTGAATTAGAGGGTCCGATGTTGGATTGA

YLR241W, 782 aa (SEQ ID NO 192)

MTSYIERLKSAAASYLDTVPDEHDFRKP TAKVVTQ LTIATSLGIFALLSFSILLKKWPR
LYASRRYKDDGNLRLPSWNQSSLFGLTVLYKIRDEQILEYAGLDAYVFLSFFKMCIKLL
SIFCFFSVCVISPVRYHFTGKIDDDDDSESSLHLVKRIVEGSGDGDNHSAPERTNV
YLWMYVLFYFFTFIAIKMAVAETKHVVSTRQAYLGKQNTITDRTIRLSGPIELRDSEA
LKTRIEQLKIGTVSSITICREWGPLNKLHCRKKILKNLELKYSECPRELRTROPYSENY
HLLGNEQSGAVTHGENVPSSNNNDEDTILYSQISLGERPKMKIGYRGIFGKEVDAIEYLE
QQLKFIDAEIIEARKQHYSATPTAFVTMDSVANAQMAAQAVALDPRVHYFITRLAPAPHDI
KWDHVCLSRKDRLTKVYSTTVFIGLSSLFLVIPVSYLATLLNLKTL SKFWPSVGQLLKD
QWAANIIVTGLLPTYLFTLLNFGIPYFYEYLT SYQGLVSYSEEEISLVSKNFFYIFVNLFL
VFTLAGTASNYWAYLSDTTKIAYQLATSVKEFSLFYVDLIILQIGMFPFKLLLVGSLIG
FPLVKIKAKTPRQRNELYNPPIFNFGQLQPILILIITLIYSVMSTKILTSGLAYFIIG
FYVYKYLIFATDHLPHSTGKVWPLIFRRIIVGLLLFQLTMTGTLAGFEGGWVLSCLFP
LPVVTLCLFLYDFEKNYLPLSKYIALSSIREYERD NSTVNSANEEESYAYPYAVSELEGPM
LD

YLR321C, 1781 bp, CDS: 501-1781 (SEQ ID NO 193)

TTCAAGTGCACCTCTTTGTAAGGAAGATTACAAGTCTCCAGTGGTCACAACTGTGGCCAT
TATTTTGTGGATCGTGTTTTGCCAAAGATATGAAAAGGGCACCAAATGCTTTATATGC
CACAAGGAGACCCACGGCAGTGCAAAAGTAGCATCTGACTTACAGAAGATGCTAAATAAA
AGGAAAAGTTGATGGAGAATGCCATATCACCCCAAAAATTACACGCACCCGATGCTAATG
TACAGGAATTATAGAGCACATGACCCATAGATTTATCGAGCATTGTTGCAATTTGAAAG
ACTCTTTCACATAATAAAGTATGTAACTATATAGATAGAAGATGTCCCGTGTCTTTTG
TCTACTAAATGATGATCTGCTCATTTAAAGTCGCCGCGACTACTTTGACAAAAA
ACTTAGAAAAACGACAAATAGAGATTATTGAATGAAGTACATTGAAAAAAGAAAGA
AAGGCACATAGCAGCACACAATGTCGCACCAAAACCAGCTTATTCCACAAGCTTATATTT
CTAACTTTCATAACAGATTGACAAACGAAGATGATGGTATCCCCATCTTTACAATGGCTC
AACAAACAAGGCAGCATAAAAGGGCTAAAGTGGTCAACTATGCGGAATATGACAACGATC
TCTTTGATGAATTCAATATGAACGGTTCTAATTTCAACAATGCTGATACACACTATAAAG
ATAATGCAGTGTCTCATGAAAATACTCCGGCACTTACAAATGGTGTACCATGGACGGTT
CCGAATACAATGTCCTAGAGAACATGAATGGAGCTGATAGTATTATCTCTAACAACAAAT
ACGATGCGGGTTCAAACATGGTTGTGGAATCTTTATCCGGTTTGAATAGCAATAACAACG
CCAGCAATGGTCCGAGCAACAAAGCGCAGGCACAGGATATTGGAAACGCCGTTCTACCGG
ATCTGCAAGACCAACACCACAACCCCTTCAACATATTGAGATACCCTAAAATAAGAGATA

CTTTCATTAAACGGAAAAGTGGTGTCTCCATATAGACTCAACACTGATCAAGAAACGAAGG
CAAACGCCAATTCTGGAGAGGCAATCATGATACCAATTACTTTGGATATAGAACATATGG
GTCATACCATAAAAGACCAGTTTCTCTGGAACATAATGACGACTCCATATCTCCGGAGG
AATTTGCCTCTATATACTGTAAAGATCTTGATATGACTTCCGCTACCTTACAACTCAAA
TTGCGAATATAATAAAAGAGCAGTTGAAAGACCTCGAAAATATTGCAGCCACTGAGATAA
TGTCTGACCTCCACGTGATAATCAACCTAACCTGCAACTTACAAGACAGATTTTGTGAAG
ATAACTTCCAGTGGAACCTTGAACGACAAATCACTTACTCCAGAAAGATTTGCTACATCCA
TTGTACAGGACCTTGGCTTAACAAGAGAGTTTATCCCTTAATATCTCAATCGCTTCATG
AAACTATCTTGAAGATAAAGAAGGACTGGGTAGATGGCCACTTGATTGAGGACCATGTCC
CAAACGATGCCGCATTTGGGTACTTATCTGGTATAAGGCTGGATATTGATGAACTGGGCT
CCAATTGGTGCCCAAGGGTGGAAATATTAACAAAAGAAGAAATACAAAAGAGAGAAATTG
AAAAAGAAAGAACTTAAGAAGATTGAAAAGAGAACTGATAGATTATCTAGAAGGGGCA
GGAGAAGATTAGATGACTTAGAAACCACAATGAGAATGTAG

YLR321C, 426 aa (SEQ ID NO 194)

MSHQQLIPQAYISNFHNRLTNEDDGIPIFTMAQQTRQHKRAKVVNYAEYDNDLFDEFNM
NGSNFNADTHYKDNAVSHENTPALTNGVTMDGSEYNVLENMNGADSIISNNKYDAGSNM
VVESLSGLNSNNNASNGPSNKAQAQDIGNAVLPDLQDQHNPFNILRYPKIRDTFINGKV
VSPYRLNTDQETKANANSGEAIMIPITLDIEHMGHTIKDQFLWNYNDDSI SPEEFASIYC
KDLDMTSATLQTQIANIIKEQLKDLENIAATEIMSDLHVIINLTCNLQDRFFEDNFQWNL
NDKSLTPERFATSIVQDLGLTREFIPLISQSLHETILKIKDWDGHLIQDHPNDAAF
YLSGIRLDIDELGSNWCPRVEILTKEEIQKREIEKERNLRLKRETDRLSRRGRRRLDDL
ETMTRM

YLR322W, 815 bp, CDS: 501-815 (SEQ ID NO 195)

GTCATATCAAGATCTTTACAGTATATAGAGGCAAATTCCTCCGGAGATATGGAGTCGTCA
TTGTAGTTCAGAGAACTGGTCTTTTATGGTATGACCCATATGTTCTATATCCAAAGTA
ATTGGTATCATGATTGCCTCTCCAGAATTGGCGTTTGCCTTCGTTTCTTGATCAGTGTTG
AGTCTATATGGAGACACCACTTTTCCGTTAATGAAAGTATCTCTTATTTTAGGGTATCTC
AATATGTTGAAGGGGTGTGGTGTGGTCTTGCAGATCCGGTAGAACGGCGTTTCCAATA
TCCTGTGCCTGCGCTTTGTTGCTCGGACCATTGCTGGCGTTGTTATTGCTATTCAAACCG
GATAAAGATTCCACAACCATGTTTGAACCCGCATCGTATTTGTTGTTAGAGATAATACTA
TCAGCTCCATTCATGTTCTCTAGGACATTGTATTCCGAACCGTCCATGGTAACACCATTT
GTAAGTGCCGGAGTATTTTCATGAGACACTGCATTATCTTTATAGTGTGTATCAGCATTG
TTGAAATTAGAACCGTTCATATTGAATTCATCAAAGAGATCGTTGTCATATTCGCGATAG
TTGACCACTTTAGCCCTTTTATGCTGCCTTGTGTTGTTGAGCCATTGTAAAGATGGGGATA
CCATCATCTTCGTTTGTCAATCTGTTATGAAAGTTAGAAATATAAGCTTGTGGAATAAGC
TGGTTTTGGTGCGACATTGTGTGCTGCTATGTGCCTTTCTTCTTTTCAATGTAC
TTCATTCAATAATCTCTATTTGTCGTATTTCTAA

YLR322W, 104 aa (SEQ ID NO 196)

MRHCIIFIVCISIVEIRTVHIEFIKEIVVIFRIVDHFSPFMLPCLLSHCKDGDIIIFVCQ
SVMKVRNISLWNKLVLVRHCVLLCAFLLSFFNVLSHSIISICRIF

YLR325C, 737 bp, CDS: 501-737 (SEQ ID NO 197)

CCACATGTCACAACACTACTTTGTGAAGTTGCAATGCGTGATTAGTATTATAAAACATCATA
GCCTTGCCAAATAAACTCGCTTCCCAGAAAAGACGCCAAATTAAGTCCGCTGTTATGTG
ACAAAACAGGGCATCTCACATATTCGCGTACTGGTGTCTTTTAGCTCATTCCGATATTA
TTCCAAGACGGAATTTTCATCTAGAGAAAATGCATCCGTGCATTTTCATAAACCACACA
ATTAAATGCCTTGCGAAAAGGAGGACTCGTCCGTGCAACTGTTGAAAAAATAGACGGA
GCATCATACGTTTCGAGTGGAATTTATGGAGAGTTTCCAAGCTCTATGGCATGTAGAGT
CGTGATTGCTGCTGTACGCTTTTGCACAATATTGAATCTTCAATCTAAAGAATTAAATTT
TCTAATTTCAATGTAGAAATATTTCAACTGTTAGTTTATTTCAGGTGGAATATAGTA
CGACAAAATATCAAGGAAAATGGCTAGAGAAATCACCGACATCAAACAATTTTGGGAAT
TGACCAGAAGAGCTGACGTTAAGACCGCCACTGTTAAGATTAACAAAAAATTGAACAAGG
CCGGTAAGCCATTCAGACAAACCAAGTTCAAGGTTAGAGGCTCTTCTTCTTTGTACACTT
TGGTTATCAACGATGCTGGTAAGGCTAAGAAATTGATCCAATCTTTGCCACCAACTTTGA
AGGTTAACAGATTATAA

YLR325C, 78 aa (SEQ ID NO 198)

MAREITDIKQFLELTRRADVKTATVKINKKLNKAGKPFRTKFKVRGSSSLYTLVINDAG
KAKKLIQSLPPTLKVNRL

YLR344W, 1331 bp, exon1: 501-519, intron1: 520-966, exon2:
967-1331 (SEQ ID NO 199)

TAAGGGCTGTCAATTTTTCATTTCCCTCAAAGTTAATGCGCAAGAGTTAGGATGATCTTG
ATTATTAGTTATTTGTTTGTTCATCAATTATGCCGACGTCCATGAATGCTATTGAAGTA
TCGATTACTTATGCTATTCTATTGTATTTGAGCCGGCGGCTAGTAAACAAGACAGCATAC
CTTTCCAACATCCGTACATATTGATTATTGTATCTATGATTTTCATGTAATGTATGGGTT
AACTAATCCTTTCTCTTCTTTTCTTCTGAAAATCAGTAGCTAGAGGAACCTGTTTC
GTGAAAGATATGGAATATTCGCTCTAGGGAAGAGCCGAGAGCTGAGAGCAGTATCCATCG
GATGGAATCTTGCCTGGATGCGTAACGACGACAGCTTGTCTAGAAGGCGAAGTACAAGAT
ACTAAGAAGACTATAACAACAGAAGACAATTTTGTAGTGCGATTCTATATTATTGACGTA
ACCAACAAAAAAGTATCAGAATGGCTAAACAATCATTAGGTATGTGCACAAATGCTAAAT
CACTGAAACCCTGTAGAGCTGGAATTGAAAATATAGTTTGTACCTTTTGCCTGAGGGCAG
AATGACTCAATGTTATCTTAATTCGATTAGAAAAAGAAGGTGCGTTATCCAAGGTTGAAA
CTTGTAAGTATTTAGGTGATGTCTCATAACTGCAACCACTGGAAAATGACGCAAATATC
AAAATAATAGGGAGATAAAGTCTCACGACATGAAAAAATCATAGAATTATTGTTCAATTT
ATCTAGCCGTATCTTACCTTATGGAAAAAGTGTGAATATGTTTTTCTAAATCGAGCTTCC
CGGAAATTACACTATATTATGCATCCGTGATACATCTGAAATTCAATACTTTCTCCAAGG
TCCTGCTTACTAAGAGGGTAAGATTTGTTGAAACTCGAAATACTAACATTATTTTCATTA
TTTTAGACGTTTCTCCGACAGAAGAAAGGCTAGAAAGGCTTATTTACCGCCCCATCCT
CCCAACGTCGTGTTTGTCTATCTGCTCCATTATCTAAGGAGTTGAGAGCTCAATACGGTA
TCAAGGCCTTGCCAATCAGAAGAGATGATGAAGTTTGGTTGTTCTGTTTCCAAGAAGG
GTCAAGAAGGTAAGATTTTCTGTTTACAGATTGAAATTTGCCGTTCAAGTTGACAAGG
TTACCAAGGAAAAGGTCAACGGTGCTTCCGTTCCAATTAACCTTGCACCCATCCAAGCTTG
TCATTACTAAATTACATTTGGACAAGGACAGAAAAGCTTTGATCCAAAGAAAGGGCGGTA
AGTTGGAATAA

YLR344W, 127 aa (SEQ ID NO 200)

MAKQSLDVSSDRRKARKAYFTAPSSQRRVLLSAPLSKELRAQYGIKALPIRRDDEVLVVR
GSKKGQEGKISSVYRLKFAVQVDKVTKEKVNGASVPINLHPSKLVITKLHLDKDRKALIQ
RKGGKLE

YLR367W, 1376 bp, exon1: 501-633 intron1: 634-1116, exon2:
1117-1376 (SEQ ID NO 201)

ACTTTTTGTCTGCTGCTGGTCTGTTTGTCTTTTAAAATTGCGCTAGACAAGTAAAC
AGGGATTGCTTAAGAATCAAAGTAGCTTAACTCTAAAGTATTATTTTCTCAGTTGTGGG
CCCATGTGTTGGAGGGAAGGAATATATTGAAATGTAAATGTTCTTAAGTTCCGTTGAACT
TGGATATTGTTACAAGAGTTCTAGTCTTTGATACCATTTTACGCAATTACAACCGCATT
ATTTACCTTTTCATCTTCAGTTTACGGTTCAGTTTATTCTGTTACGAAAGAACTATGGT
GATTCAAAGGCGAAGTGCGTAGGATTGTAACCTCTATATCTTTAGGATACTTACAATTTT
GTACTGTTTTCAAGACCACTGTAACCGATAATAAACCGGAGGACACATTTTAACCCACTA
TTTTTTTTCAGAAGATCAGATGCGAGAGCTCGAAGCATAAGTATAATACTAACGTTTCAAA
ACATAGTAATTAGGTAAAAAATGACTCGCTCTTCCGTTTTAGCTGATGCTTTGAATGCCA
TTAATAACGCCGAAAAGACCGGTAAACGTCAGGTTCTATTGAGACCTTCTTCCAAGGTTA
TCATCAAGTTTTTACAAGTTATGCAAAAGCATGGTATGTTCCAACCTATTTTCAATATTT
TCACATGTGTTTCAATTTCTGCTTATTTTTTAAATGTTACCACGAGGTTTGTCCAAGTTCA
ATGTTGCGCAACTCTAACGAAGAAATAATTATTGCCATTGTTTTTTACTCCGGGCTGATA
ACTAGATGGTGTGATCGGGCAGTATACTAATTTATACTGGACAAAGACTCGTAAAAGATG
TTCTTTGTGCTTAGTCCCATACTGTTTTTTAAGTGTCCGGGATATTTAATCCCATGTGGA
AATGCTTCTTACACGGTTATGGATTACACCTCATGTGTAGCTACTATATCCATTACCGTT
TACTTTTCTCAAATCTCACTCTTAAATTTTCAATGGCAAAATTTCTCCGCACAACCTT
AGACAACATTTTCTTGTTTTTTATGAAGTAAGCAAAATTTTCAATCAACAACGCTCCAT
GAGATTCTTCAATACTAACATTTACTCCTTATTTAGGTTACATTGGCGAATTCGAATACA
TTGACGACCACAGATCTGGTAAGATTGTCGTCCAACCTGAACGGTAGATTGAACAAATGTG
GTGTTATTTCCCCAAGATTTAACGTTAAGATTGGTGACATTGAAAAATGGACCGCAACT
TATTGCCAGCCAGACAATTCGGTTACGTTATTTTGACTACTTCTGCGGGTATTATGGACC
ATGAGGAAGCTAGAAGAAAGCACGTTTCCGGTAAATCTTGGGTTTTGTCTATTAA

YLR367W, 130 aa (SEQ ID NO 202)

MTRSSVLADALNAINNAEKTGKRQVLLRPSSKVIIKFLQVMQKHGYIGEFYIDDHRSBK
IVVQLNGRLNKCGLVISPRFNVKIGDIEKWTANLLPARQFGYVILTSAGIMDHEEARRH
VSGKILGFVY

YLR393W, 1340 bp, CDS: 501-1340 (SEQ ID NO 203)

CCCTCAACCCGCATTTTGCTGAGAATTTTCACCAAGGCCCTAGGTGATATTAGATTCCAC
CTGACTAATTGCATTACAGCCGACCCAAGGCAATATCAGTTTAATAAAATATCATGTATC
TCACCCTCTTCTTGGTATTAGTAAAGAGACGCCTGATCTTGTAACAGTGGTGAAGATTGT
ACTAGAGCAGAATCAAGAATTTAAAAAGTGTAAGGCAAGGCAGAGGCGATGTACATAAA
ACTTCGAAGTAAGAAATATTTAATAGTTCTCGCCACATCACTATGCAGCTATATAAAAC
TACTATAAACGTTTGTGTTTGTTCCTTACGCACAATATCCTTGCTAGAAATCGTTTGTGA
AATTTAAATTTTATTACCATTTATTTGATTGCGCTTCAGAAAAATATGGAAGAGTGCAT
ATTTAAAAAGGACTATTTTACGATATAGTAAAGTCAGGTTATTTGTTTATTTGCGATAT
CAGAGTAACTTAACTAACTATGCAGGGCACTTTTAAAAGGTTTACCATCCCACGCTTA
CGCGGATGTCCTTCTTGATAAATTCCTCAAGCCTATGATGGCAACGGCTTCCCCAAAGG
AATACCAGATCAACAACCTGGTCAAGCCAATAGGCTTAACACAAGCACCAGGAAAAGCA
CCAAATACTCCCAGGGGAACCTCTTGAGGGATATGTTTGATTGCGAAAAGACAAACCACA
GAGTTAAAGAGTTGGCCGTTGAATTCAGCAAATCTGGACTTTATGACGTGCAAGTCTTCC
AAAAGACAAAGGGGAAATGTTTATAGCTCCAGTTTCATATTGGAAAGAAGATAAAGCTT
TGTTTTTCTCTCATTTGATAGGAACGGCAATGGATGGTACGAAACAACAGAATATCGAGG
ATATGTTAAGGGGTAAACAGTATAGTGAGGTTATTTAGTACAGCATCTGGCGATAAGT
TGAGTAGTTCATACTTCCAAGGAATCGTAGACGATAACAAAAAACTGACTACTTGACTG
AAGCTGATGCGCGTTTAAAGTTTAAATGACAGTAACGTCCAAATCATCGAGGTCAATCTTG
TAGAAAACGCTGTGAAAAGTGCTCTAGTGAAAACGCTTGCTCGTTGGGCCAATCGCGTTC
CATCCTGGCGCCAGCCATTTTATTTTGAATGTTCTAGAGGCCAATGGCCATTTTCCGTCA
GGGAAGAGCTCTTTTGCAATAATGTCTTTTCTGGATACGTCTTTCTTGTGGACCAGCAGT
TAAAAATTAGGTGGGCAGCTTGCAGGGGAGGCTACTCCATCTGAAAAGGAAGCATTTGTGGA
AGTTTGCCAAACGTCTGTGA

YLR393W, 279 aa (SEQ ID NO 204)

MQGTFKRFYHPTLTRMSFLDKFLKPMMATASPKYQIKQLVKPIGLTQAPRKSTKYSQGN
SLRDMFDSEKTNHRVKELAVEFSKSGLYDVQVFQKTKGKLFIAVPSYWKEDKALFFPHLI
GTAMDGTKQONIEDMLRGKTSIVRLFSTASGDKLSSSYFQIVDDNKKTLDYLTADARLS
LNDSNVQIIIEVNLVENAVKSALVKTLARWANRVPSWRQPFYFEC SRGQWPF SVREELFCN
NVFSGYVFLVDQQLKIRWAACGEATPSEKEALWKFAKRL

YLR423C, 1754 bp, CDS: 501-1754 (SEQ ID NO 205)

TTCTATTGGTGTAGTTATACCAGAACCATCCTTCCCAAGGCCTTTTCCCGCAACATATCC
CATACTCGAAAGTAACTTCGCACCAATACCATATGTCTTCGTTAATTTTGAGATCGTTGG
GGCATTGCCGCTACTAGTTTCAAGGCATCATTAGTGTATGTCATGTCACCTATTCATGCT
TGAATTATTATCTTCTCATCGCTATAATTATAGGAATCGATTCTTCTTTTTTTTGAAAAA
GAACTTTTTATCTGTGTTGGAGTCCGAATCCTCCATGTTTTGGCGTACTGAAGGCTTAAG
TTCTTCGACCTCTCTCGGTTGTACTATTTGCAAATTTTGGAATTTTGTATTGTTTTGAC
ATAATGTAAATACTAGATGCGCGCTCTAAGGCCTCAGTATTAAAAATTGCAAGATATCCC
TAACTTGATAATTATTTGAAAGTCGCATAACGTACGATAAATTCGATACTGCGAGGATAT
TATCAACGTATTTAACACCTATGAACGAAGCAGATGTTACAAAATTTGTTAATAATGCCA
GGAAAACGCTGACCGATGCTCAACTTTTATGTTCAAGTGCTAATTTAAGGATTGTAGATA
TTAAGAAAAAATTGTCATCTTGGCAGTTGAGTATTTCAAACTCAATTTTCTAATAGTTG
GCTTGAGACAGCAAGGAAAGTTTCTTTACACTATTTTAAAGGAAGGCATTGGGACAAAGC
TAATCCAGAAACAATGGAATCAAGCTGTCTTAGTGGTCTTAGTTGATGAGATGAAGTACT
GGCAATATGAAATCACTTCTAAAGTACAAAGGTTGGATGGTATAGTAAATGAATTGAGCA
TATCAGAAAAAGATGATACCGATCCCTCTAACTAGGAGATTACATCTCGAGAGACAACG
TTAACTTATTGAATGACAACTGAAAGAAGTGCCAGTAATTGAGCGTCAAATTGAAAACA
TTAAGCTTCAATACGAAAATATGGTCAGAAAAGTTAACAAAGAACTGATTGATACCAAGT
TGACGGACGTAACCTCAAAAATTCCAAAGTAAATTTGGTATAGATAACCTGATGGAAACAA
ATGTTGCAGAGCAGTTTAGCAGGGAACCTAACGGACCTTGAAAAGATTAGCAGAGATAA
TGAATTCATTGACACAGCACTTTGATAAGACATTGCTGTTACAAGATAAAAAAATTGATA
ACGATGAACGTGAGGAGCTGTTTAAAGGTGGTACAAGGCGACGACAAAGAACTATACAACA
TTTTCAAACTCTGCATGAGGTAATTGATGACGTGGACAAACAATTCCTTAACTTGGGTC

AATTTTTCAGGCCAAAAATAAAGGAAAAGACAGAACTACACAGCGAAGTTTCTGAAATAA
TAAACGATTTCAATAGAAATTTGGAATATCTATTAATCTTTAAAGATATTTCCAATCTGA
TTGATAGCTTCAAAAATTCCTGTACACAAGATATTCAAACAACCTAAGGAACTTTGTGAAT
TTTATGATAATTTTGAAGAAAGCTACGGTAACCTTAGTTCTAGAAGCAAAGAGGAGAAAGG
ATGTGGCAAACAGAATGAAAACCTATATTGAAAGATTGTGAAAAGCAGTTGCAGAATTTAG
ATGCTCAGGACCAGGAAGAACGTCAGAATTTTATAGCGGAAAATGGAACCTATCTTCCTG
AGACAATCTGGCCCGGTAAAATTGACGATTTTCTTCCCTGTACACTTTAAATTACAACG
TGAAGAATCCTTAG

YLR423C, 417 aa (SEQ ID NO 206)
MNEADVTKFVNNARKTLTDAQLLCSSANLRIVDIKKKLSSWQLSISKLNFLIVGLRQOGK
FLYTILKEGIGTKLIQKQWNQAVLVVLVDEMKYWQYEITSKVQRLDGIVNELSISEKDDT
DPSKLGDIYISRDVNLNDKLKEVPVIERQIENIKLQYENMVRKVNKELIDTKLTDVTK
FQSKFGIDNLMETNVAEQFSRELTDLKDLAEIMNSLTQHFDKTLQLQDKKIDNDEREEL
FKVVQGGDKELYNIFKTLHEVIDDVDTILNLGQFLQAKIKEKTELHSEVSEIINDFNRN
LEYLLIFKDISNLDISFKNSCTQDIQTTELCEFYDNFEESYGNLVLEAKRRKDVANRMK
TILKDCEKQLQNLDAQDQEERQNFIAENGTYLPETIWPGKIDDFSSLYTLNYNVKNP

YML026C, 1342 bp, exon1: 501-547, intron1: 548-948, exon2:
949-1342 (SEQ ID NO 207)

ATCTGTAAATAATAAGCCCATGAAATATCAATCTCACAATGAAAGAATTGTATAATTCAG
AATGATTTGACGTAAAAGCAAGTCTCATTCAAGAACTGTAAAATCCGTACACACTACTG
AATTTTACATCCATACATTTTGTGAAATTTTCATGTTTTTTTGAAAAATTGGAAAAGGGC
TAAATTATCCGTCCGGGTGTCTCCTAGCTCGGCTCAACCTAGGCAAATGCGTTTACTGG
GGCCATCCAAGCTCATCCTTCCAGAGATTTCGCTTTCAGAGGCAAAGAACTCGTCTCCGC
AGGCCTCTTGTTCGGGAGGAGGAGAATTCTTGCGCGGAAACTGGTTGATGCCTGGGCTA
TGGTAATTCTGACACCTTTGCTATCCTAACTGGAAAAGGTCCTTAGTAATAACAATATCA
GGTACTTTAACATTGTTAAAGATATACTATTAGTGAAAACCGATCTTACGAAAAGCCAA
TAGAGCAGAAAGTGGTAAAGATGTCTTTAGTTGTACAAGAACAAGGTTCTTCCAACACA
TTTTACGGTATGTTTTACGAGTACAGTGCAGATATGTTGAGAGAGTTTCACATTACATGG
GATAATAGCTTAATATTGCGATTGAAAATATGTGAGTGCCTCCGATGGAATAATAAACG
TCACGGGTACCAAATACGAGGCCGAATTAACCTCTACGCTACTATAAAAATTATCACTAG
ATTTTAAAGTAATACACAGTTTATTGAAAATACAATATATGACTCAATGCGAATTTAAA
AATTTCAGTCAATACAGCTTGACAAATTCATATTTATCGTCCCTCCATGTTTCGTACGCCA
TTCCAAAATGATGCGCCATGTTGAAAATTTCTCGAAGAACCCTAGCAGTGGTGTGAAATAA
ATTACTAACAATAAGATGTACAATTTTTTGTGCGCCCATTAACAATCAGTTTGTGTAACAC
CAATGTGATGGTAACATTAAAATTGTTTACGCTTTGACCACTATTAAAGGGTGTGGTTCG
TCGTTACTCCAACCTTGGTCTGTAAGAAGGCTGATGTTGATTTGCACAAGAGAGCTGGTGA
ATTGACCCAAGAAGAATTGGAAGAATTGTCCAAATCATGCAAACCCAACCTCATTACAA
GATCCCAGCCTGGTTCTTAAACCGTCAAACGACATTACTGATGGTAAGGACTACCACAC
TTTGGCTAACAACGTCGAATCCAAGTTGAGAGATGACTTGGAAGATTAAAGAAGATCAG
AGCCACCGTGGTATTAGACACTTCTGGGGTTTACGTGTTAGAGGTCAACACACCAAGAC
CACTGGTAGAAGAAGAGCTTAA

YML026C, 146 aa (SEQ ID NO 208)
MSLVVQEQGSFQHILRLNLTNVDGNIKIVYALTTIKGVGRRYSNLVCKKADVDLHKRAGE
LTQEELERIVQIMQNPHTHYKIPAWFLNRQNDITDGKDYHTLANNVESKLRDDLRLKKIR
AHRGIRHFWGLRVRGQHTKTTGRRRA

YML063W, 1268 bp, CDS: 501-1268 (SEQ ID NO 209)
TATATTATTTTTTCCCTTCTGGGTCTTTTCTTCTTCTTCTTGTACCTTTTTTGCTTT
TTCATAAAATAATTTCTCTAGATTTGAAGACAGCATTTTGTACATCCATACACCATAACA
CCATACACCATAGCACCAGTACACTATATTTTATGAATTTTACTAAGAATTATTCCTGC
AGGAGCTCCACTGAAAAAAAAGAGCAGCATGGATGTCCGGTAGAAGTGCTACTGAGTAA
ATGGGAAGGACGCGGTAGATCCAGTGTGGAATCAAGGTGGTGCCGGTGTGAAGCCGCCTC
GGCCGGCTGGACTCTCCAGGCCGGAGTGATGATTGCCACGCTGAACGTAACACAGTTTCA
CAATACCAGTGTCTCATTAGTGAGTTCCAATGTATAGTTAGTAGTGGTATTTTGATATA
TGTGAGTGGTAGCAGATTTGAACTTAGTTAGTTGTATTTCGCTTTGAGGAAACCAAGCAA
AAAACCGATCTAGACTAATCATGGCTGTTGGTAAGAATAAGAGACTATCCAGAGGTAAGA
AGGGTTTGAAGAAGAAGGTCGTTGACCCATTTACCAGAAAGGAATGGTTCGATATTAAAG

CCCCATCCACTTTTGAACAGAAATGTTGGTAAGACTTTAGTTAACAAGTCCACTGGTT
TGAAGAATGCTTCCGATGCTTTGAAGGGTAGAGTTGTGCGAAGTTTGTGGCTGACTTGC
AAGGTTCTGAAGACCATTCCTTTCAGAAAGGTCAAGTTGAGAGTCGATGAAGTTCAAGGTA
AGAACTTGTTGACCAACTTCCACGGTATGGACTTCACTACCGACAAATTGAGATCAATGG
TCAGAAAATGGCAAACCTTGATCGAAGCTAATGTTACCGTTAAGACTTCCGATGATTACG
TTTTGAGAATCTTTGCTATTGCCTTCACCAGAAAGCAAGCTAACCAAGTTAAGAGACACT
CTTACGCTCAATCTTCCCACATCAGAGCTATCAGAAAAGTTATTTCTGAAATCTTGACCA
GAGAAGTTCAAAACTCTACTTTGGCTCAATTGACCTCCAAATTGATTCCAGAAGTTATCA
ACAAGGAAATCGAAAATGCTACCAAGGACATCTTCCACTACAAAACATCCACGTTAGAA
AGGTTAAGTTATTGAAACAACCAAGTTTCGACGTTGGTGCTTTGATGGCTTTGCATGGTG
AAGGTTCCGGTGAAGAAAAGGTAAGAAGGTTTCTGGTTTCAAGGATGAAGTCTTGAAA
CTGTGTAA

YML063W, 255 aa (SEQ ID NO 210)

MAVGKNKRLSRGKKGLKKVVDPFTRKEWFDIKAPSTFENRNVGKTLVKNSTGLKNASDA
LKGRVVEVCLADLQSEDHSFRKVKLRVDEVQGNLLTNFHGMDFTTDKLRSMVRKWQTL
IEANVTVKTSDDYVLRIFAIAFTRKQANQVKRHSYAQSSHIRAIRKVISEILTREVQNST
LAQLTSKLIPEVINKEIENATKDIFPLQNIHVRKVKLLKQPKFDVGALMALHGECSGEEK
GKKVSGFKDEVLETV

YML128C, 2042 bp, CDS: 501-2042 (SEQ ID NO 211)

TTAATAGGGTTAGCCACCATTGTCTCGAACATGTTACAGGCTCGGAGCTTGTGGCGGGT
GCCTCGCTTACTGGAGTACCATTAGCGGTGTGTTTGAAGCTAACGAGTTCATCTTCAAT
CTTTATTTCCACTTCTTTACAAGCTTTCTGCCTTTCTCTATGACGTCTTTCCCAAACAC
TACCTCTTGACACGACTTGTGTTTTCTGTTTTCTCTAAGAATATCACTATTTTCACTTT
TTTCACTTTTCCACCATTACGTGCGTAAGCAACAGCATTACGCCGGCCTCACCTTAGAG
GGGAAGAATAAGGGATCTTTGGAAGTGAAGGAAAATAAGGGAGAGGGAGGAAACAAGGAG
GCGGTGAAAGGGGATCGACAGGGTATTTAAAGCCACTCATGGAGTCGTATTCCTAGCATG
ATTAGATTACCGGAGTTTGAAGAGGATCTGCAATAGAAGAGGAGACAACACTACAAAAGAA
CTGTTAATTAAGAGAAGAAGATGAAGCAATTCAAGTTGGTTAATGCGGTTCGCGCATCAT
TTGTGCTTATTGGCTTAGTGTTGGCCAATTCAGATTCAAGTGTTCGACAAGTGGACGCAGG
AAGACCTGGCCGATTATTTACGTGATAATAAGAAGAGCTTGGAAAAGTACGCTACAGACT
CCATTGAGGACTTGAAAACGGAGGCATCGCAGGTATGGGACAAACACGCGCAGCCCAAAC
CATGGTGGCAGGTGTGGTCTAGTGACAGCAGTAGCGTGAGCAACAGTAACCCCGGATGGT
TTGGTTATACTGGTTCTTCGGATCACCCAGTTTCTGACTGGCTCTTTGACACCTGGTCCA
CAGACAGTCTACGTAACCTTCTTGAAGAAAACGGCGTGATGTTGACGACGCTAAGGCTT
CCAAGGACTCGCTGGTGAAGACTGCTAAGGAGAACTTCAACAAGATTTCCAAATCTTTGA
AGTCGTGCGGATACTATCCTTCTAGCTCTTACTTTGATAGCTGGTCAACCAAAGATTTGC
AAAAGTGGTTGAATGACAATGGTATCGACTACGACAAGGCAGTTCAAAGCAAGGACGAGC
TAGTTTCAGAAAGTCAAGGAAAACATCTACCGAACTTCAGAAAAGGCAGAACAGCAGCGTC
TGGGTTTGCTAGAAAGCTTGGATTGGGCTCACCAACAAATATTAGACACATCGGGACAAA
TAAAAGACACTGTATTTGACAAGTGGTCTAGTGATCAGTTAACCAATTGGTTGGAGAGCC
ACAAGGTCAATATTGACAAGAATATGGCCAAGAAACACGACTATTTGGTTAGAATGGCCA
AAGAAAATTCTGCCAATTTGAAAGATGATATCTACTGGTACCTGGACTATATGAAAAGAG
AGTCTTCTCCATTTTGGACCAAGACCCAGAAATACGTTGGTTCCGTTTGGGACTCTTCTA
AAAATTTCTCACAAATTTGTAATCTCAAGTTTCAGAGGTAAGACTGACAATGTGATCAATG
ATACTTTTTTGGTTGGCCTAGACTCTTGGCCAAAGGACAAATGAAAATGTTTTTAGATG
CTCGTGGTATTAAGTACTCAATGCTGTCTACTGAACATCAATTGAGAGAATTAGTCAAAA
AATCCAGAAACGAAAACTCAAGATCCTGCCAAAAGACTACCAAAAATACTTTGACAACA
GTAATGGTCTTTGGATGACATAAAGGGTGGTTTGGTGACAAAAGGACGACTTCCAAG
ATTCTCAGACTTACTCCACAATTATGCAGGATTTTGACAAGGTTTCCAAAACACAAATG
ATGCTAAGGACCAATCGCTAAGACCTGGTCAAATACCTTTTCAGAGCTGGTCTCAAGAAG
ACCTATTGCAGTACCTAAAATCATTCGGTGTTCGGGTTAAACAGACTTCTACGAAGGACG
ACTTAATCAACTTGGCCAAGCAGAAATACGCAATGGTTGTTCGGCACTGTTAAGGAGCCTG
CTTACAAGAGGTACCTACATAACGTTAAAACTGGTCGAAAAGCATATTAGGGTTCAACT
AA

YML128C, 513 aa (SEQ ID NO 212)

MKQFKLVNAVSAFVLIGLVLANSDSVFDKWTQEDLADYLRDNKKSLEKYATDSIEDLKT
EASQVWDKHAQPKPWWQVWSSDSSSVSNPNPGWFGYTGSSDHPVSDWLFDTWSTDRLNF

LKKNQVDVDDAKASKDSLVTAKENFNKISKSLKSSGYYPSSSYFDSWSTKDLQNLNDN
GIDYDKAVQSKDELVQVKENIYRTSEKAEQQRLGLLESLLAHQQILDTSQIKDVTVD
KWSSDQLTNWLESHKVNIDKNMAKKHDYLVMAKENSANLKDDIYWYLDYMKRESSPFLT
KTPEYVGSVWDSSKNFLTNLYSKFRGKTDNVINDTFLVGLDSWPKDKLKMFLDARGIKYS
MLSTEHQLRELVKSRNEKLKILPKDYQKYFDNSNWSLDDIKGWFADKKDDFQDSQTYST
IMQDFDKVSKNTNDAKDQIAKTWSNTFQSWSQEDLLQYLKSFGVPVKQTSTKDDLINLAK
QNTQWLFGTVKEPAYKRYLHNVKNWSKSLGFN

YML130C, 2192 bp, CDS: 501-2192 (SEQ ID NO 213)

ACGAGATCATTTTCTTATCTATCTATTGAGTAATGCTTACTTTTCATATTTTCAATGAAC
AATAGGATATGTAGGAGAATTGATATATTCAGTGCCTATCAGAGAAAAGGTCTACTGACA
TTTTATGGCAAATGTATTCTACACAAATCGAGAATACCACAGACAATGGTACAAGACATA
CACAAAGAGAAGACTGTTCTAATTAACAAATAATATTGAGCTACCTGCTAAGTATGTCC
TTTTCCCTTTGTCCTTTGGTTTCTCTTATAGAAGACCCTGGAAATTTTTCGCATTTTCC
GGCTTTGGCGTTAGTAAGAACAAAAAGAAAGAGAACAAAAAGAAACGATACGGA
GTACGTGTCATAAAACTTGTTCATCCTTGAAGCTAAGTATAAAGAGCTTGAAAAG
GTTTACCACTTAACTGGTTATACTATTTCAAGAGTGTAACATTTTATTGCATATACCA
CAGTAACGTGCAGGTAAACATGAGATTAAGAACCGCCATTGCCACACTGTGCCTCACGG
CTTTTACATCTGCAACTTCAAACAATAGCTACATCGCCACCGACCAAACACAAAATGCCT
TTAATGACACTCACTTTTGTAAAGTCGACAGGAATGATCACGTTAGTCCCAGTTGTAACG
TAACATTCAATGAATTAATGCCATAAATGAAAACATTAGAGATGATCTTTCGGCGTTAT
TAAAATCTGATTTCTTCAAATACTTTCGGCTGGATTTATACAAGCAATGTTTCAATTTGGG
ACGCCAACGATGGTCTGTGCTTAAACCGCGCTTGCTCTGTTGATGTCGTAGAGGACTGGG
ATACACTGCCTGAGTACTGGCAGCCTGAGATCTTGGGTAGTTTCAATAATGATACAATGA
AGGAAGCGGATGATAGCGATGACGAATGTAAGTTCTTAGATCAACTATGTCAAACAGTA
AAAAACCTGTAGATATCGAAGACACCATCAACTACTGTGATGTAAATGACTTTAACGGTA
AAAACGCCGTCTGATTGATTTAACAGCAAATCCGGAACGATTTACAGGTTATGGTGGTA
AGCAAGCTGGTCAAATTTGGTCTACTATCTACCAAGACAACCTGTTTTACAATTGGCGAAA
CTGGTGAATCATTGGCCAAAGATGCATTTTATAGACTTGTATCCGGTTTCCATGCCTCTA
TCGGTACTCACTTATCAAAGGAATATTTGAACACGAAAACCTGGTAAATGGGAGCCCAATC
TGGATTTGTTTATGGCAAGAATCGGGAACCTTTCCTGATAGAGTGACAAACATGTATTTCA
ATTATGCTGTTGTAGCTAAGGCTCTCTGGAATAATCAACCATATTTACCAGAATTTTCAT
TCTGTGATCTAGTCAATAAAGAAATCAAAAACAAAATGGATAACGTTATTTCCCAGCTGG
ACACAAAAATTTTAAACGAAGACTTAGTTTTTGCCAACGACCTAAGTTTGACTTTGAAGG
ACGAATTCAGATCTCGCTTCAAGAATGTCACGAAGATTATGGATTGTGTGCAATGTGATA
GATGTAGATTGTGGGGCAAATTCAACTACCGGTTACGCAACTGCCTTGAAAATTTTGT
TTGAAATCAACGACGCTGATGAATTCACCAAAACAACATATTGTTGGTAAGTTAACCAAT
ATGAGTTGATTGCACTATTACAGACTTTCGGTAGATTATCTGAATCTATTGAATCTGTTA
ACATGTTCGAAAAAATGTACGGGAAAAGGTTAAACGGTTCTGAAAACAGGTTAAGCTCAT
TCTTCCAAAATAACTTCTTCAACATTTTGAAGGAGGCAGGCAAATCGATTTCGTTACACCA
TAGAGAACATCAATTCCACTAAAGAAGGAAAGAAAAAGACTAACAATTCTCAATCACATG
TATTTGATGATTTAAAAATGCCCAAAGCAGAAATAGTTCCAAGGCCCTCTAACGGTACAG
TAAATAAATGGAAGAAAGCTTGAATACTGAAGTTAACAACGTTTTAGAAGCATTCAGAT
TTATTTATAGAAGCTATTTGGATTTACCCAGGAACATCTGGGAATTATCTTTGATGAAGG
TATACAAATTTTGAATAAATTCATCGGTGTTGCTGATTACGTTAGTGAGGAGACACGAG
AGCCTATTTCTTATAAGCTAGATATACAATAA

YML130C, 563 aa (SEQ ID NO 214)

MRLRTAIATLCLTAFTSATSNNNSYIATDQTQNAFNDTHFCKVDRNDHVSFSCNVTFNELN
AINENIRDDLSALLKSDFFKYFRDLKYQCSFWDANDGLCLNRACSVDDVEDWDTLPEYW
QPEILGSFNNDTMKEADDSDECKFLDQLCQTSKKPVDIEDTINYCDVNDNFNGKNAVLID
LTANPERFTGYGGKQAGQIWSTIYQDNCFTIGETGESLAKDAFYRLVSGFHASIGTHLSK
EYLNKTGKWEPNLDLFMARIGNFPDRVTNMYFNAYVAKALWKIOPYLPESFCDLVNK
EIKNKMDNVISQLDTKIFNEDLVFANDLSLTLKDEFRRFKNVTKIMDCVQCDRCRLWGK
IQTGYATALKILFEINDADEFTKQHIYVGLTKYELIALLOTFGRLSESIESVNMFEKMY
GKRLNGSENRLSSFFQNNFFNILKEAGKSIRYTIENINSTKEGKKKTNNNSQSHVFDDLKM
PKAEIVPRPSNGTVNKKWKKAWNTEVNNVLEAFRFIYRSYLDLPRNIWELSLMKVYKFWNK
FIGVADYVSEETREPISYKLDIQ

YMR022W, 998 bp, CDS: 501-998 (SEQ ID NO 215)

AACAGTATTGGCTGTTGATTTCATTGCGCTGCAGCAGTCACCTTCAATTTGTGCACCATTT
TCGTATTCTGTACTTTGCGATGTAGAGTCTACTAAAATAGCGTCTCTGATAGCCATGGGT
GAAGGTCTTCCTCTAGTTCTCACCTTAATTAGCATTCGGTGAGAATGCCTGCATGTTGAA
GAGCGATGCCCTCTGATGCACGATGCACACGCATATTTGTTCCCATTAATATTATCATC
TCTGATAGAGCTTGAAGAACTTACCAGACTGTTTCAAGTTTAAAACAAGGCGCCTCATCG
CATCTACCTCACGAAGATGCAGCAGCTTATTGTCTCGAGATCCTTCTTATAACTCCTTTT
CGCCATTACCCGAAAACGAGATTACAGCCTCTAAACCAAGAGCTCGAAAAGCGCCAAAGT
AAACTCTGGCGTTTAGCGTACGAAGGAGATTATCCTAAAAGGAACCTCCCTAGTAATAGT
GTAATTTGGAAGGGCATAGCATGTGCGAAAACCGCTCAGAAACGTCTCCTCAAGGAGCTTC
AACAGTTAATTAAAGATTCTCCACCTGGTATAGTGGCTGGTCCCAAATCGGAGAATAACA
TATTCATTTGGGACTGCCTAATTCAAGGGCCTCCAGATACGCCATACGCTGATGGTGTTT
TTAATGCTAAGCTAGAGTTTCTTAAAGACTATCCGTTATCTCCACCTAACTTACTTTCA
CACCCAGCATACTACATCCAAATATTTATCCAAATGGGGAAGTGTGCATATCCATTCTAC
ACTCCCTGGTGATGATCCTAACATGTACGAATTAGCGGAAGAAAGATGGTCGCCAGTGC
AAAGTGTAGAAAAAATTCTATTAAGTGTTATGAGCATGTTGAGTGAGCCCAATATCGAAA
GTGGTGCCAACATTGATGCTTGCATCTTGTGGAGAGATAATAGACCTGAATTTGAGAGAC
AGGTAAAGTTATCCATTTTGAAATCATTAGGATTCTGA

YMR022W, 165 aa (SEQ ID NO 216)

MSKTAQKRLLELQQLIKDSPPGIVAGPKSENNIFIWDCLIQGPDPYADGVFNKLEF
PKDYPLSPPKLTFTPSILHPNIYPNGEVCISILHSPGDDPNMYELAEERWSPVQSVEKIL
LSVMSMLSEPNIESGANIDACILWRDNRPEFERQVKLSILKSLGF

YMR118C, 1091 bp, CDS: 501-1091 (SEQ ID NO 217)

GTCCTTCCGCTTTATATGTTTCGTTATCCTATCACATTATCAAATGACTTTGTGCCACTG
TGTTTTGACAAAATTACTGTAATATAATCAATAGTATTTACATGTTTGTACCAGAAGTAC
TTGCATCGCATCCAGTTCTCATGCAATATAGTTGTATACCATGTCGTTGAAAGGAACCAG
AGTAAACACTTCTACCAGTATTTCTTTACGGTTCGGATCAAAACCATCACTCATTCCGTC
ATTCTTACCGTACGATAAACCAAATTACAAGGAAAAGTATCCCTAATTAGAGATCACTGC
ATCCGTAATAGTTTTTTTTCTATTTTGGACTTTTGTAAAAAAGGGATTAGGGATACGTTG
CTCATAAAAAAATTGACGAAGATTTTAGATAATGGCAAATAAAAAATGAAATAGTATCAAT
ATACCGAAAAATTAATCACACTCAATGCGACTGTGATAGCTGATAAGTGGAGCTCAGAAA
TATTCAGAAGCGTAAGAATAATGAAAGCAACCATTCAAAGAGTAACATCTGTATTTGGAG
TTCCCGGAGCATCTGTATTCGTGCCAAGAATCAGCACACCATTTATTTTGCATAATTATA
TCTCTAATGGCAGAATGGACCTTTTTTCCAAAGAATTCCACAATGGCCGCGTATCCAAAT
CTGATCTTTGGTCAAGCAACAAGGAAGAGGAGCTCTTAGTATCTCAAAGGAAAAAAGAC
CGATCTCTCCTCATTTAACTGTTTACGAACCTGAAATGAGCTGGTATCTTTCCTCTTTAC
ATCGTATATCTGGCGTTTTACTGGCTCTTGGATTCTATGCTTTCACAATTACTTTGGGTG
TGACGACAATAATGGGAATGGATACGACTTTTCAGGATCTAAACAAGTGGTATCACGAAA
AGATGCCTAAGTGGTCCCAATGGGTGGCCAAAGGCTCTGCAGCATATCTGTTTGCATTCC
ATTTTGGTAACGGTATAAGGCATCTCATCTGGGATATGGGCTACGAATTGACCAACCGTG
GGGTATATAAAAACCGGATCAATCGTTTTAGCCGGGCACACTCGTCTTAGGAACGTATTTAC
TGGCTCAGTAA

YMR118C, 196 aa (SEQ ID NO 218)

MKATIQRVTSVFGVPRASVFPRISTPFILHNYISNGRMDLFSKEFHNGRVSKSDLWSSN
KEEELLVSQRKKRPISPHLTVYEPEMSWYLSSLHRISGVLLALGFYAFTITLGVTTIMGM
DTTFQDLNKWYHEKMPKWSQWVAKGSAAYLFAFHFGNGIRHLIWDMGYELTNRGVIKTGS
IVLAGTLVLGTYLLAQ

YMR143W, 1121 bp, exon1: 501-524, intron1: 525-713, exon2:
714-1121 (SEQ ID NO 219)

CCGCTTAGCGCAAACCTATCGTGAACCTCGCTGCAACAACCTGAGAGGGCAAGGATATACATA
AAAATAGCCTACAAATCTGAACTCTGTAAAGGAAGCCTCATAAATAAAGGTAGATAGTA
AAGTATACAAGAGAAGAATCCCAAGATGTCAGCTGTCCCAAGTGTTCAAGTATGTTTTCA
GTTCTGCAGAATGATGTTTGATAGTATCGATAATGGAGTGAGATCAAGAGAAAAAATG
AATATGTCAGCCAACCAAGTTCTGAGTAGGCAGTAAATGAGTACGCATAGTGATTTATC
CAAAGGAAAGAATTGTTATTTTTACAAGCCGAATTGAGATCCAATTAGGCAATGTTTTGG
GGAGAGTATTTTGACAAGATTGGTTAACTACTACGGTCAGTTCGTAACCAGTACGATT
GTACACATAAGGAAACAACCTGTAAAGATAACAATAAGGGCTTCCAATGCCATTGTAAGA

TATCATATTTCCTAAACAAAAATGTACAGCGAATATAAAGCCAGCGTCAGTGTCTTCCTGG
AAGGTTGCGCAACTAAAGAAGTTGAAATTAAAATGGCAAGCGCTACATTTTCATCCATTT
TCACTCATCAGATGTCCAAGATTTTCGAAAAATAAATATTCTCATTTTTCTCTCAATGAA
ATAATTGTTACTAACATTGAATTTCTCGTAACTAATTGCATTACTTCTTTAGACTTTTG
GTAAGAAGAAATCAGCTACTGCTGTTGCCCATGTCAAGGCCGGTAAGGGTTTGATCAAGG
TTAATGGTTCTCCAATCACTTTGGTTGAACCAGAAATCTTAAGATTCAAGGTTTACGAAC
CATTATTGTTAGTTGGTTTGGACAAATTCTCCAACATCGATATTAGAGTTAGAGTTACTG
GTGGTGGTCATGTTTCCCAAGTTTACGCCATCAGACAAGCTATTGCTAAAGGTTTAGTTG
CTTACCATCAAAAATATGTCGATGAACAATCCAAGAACGAATTGAAGAAGGCTTTCACTT
CTTACGACAGAACCTTGTTGATTGCTGATTCTAGAAGACCAGAACCAAGAAATTCGGTG
GTAAGGGTGCTCGTTCCAGATTCCAAAAATCTTACCGTTAA

YMR143W, 143 aa (SEQ ID NO 220)
MYSEYKASTFGKKKSATAVAHVKAGKGLIKVNGSPITLVEPEILRFKVYEPLLLVGLDKF
SNIDIRVRVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEQSKNELKKAFTSYDRTLIIAD
SRRPEPKKFGGKGARSRFQKSYR

YMR174C, 707 bp, CDS: 501-707 (SEQ ID NO 221)
GTCCCATCATTTCTTTACACCTCGTACTGTATTCATGATCATCTATCCATTTTACATACCG
CTCCCTTTAAGATACGTTTATTCGTAACCTCCATTTACCAATCACTATGAGCCGTCACG
TTTCCAAAAAACCTAAACATATGATGCAAACCTCCAATGAGACTCAACGTAACATGCAA
GTAAATACAGAAGGTTAAGAGATAGTTGTCTTAAAGGGGTACCGAAAGCATTTAGGGGAG
GCTTAAGGGAGGGTGCCGATCCTATGAAGTATTAATACGTAATGCCAAAAGGAATTGTTG
AACATCTGAAGTGGATAGATTAATCGTACAGTAATCGTACAGTACTATGTCTTACTGATG
TCGGGAATCTCAGGGGCGACCGCCCCCGGCTAGAATTATCTATATAACGGTAAAAAGAAT
AAAACCTCTATTCTAGTTCTCGCCATTTACCTTGACTTTAATGAACCAATAAAAGAAATTT
CTACAACCAAGACATCCAGAATGAATACAGACCAACAAAAAGTGAGCGAAATATTTTACA
GCTCAAAGGAAAAATTGCAGGGCGATGCAAAGGTAGTGAGTGACGCTTTTAAGAAAATGG
CTAGTCAAGACAAGGACGGCAAGACTACCGATGCTGATGAAAGTGAAAAACACAACATATC
AAGAGCAATACAACAAGCTCAAAGGGGCGGGGCATAAGAAGGAGTAG

YMR174C, 68 aa (SEQ ID NO 222)
MNTDQQKVSEIFQSSKEKLQGDQVSDAFKKMASQDKDGKTTDADESEKHNYQEYQYNKL
KGAGHKKE

YMR191W, 1877 bp, CDS: 501-1877 (SEQ ID NO 223)
GGTTCGATACAACACTTGTGCTGGCTGGTATATCAACCATGGGTACGTCAGCATATTGAT
TCGATGTGGCAGTGTACGAGAGCCATTCTGTATCGTTTCGACAAAGTTTGCATGACTTCAT
GTTGTTTCGTAGCAGTATTCGTTGGTCCAGATGCAGGAATGCTGGTTATAAAGTTTGTTG
TTCTCTGGTCCACATTCATCTTTGGATGGCGTTGTTGGTGGCGAATTTGTCTTAGGCCTTT
TGTTTCGCGATGTGCTTTTGGATAGCCTGGAATACGAAATCTTTGTCTTCTGTAAAGTCG
CCGTTTCCTTTAACCATTGTGCTCCCTTCTTAAGTTATGTGACGGCTTCGTCACCATTA
CCGCCTTGTGTGTACGTGTATGATTTTTTAAATATATACAACAATAATCTGTATTTTTTC
CTTTCCTCTAGCCAATGACTCCAAGCTGGCTGATAAAAACAACTAAACGGTAAAGCCAC
AAATCCGAAATGTATCACCAATGATCACCCAGCCTGCTAAGTGCCCTCTATTGATCCGTA
TATCAGCTTTTAGATCAGGCTCGAGTTTCTTGTATATGTGCATTGCAAAAGCATAAACA
AATCCTGGCAGCCGAAGCCGGGCAATCCACTTCGAAACGCACGGCTGAACATATAAATA
TAAAGGACATGTGGAGAGAAGCTTCTCTTCTTACATTTTCGATTTTCATGATCTAAAGT
GGTTCTTTCACAATAGAAGAGCACCAACACGAAATATGGCTGTCGGTGGTAATAACTGGA
GCATGTGGCTGCGAATGTACGGGTCCACCTCAGGCAGATCACGAAGTCTCTGGACCGAA
CGCTGATCAGTTTGAGCCATGGGAATTTTCCACCAATATAATCGCAATATTTTTGTCA
CTTGGTGGAAGAGCCTATTTGAGGCTTCTACAGCTTTTAGGAGGGCAAGTGGTTTAACGG
TATCTCCTCTCACGAGGAGAGGAATCGCAAGGTTTGACCATTTTCAGACCTGTTCCCAATG
TCAGTAAATTTGCTTCTTTTCCAGAGTGCCCAAGGAGCCCCAAGGGGCTTTTACCA
ACTGGAATATGACTACATCAAAGAGATTATTAGGGCAGAGAGCTTATTCGACTTCCAGTA
TCAAATTTACCCAAGAAGCCGTGAATAACATGACTATATCTTTGAGGTGTTTTTCAACT
CACTAGGCGGATTAAATCAGTGCTCCCACTCTAATTCCTGCAAAGCTTATCAGAATGCGT
CTAATGTTACCTCTAAACAGGATCACGTCCAACCAGTTGCCCTTAAGAAGTTATCTCAA
AGGATATCAATTTTCATTCGTAATTTAGAACTATTTAAGATAATGAAGACCCAGAATGAAG
TCGTTGATGAAACAAGCGCATATTACATGAAAAACCAGGTTCTTATATTGAATTTACCA

TTTCAGAATTTAACGTTAATGGGACATTCTCCGCACCTTTGTCATTTTTTAGATCCTTCTT
TGTTAGCGGATTTGGATGAAATGATTAGAAATTACAAATACGAATTAATAATCAATATACA
GTAGTGTGACATGATCTTGCAGAATTATGGATCATTGCCGATAACTTTTCATCGAAATA
AGATTCGAATACATTTTCCAACTCAACTGTGGTGGAACAGAAAACTAATTGCAGGTC
TGAATATTGCTACGGGTGTTATTTACGCAGATACGTCTCCCGATATCAGTCTAGAAGGTA
CAAATTTGAATGCTCTGGTTAATGTTGACAATTCAGGAAGCGTATGGTCTTTTGTAAAGG
AGCCCTCGTTTCCCTCTAGGAGCGCTTTTTCACCTATTTTATCAGATGCATCCTATGATA
CTTATGAATTGGTCTAG

YMR191W, 458 aa (SEQ ID NO 224)
MITQPAKCPLLIRISAFRSGSSFLLYVHCKSINKSWQPKPGNPLRNARLNYINIKDMWRE
ASLPSHFAFHDLDKWWFFHNRRAPTRNMAVGGNNWSMWLRMSRVHLRQITKSLDRTLISLSH
GNFSHQYNRNIFVTWWKSLFEASTAFRRASGLTVSPLTRRGIRFDHFRPVPNVSKFASF
PRVPKGAPRGLFTNWNMTTSKRLLGQRAYSTSSIKFTQEAVNNMTISLRCFFNSLGGLNQ
CSHSNSCKAYQNASNVTSKQDHVQPVALKKLSQKDINFIRNLELFKIMKTQNEVVDETS
YYMEKPGSYIEFTISEFNVNGTFSAPLSFLDPSLLADLDEMIRNYKYELKSIYSSVDMIL
QNYGSLPITFHRNKIRIHFPNSTVVETEKLIAGLNIATGVIYADTSPDISLEGTNLNLALV
NVDNSGSVWSFVKEPSFPSRSAPSPILSDASYDTYELV

YMR230W, 1228 bp, exon1: 501-552, intron1: 553-962, exon2:
963-1228 (SEQ ID NO 225)

ATCAAATATTGATCGAGTTCATATAAAGCTAAAGAGTAGGAAATATACCATCAATGGTGA
GCACTTATTTTTTTTTTGGATTTAGATGTGAGACATACTAAAAAAAGTTGCTATCAAGCC
TATAATTTGGCTACGTTGTCTTCCGGTGTTTTTCAATTGATTTAAGTTACAACACTCAA
TCTGGGTAATTTGATCTTTTTTAATAATTATTTTAGTGACATATAGTTCTTAGAGTTTCGC
AGATTTATTTTGTCAATTTTTTGGATCGGCGTCTTATAAAATCAAGACATAATACATCCGC
ACATCGCGCATGTGTGGGTGTATATGCCCTTTTCACGATTTTTAAGTTGCGTCTCAAAT
AGTTTCCGAGTTGGAAGCCTGAGTTTTTCAAAACAATATAGGAATTAAGGTATACGTCT
TTGGATACATGTTATTTGAAATGGGGTAGAACTAGCACAACTGAAACCAAGAAAACACAG
ATCATAACTAACCCTTCAAGATGTTGATGCCAAAGCAAGAAAGAAACAAAATTCACCAAT
ACTTGTTCAGGTATGTTTGCATTTTTTAGGTGAAATATGCAGTGATATGCTCCGAAAT
GGATAGCAAAGATGATAAATGAAAATACAATTAATTTGAACCTGAATATCATTAAAAGTG
GTAGAAAACCGATTGTTTCAAAAAGATCTTTGTGGACAAGTACGGCAGTGCATGAATCCG
AAAGAAAAGTGCAACCTAAGCAGAATTCCATTATTTACGCGTCCATTTTTATAATGTTT
GAACTTTTGAGTCCTTATAGAAATGCTAATATTATGATCAAAGCGATTATATCATTTACT
TTACAGTTTCCGGAGTTTCCGTATTATTGCAAAAGGACCACAAACAATTGAAATCATGAT
ATCGTAAGAAATATTATTACTAACAAGGAAGATCATTGAATTACGATCGCATATCGAAAT
AGAAGGTGTTGTCGTCGCTAAGAAGGATTTCAACCAAGCTAAGCACGAAGAAATTGATAC
CAAGAACTTGATGTTATCAAGGCTTTGCAATCCTTGACTTCTAAGGGTTACGTTAAGAC
TCAATTCTCATGGCAATACTACTATTACACTTTGACTGAAGAAGGTGTTGAATACTTGAG
AGAATACTTGAACCTGCCTGAACACATTGTCCCAGGTACCTACATTCAAGAAAGAAACCC
ATCCCAAAGACCTCAAAGAAGATACTAA

YMR230W, 105 aa (SEQ ID NO 226)
MLMPKQERNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLRREYLNLP EHVPGTYIQERNPSQRPQRRY

YNL054W, 3998 bp, CDS: 501-3998 (SEQ ID NO 227)
CCCTTCGCTAAATCATTAAGAGGTCAATTCATGAAGTTAATTCAGCACCAAAGTTGGACTG
TTAGACACGAGATACACATTGCAGTCCAAATGTGCAGATTTTTTCAGATAATTGTCGTCGC
ACAAGACTGCCCTCCCGTCTCAGACAGACACAAAATTAGATTTTACGTTTACATAAAG
ATGTACATAACTTGAAAAACGTTAATCCCTCTTAAATTTAGACCTTGTAAGTCTTCCTG
GCCACTCTTTGTGATATATTGTAGTGCAATATATTGATTCGTTCTTCTTATTTCTTTGTT
CTTAGGCATTTCCGCTTTAGAAAATTCGTTGGGTGGTTTCTGCGACGGGTATCCCCTTCG
ATTTTGCATAATGATCTTCAATCTACAATAAAATCAAGTAGATACAGGAAAATATTCC
ATAAATTATAGTGTAATCGCCCTGTATACACCTTATCGTTTCATCTCAGGCAAGTTAAA
GCATTTGGGAAACGTGCTAGATGACAGAAGAAGATAGAAAGCTCACTGTAGAGACAGAAA
CAGTTGAGGCACCCGTGGCAAATAATCTTTTATTGTGCAATAACAGTAATGTAGTAGCAC
CTAATCCTTCTATTCCTCTGCCTCCACATCTACCTCTCCGCTACACAGGGAAATAGTTG
ATGATTCTGTGCTACTGCTAACACCACCAGCAACGTTGTACAGCATAATTTGCCACCA

TAGATAACAATTTAATGGATTCCGATGCCACGTACATAATCAAGATCATTGGCATTTCAG
ACATAAACAGGGCAGGAACATCAATGTCAACGAGTGATATCCCAACAGATTTACATTTAG
AACATATCGGCTCTGTTTCATCAACTAATAATAAGTAACAATGCCCTAATCAACCACA
ACCTCTGTCTCATCTCTTTCCAATCCGTCATCTTCATTACGAAACAAGAAGAGCTCTT
TGTTGGTAGCTTCTAACCTGCGTTTGCTTCAGATGTTGAACTCTCGAAGAAGAAACCTG
CCGTCATCTCCAATAATATGCCTACAAGTAACATTGCCCTTTATCAAACAGCGAGATCGG
CGAATATTCATGGTCCATCATCAACTTCCGCATCTAAAGCGTTCAGAAAGGCTTCGGCCT
TCTCCAATAACACGGCACCCAGCACTAGTAATAACATCGGCTCGAATACACCTCCAGCTC
CTCTTTTACCTCTACCTTCACTATCACAAACAAAATAAGCCAAAAATAATAGAGAGGCCCA
CAATGCACGTCACTAATTCAAGAGAAATACTTTTAGGTGAAAACCTGTTAGATGATACAA
AGGCGAAGAATGCTCCCGCGAATTCACCACACACGATAATGGTCCAGTAGCAAATGATG
GGCTGCGTATACCGAATCACTCGAACGCAGATGATAATGAAAATAACAACAAAATGAAGA
AGAATAAAAACATTAATAGTGGGAAAAATGAACGTAATGATGACACCAGCAAAATATGCA
CTACATCTACTAAAACAGCGCCTTCAACCGCACCTTTGGGCAGTACAGACAATACTCAGG
CTCTCACTGCTAGTGTCTCCAGCAGTAATGCTGACAATCACAATAATAACAAGAAGAAAA
CCAGCAGCAACAACAACGGCAATAACAGTAATAGTGCATCCAATAAAACCAATGCCGATA
TCAAGAATTCTAACGCCGACTTGAGCGCTTCTACCTCTAACAATAATGCAATAAATGACG
ACTCACATGAGAGTAATTCAGAAAAACCAACAAAGGCGGATTTTTTCGCTGCAAGGCTGG
CTACAGCTGTAGGTGAAAATGAAATTAGTGATTCTGAGGAAACATTTGTTTATGAATCGG
CAGCTAATTCGACTAAAAACCTAATATTTCTGACTCCTCCAGCCAGCAGCAGCAGCAGC
AACAGCAACCTCCAAAACAACAGCAACAGCAACAAAATCATGGAATAACCTCAAAGATAA
GCGCCCCATTGCTAAACAATAACAAAAAATTATTAAGCCGACTGAAAAATTCAAGACATA
TTAGCACTGGTGCCATATTGAATAACACAATCGCGACTATAAGCACAAATCCGAACCTGA
ATTCTAATGTGATGCAGAACAATAACAATCTGATGTCGGGACACAATCACCTGGACGAGT
TGAGCAGTATAAAACAGGAGCCACCGCATCAATTGCAGCAGCAGCAACCACCAATGGATG
TACAATCGGTAGATTTCGTATACCTCTGACAACCCAGACAGCAATGTTATTGCCAAGTCGC
CTGATAAGAGGTCAAGCTTAGTATCCCTATCTAAAGTTTCTCCACATTTACTTTTCATCCA
CATCAAGCAACGGTAACACAATATCGTGTCCCAATGTTGCCACAAATTCGCAGGAATTGG
AACCAACAATGATATTTCAACGAAGAAATCTCTTTCCAATTCTACTTTGAGACATTCCT
CTGCTAATAGAAATTCTAATTATGGTGACAACAAAAGGCCTCTTAGAACAACAGTGTCAA
AGATATTTGATTCAAACCCTAATGGAGCTCCTTTACGGAGATACTCTGGGGTACCGGATC
ACGTTAATCTAGAAGATTACATCGAACAGCCGCATAATTATCCAACAATGCAAAATAGTG
TGAAAAAGGATGAATTTTATAACAGCAGGAACAATAAGTTTCCCCATGGTTTAAACTTTT
ATGGTGATAACAATGTTATTGAAGAGGAAAAATAATGGTGACTCGTCTAATGTAAATCGAC
CGCAACACACTAACCTTCAGCATGAGTTTATTCCAGAAGATAACGAAAGTGATGAAAACG
ATATTCACTCCATGTTTATTATAATCATAAGAACGATTTAGAAACAACAAACCGCTAATAT
CCGATTATGGTGAAGATGAAGACGTAGATGATTATGATCGCCCAATGCTACTTTCAACA
GTTACTATGGCTCAGCATCCAACACGCACGAACCTTCATTACATGGAAGGATGCCTTCAA
GATCAAATAATGATTACTACGATTTTATGGTTGGCAACAATACTGGCAATAACAACCAAT
TGAATGAATATAACCCCTTAAGAATGAAACGTGGTCAAAGACACCTATCAAGAACAACA
ATAGCATAATGAATGGTAGCATCCATATGAATGGTAACGATGACGTTACCCATTCCAATA
TCAATAATAACGATATTGTTGGTACTCACCGCACAACTTTTACTCAAGGAAGTCCCCAT
TTGTGAAAGTAAAGAATTTTCTTTATCTTGCAATTTGTTATATCATCACTATTGATGACAG
GATTCATTCTGGGATTTTTATTGGCCACTAATAAAGAACTACAAGATGTAGACGTGGTAG
TGATGGATAATGTGATTTCAAGTTCGGACGAGTTGATCTTCGACATCACAGTAAGTGCTT
TTAATCCAGGATTCTTCAGTATAAGCGTTTCCCAAGTCGATTTGGACATTTTTTGCAAAAA
GTTCTTACCTGAAGTGCGATTCTAATGGTGACTGTACAGTAATGGAACAGGAACGGAAAA
TTTTACAAATAACGACAAATCTTTCGTTAGTTGAAGAGAGTGCTAATAATGATATTAGTG
GTGGGAACATAGAGACGGTATTACTAGGAACCGCTAAAAAACTAGAGACACCATTAAGT
TCCAGGGCGGCGCATTTAATAGGAACCTACGATGTGTCAGTCTCGAGTGTCAAGCTTTTAA
GTCCTGGGTCTCGTGAAGCCAAGCACGAAAACGACGATGATGACGATGATGATGGCGACG
ATGGTGACGATGAAAACAATACTAATGAAAGACAATACAAAAGCAAACCAATGCTAGAG
ATGACAAAGAAGATGATACTAAAAAATGGAAGCTACTAATCAAGCATGATTACGAATTGA
TAGTCCGTGGAAGCATGAAGTATGAGGTGCCCTTTTTCAATACGCAAAAATCTACGGCTA
TTCAAAAGGATTCCATGGTCCATCCTGGTAAGAAGTGA

YNL054W, 1165 aa (SEQ ID NO 228)

MTEEDRKLTVEETETVEAPVANNLLLSNNSNVVAPNPSIPSASTSTSPLHREIVDDSVATA
NTTSNVVQHNLPIDNNLMDSDATSHNQDHWHSIDINRAGTSMSTSDIPTDLHLEHIGSVS
STNNNSNNALINHNPLSSHLSNPSSSLRNKKSSLLVASNPAFASDVELSKKKPAVISNNM

PTSNIALYQTARSANIHGPSSTSASKAFRKASAFSNNTPSTSNNIGSNTPPAPLLPLPS
LSQQNKPKI IERPTMHVTNSREILLGENLLDDTKAKNAPANSTTHDNGPVANDGLRIPNH
SNADDNENNNKMKKNKNINSKNERNDSTKICTTSTKTAPSTAPLGSTDNTQALTASVS
SSNADNHNHNNKKKTSSNNNGNNSNSASNKTNADIKNSNADLSASTSNNNAINDDSHESNS
EKPTKADFFAARLATAVGENEISDSEETFVYESAANSTKNLIFPDSSSSQQQQQQQQPPKQ
QQQQQNHGITSKISAPLLNNNKKLLSRLKNSRHISTGAILNNTIATISTNPNLNSNVMQN
NNNLMSGHNLDELSSIKQEPHQLQQQPPMDVQSVDSYTSNPNDSNVIKSPDKRSSL
VLSKVSPhLLSSTSSNGNTISCPNVATNSQELEPNNDISTKKSLSNSTLRHSSANRNSN
YGDNKRPLRTTVSKI FDSNPNGAPLRRYSQVDPDHVNLEDYIEQPHNYPTMQNSVKKDEFY
NSRNNKFPHGLNFYGDNNVIEEENNGDSSNVNRPQHTNLQHEFI PEDNESDENDIHSMFY
YNHKNLETKPLISDYGEDEDVDDYDRPNATFNSYYGSASNTHELPLHGRMPRSRNNNDYY
DFMVGNNNTGNNNQLNEYTPLRMKRGQRHLSRTNNSIMNGSIHMNGNDDVTHSNINNNDIV
GYSPHNFYSRKSPFVKVKNFLYLAFVISSLLMTGFILGFLLATNKELOQVDVVMNDNVIS
SSDELIFDITVSAFNPFFSISVSQVDLDIFAKSSYLKCDSDNGDCTVMEQERKILQITTN
LSLVEESANNDISGGNIETVLLGTAKKLETPLKFQGGAFNRNYDVSVS SVKLLSPGSREA
KHENDDDDDDGDDGDDENNTNERQYKSKPNARDDKEDDTKKWKLLIKHDYELIVRGS MK
YEVPPFFNTQKSTAIQKDSMVHPGKK

YNL067W, 1076 bp, CDS: 501-1076 (SEQ ID NO 229)

GACGACTATTGATGCCAGGCAAATTTTGGATTTACTGCTCCTCTTTTAAGAAGACAAGTG
TGTGATATCGTAGCGGTAGGAACCAATTTTGCAATCGATTTACTTACAGCCAAGAAAATC
TATTTTCATGTTTAGCATTGCCATTTCTTCTGTGTACACGTTGTGCTTGCCAGGAAC TA
TAGGAGAGACGTATACAAGCATCAATGTTACGAATGTACGATCCCGTTTGCATCTGATGT
GTAAACTCATGTGGTGCAC TGGTGTGTTTCCAAGACTGCAC TATTA ACTGGGAATTTT
TTTTTTCTTCTAGTGAATTTTTTTTAAAGCGACGCACAGGAAAAGTGAAAATTATTTAA
ACGGACGGCAAACATGAAAAAAAATTACCAACCATATTTCTATTTCTTTCCCTTTAC
CTATTCTCTTTTGAAGTAGTTCAATTTCTCTCTCTGAAACGACAATAAACCAAACTCTA
GCCTCCAATAGTCACTAAAGATGAAGTACATTCAAACCGAACAAATGAAATCCAG
AAGGTGTTACTGTCAGCATTAAGTCCAGAATCGTCAAGGTGTGCGGTCCAAGAGGTACTT
TGACCAAGAACTTGAAGCATATTGATGTTACCTTCACCAAGGTCAACAACCAATTGATCA
AGGTGCTGTTCAACACGGTGACAGAAAGCACGTTGCCGCTTTGAGAACCGTTAAATCTT
TGGTTGACAACATGATCACTGGTGTACCAAGGGTTACAAGTACAAGATGAGATACGTCT
ACGCGCATTTCCCAATCAACGTCAACATTGTTGAAAAGGATGGTGTCTAAATTCATTGAAG
TCAGAACTTTTTGGGTGACAAGAAGATCAGAAACGTCCAGTTAGAGATGGTGTACTA
TCGAATTCTCTACTAACGTAAAGGACGAAATCGTCTTATCTGGTAACTCTGTTGAAGACG
TTTCCCAAATGCCGCTGACTTGCAACAAATCTGTCTGTGTTAGAAACAAGGATATCCGTA
AGTTTTTGGATGGTATCTACGTTTCCCAAGGGTTTCATTGTGCGAAGACATGTAA

YNL067W, 191 aa (SEQ ID NO 230)

MKYIQTEQQIEIPEGVTVSIKSRIKVVGPRGTLTKNLKHIDVTF TKVNNQLIKVAVHNG
DRKHVAALRTVKSLVDNMITGVTKGYKYMRYVYAHFPINVNIVEKDGAKEIEVRNFLGD
KKIRNVPVRDGVITIEFSTNVKDEIVLSGNSVEDVSQNAADLQQICRVRNKDIRKFLDGIY
VSHKGFIVEDM

YNL075W, 1373 bp, CDS: 501-1373 (SEQ ID NO 231)

TCGATGGATATCCCATCCAAGAACAGGAATACTGGGTTTTTGAAGACCAGAATGGAGATC
TCTGAGGAAGAAAAGATGGTACGTACAATATCACGGCTTGACAATACGAGTATTGCAAAC
AGTAATGGAAATGGTAATGATGACACCTCTAATCAGAGAACGGAAGCACTGGGGCGTAAG
ACGAGTAATGGAGGGCGAATATGATTACTAAGTTAAATAAATCAGATACAGTATTTAAAG
TTCTTTCAAAAAAAGATAATGTCATATATTTTACTATCTACGCAGTGAAAGAGTTCCTTC
TAATGACACACTATTCACCTTCGGGTAACGGATATTGTGTACTGAAAAATATAAAAAATTT
TATCCCGGAAATGCCGATGAGATGAAAATGCATGAAGTAGCGTATATATTGATTGCATGAG
GTTGGACTTGAAAGGGCATATATACTCGGTTTTATCATTGATTCAAGTGTTCCCATAAAT
AATAAAACAGTTAAATCGAAATGCTAAGAAGACAAGCCCGTGAAAGGAGAGAATATCTAT
ACAGAAAAGCGCAAGAATTACAAGATTCTCAACTGCAACAAAAACGTCAAATAATTAAAC
AAGCGCTAGCTCAGGGGAAGCCATTGCCAAAGGAAGTAGCAGAAGATGAGAGTTTACAAA
AGGATTTTCAAGATATGACCAAAGTTTAAAGGAGAGCGAAGAAGCAGATGATCTACAGGTTG
ATGATGAATATGCTGCCACAAGTGGTATAATGGATCCAAGAATCATCGTCACAACATCTC
GTGACCCAAGCACTCGTCTCTCGCAATTTGCCAAAGAAATTAAGTCTATTTCCAAATG
CTGTCAAGGCTGAACAGAGGTAATTATGTGATGCCAAATCTAGTGGATGCTTGTA AAAAAT

CCGGTACTACAGATTTGGTGGTATTACATGAACATAGAGGTGTTCCAACCTTCTTTGACCA
TATCACATTTTCCACATGGACCCACTGCACAGTTTAGTTTACACAATGTTGTTATGAGAC
ATGATATTATAAATGCTGGTAACCAAAGCGAAGTGAATCCACATCTAATATTTGATAACT
TTACTACCGCTTTAGGGAAAAGAGTAGTCTGTATTTTAAAGCACTTGTTCAATGCGGGGC
CCAAAAAAGATTCCGAAAGAGTAATCACTTTTGCGAATAGGGGTGATTTTCATTAGCGTTA
GACAGCATGTATATGTGAGAACAAAGAGAGGGAGTAGAGATTGCCGAAGTTGGTCCTAGAT
TTGAGATGAGGTTGTTTGAAGTGAAGTTGGGAACCTTAGAAAATAAGGACGCTGATGTTG
AGTGGCAGTTGAGAAGATTCATAAGGACTGCCAATAAAAAAGACTATTTGTGA

YNL075W, 290 aa (SEQ ID NO 232)

MLRRQARERREYLYRKAQELQDSQLQQRQIIKQALAQGKPLPKELAEDESLOKDFRYDQ
SLKESEEADDLQVDDEYAATSGIMDPRIIVTTSRDPSTRLSQFAKEIKLLFPNAVRLNRG
NYVMPNLVDACKKSGTTDLVVLHEHRGVPTSLTISHFPHGPTAQFSLHNVVMRHDIINAG
NQSEVNPHLIFDNFTTALGKRVCILKHLFNAGPKKDSERVITFANRGDFISVRQHVYVR
TREGVEIAEVGPRFEMRLFELRLGTLENKDAADVEWQLRRFIRTANKKDYL

YNL096C, 1418 bp, exon1: 501-644, intron1: 645-989, exon2:
990-1418 (SEQ ID NO 233)

AAACACCTACTTATAGACACGACCAAACCTTCCACAACCTTTCATCAGAGAGAAATGTTG
ATCAAGTTGAATGCGTGAAAGTAGCAATTCGAAACAACAACCTACCTGTCATTCTGCATAG
TAGTAGTTACGAAAGGCACAGAAAATAACAAAAAAGTCAATTTTCTACGGT
CTCCATCCGTACCTCTTTAAATCCGTACATTATTGTTTTGCTTAATTTCAATATTTTCGGA
AAAAGCGAGCGCCCTGGTAAATGTGGTTCAAGCCTGCGAGCCTTTGCTTGGTAACTCAC
CAAATGCAATTCAGTCACGTTCCACACAGTTTGGGTTCAGCCTGGCTTTAGGGAAGAA
TGGGCTCACTAGGCGTTTATAATACGCGGAGGGGAAATACCAAATGCTATTGATTATGG
TTAAATATGTGTTATTTGACTTTGTATATACAAACAGAAGAGAAACCAACACACTAAAG
ACTAGACACATAACTGACCAATGTCCTCTGTCCAATCCAAGATCTTATCCCAAGCTCCAA
GTGAGTTGGAATTACAAGTCGCCAAGACCTTCATCGATCTAGAAAGCTCCTCTCCAGAAC
TAAAGGCTGACTTGAGACCATTGCAATCAAATCTATCAGAGAAGTATGTTAAAAGTTAT
ATAATTTGGAAGCAGCAACATTGTGATTTCTTCTAAAGGGTCTTTGTCAGTAATTTTTT
CAAAAAAGAGTGATTTTGAGCAGTATCTGTATGAAATTTTCATGTGTTGAGAAAAATAG
TAATTCGAGAGCTGTCAATACCATGAACGTTGCGATGAGCCTTTGAACTATAAAGGCCT
CCTTGGTCACTACCAATATCGATGAATAAAATAGAAGCACGCGAAAAAGACCTTACCCCA
AGGAGAAGAATCACAAACCCTTTTTTGTATGAATGAACCAATTCAGTTACTAACTTTAT
TTCAACGCTGCTTGATTCTTATTGTTTAGATTGATGTCACCGGTGGTAAGAAAGCACTAG
TCCTTTTTGTCCCAGTTCCAGCTTTGTCTGCATACCATAAGGTCCAAACCAATTGACCC
GTGAATTGGAAAAGAAATTCCTTGACCGTCATGTTATTTTCTTGGCTGAAAGAAGAATCT
TGCCAAAACCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACTTTGA
CTGCTGTTACGACAAGGTTTTGGAAGACATGGTTTTCCCAACTGAAATTGTCGGTAAAA
GAGTTAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTTGTTAGACTCCAAGGATG
TTCAACAAATCGACTACAAGTTGGAATCTTTCCAAGCTGTCTACAACAAGTTGACTGGCA
AACAAATTGTTTTTGAATTTCCAAGCCAGACCAACTAA

YNL096C, 190 aa (SEQ ID NO 234)

MSSVQSKILSQAPSELELQVAKTFIDLESSPELKADLRPLQIKSIREIDVTGGKKALVL
FVPVPALSAYHKVQTKLTRELEKKFPDRHVIFLAERRILPKPSRSTRQVQKRPRSRTLTA
VHDKVLEDMVFPTEIVGKRVRYLVGGNKIQKVL LDSKD VQQIDYKLESFQAVYNKLTGKQ
IVFEIPSQTN

YNL162W, 1333 bp, exon1: 501-504, intron1: 505-986, exon2:
987-1333 (SEQ ID NO 235)

TTCATCACC AATATAGACTAATGCGTTTTGGAACGCCAAACCGCAGTGACAAATAGCAA
TATGTAGCTGTCATATCGGCATATAATAACAGTTTTCTACCAAATGCTGTCCTACATTCA
GAGATCTTACATCCTTACATCTAAAGTAAAACCTAGACATTTACTTCGAGTTATACTTTT
TTTTTATTTATCTATTTTTTCTCTTGGCGACATTTAACACCTGAATTCCGCCTAACGCCA
GGACTGATCCTGCCAGGGAAGGGAGCTTTGTCTAGTGCCAATAGGCCGGACAGTAGGAA
GGTTACAGCAGCTGGCCCGCAGAGTGATTGGGTACAGGAAATAGCGCAACCTTCTCTTT
TGCCCGGGAAGGCGGTCAATCTACCTTCGAAGGGCTAGTACATGAGCGCGAAGGAGGC
AGATAATAGCACCATTAAAGTGGTCCAAATGCATCTTGAAATCTAATCCTTAATAGAGGAA
ACAACAATTATCAGTAAAAATGGGTATGTTATAACCATAATTCCTAATGGTGAATAAAA

TCAGGACCAATAAAGAAAAGCTAATTTGATTTTATTGTCAATGAAATTTTCATAATCGTC
ATGAATGCATAAACAGACACACCTAGCAACTGTATAATCTGCGCCTAAAAAGGGCGTATA
CACAAAACCTAAACGATGCGCAATAAAAGTTCAGCAGTCAGCAATGAAACCGAGATATGCA
GCAACAGAGTATCATATGCATGGAGGATCCTTTCTGTTTTTCTGATAATATGCTCTGAAA
AAGCTCCAAACAGCACAGTAGCCTATTTGTGAAGCTCAAAAAAGGCTTCTATTTCCCTCG
CTATCTTCAGATTGTGCAGTGATATTCTTTGAGGAAGGAAACGTAGAGGGGATAAGTTGG
ATAACTGTTATTTCTTTTCAATATGCTAGATTTTGCTTACCACCTTACTGATTTTCTA
ATAATAAACTTTTTTACTAACATTAGTACGATGTCTCATCTATTTCTTCTATTTAGTTAA
CGTTCCAAAGACCAGAAAGACCTACTGTAAGGGTAAGACCTGTCGTAAGCACACTCAACA
CAAGGTTACTCAATACAAAGCTGGTAAGGCTTCCTTGTTTGCCCAAGGTAAGAGACGTTA
TGACCGTAAACAATCTGGTTTTCGGTGGTCAAACCAAGCCTGTTTTCACAAGAAAGCTAA
GACTACCAAGAAGGTTGTTTTGAGATTGGAATGTGTCAAATGTAAGACCAGAGCCCAATT
GACCTTGAAGAGATGCAAGCACTTCGAATTGGGTGGTGAAAAGAAGCAAAAGGGTCAAGC
TTTGCAATTCTGA

YNL162W, 116 aa (SEQ ID NO 236)

MVRCLIIYFFYLVNVPKTRKTYCKGKTCRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGF
GGQTKPVFHKAKTTKKVVLRLCEVKCKTRAQLTLKRCKHFELGGEKKQKGQALQF

YNL178W, 1223 bp, CDS: 501-1223 (SEQ ID NO 237)

GGTCCACGTCAGTTCCACACAATAACATTTACGTAGTGTTCACGCGAAGCAGTTACATCT
CAACTAACATAATTGCTGGTGAGCCTACAACACTGCATGCGTAAACGTCAACGGGATTAC
GTTAGTATTTTTGGCCGCCGGTAAATTCTCTTGTTTTTTTTCTTGATTTCACTTCTTTT
CATGTTCCCTTTGGAATAATCTAATTCCTCATGATTAAATGAGACTGTTTTTTGTTTCCGT
AACATCCATACCTTTCCTGTATAATATTCTTGCTGTAAAGTTTGTTTTTTTATGAAAA
AACATTTTCTTTTCTTGAGATGAGGCGCCGCGAGCCTTCTCCCATGGGCAGTGGTAAAT
TTTCCAAATCAATGCAGCTCTTTGAAATACAACAGCATTTTTCATACATTTTAAGCAATT
TCTAGTTTGTAGATATTGTTAGATTAGTTTTTGAACATTGTTTTGATAACTGAAAATAAA
ACAGCAAACAACTACAAAAATGGTCGCTTAAATCTCTAAGAAAAGAAAGCTAGTCGCTG
ACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTGAAGAAGGTT
ACTCCGGTGTGTAAGTCCGTGTCACTCCAACCAAGACCGAAGTTATCATCAGAGCTACCA
GAACTCAAGATGTTTTGGGTGAAAACGGTAGAAGAATCAACGAATTAACTTTGTTGGTTC
AAAAGAGATTCAAGTACGCTCCAGGTACTATTGTCTTATATGCTGAAAGAGTTCAAGACC
GTGGTTTGTCCGCTGTGCTCAAGCTGAATCTATGAAATTCAAATTGTTGAACGGTTTGG
CTATCAGAAGAGCTGCTTACGGTGTGCTCAGATACGTTATGGAATCTGGTGCTAAGGGTT
GTGAAGTTGTTGTTTCCGGTAAACTAAGAGCTGCCAGAGCTAAGGCTATGAAATTTGCTG
ACGGTTTCTTGATTCACCTCTGGTCAACCAGTCAACGACTTCATTGACACTGCTACTAGAC
ACGTCTTGATGAGACAAGGTGTTTTGGGTATCAAGGTTAAGATTATGAGAGACCCAGCTA
AGAGCAGAACTGGTCCAAAGGCTTTGCCAGATGCTGTCAACCATCATTGAACCAAAAGAAG
AAGAACCAATTCTTGCTCCATCTGTCAAGGACTACAGACCAGCTGAAGAACTGAAGCTC
AAGCTGAACCAGTTGAAGCTTAG

YNL178W, 240 aa (SEQ ID NO 238)

MVALISKRRKLVADGVFYAELNEFFTRELAEEGYSGVEVRVTPKTEVIIIRATRTQDVLG
ENGRINELTLLVQKRFKYAPGTIVLYAERVQDRGLSAVAQAESMKFKLLNGLAIRRAAY
GVVRYVMESGAKGCEVVVSGKLRAARAKAMKFADGFLIHSGQPVNDFIDTATRHVLMRQG
VLGIKVKIMRDPKASRTGPKALPDAVTIIIEPKEEEPILAPSVKDYRPAEETEAQAEPEVA

YNL182C, 2168 bp, CDS: 501-2168 (SEQ ID NO 239)

CTTTGATAAATTAATACGGTAAGATACCGTGTGAACCTATTATAATAACTGCCACGCTTAT
AGCATGTACGCTATACATTTACGTGCTGAGCTCCTAGGAAAGCTCATGAGCAGCCACTGT
ATCGTGGAGCATAACTACAACAAAGAATACACAGCGTCACATAGAGGGTTTTTGAGAGGA
GAAGTTGAAATAGGACTTGATCTTGGGGGAGAGGGGATTTGAAAGCACCCATTTCAGGAGT
ATGTGTCTGTAATTGAAGTGTAGCGCGCGATTACCTGTAATAAGAGTGATGATTTGAT
AGCGCCATTCTACATCATATGGCAAATGTTGAAAACTGTACGCGCGAACTAAAATTTTT
TTTTACATCCCACTAAATGAAAATTTTAAATCGATGCCCATTCCAAATATGCTTATTCGA
AGGACGGCTCTGACAAGGGCATATGCGTTAAGATTGATTGTTCAATATTCATAAAACAGG
ATCTTTCAAGGGACGATAAAATGGATGAGCAAGTTATTTTTACAACAAATACCTCAGGAA
CAATAGCTTCTGTACACTCATTGTAACAGATAAATTTGAGGCAATGCTCCACTCAATCAA
GAAATAGCTGTGTTCAAGTAGGAAATAAATACCTTTTTATTGCTCAAGCACAAAAAGCAT

TAATCAATGTCTACAATCTGTCAGGTTCTTTCAAAAGAGAATCTGTTGAACAGCGCTTAC
CATTACCTGAAATCCTAAAATGTCTGGAAGTAGTTGAAAATGATGGTGTGCAGTATGATA
GAATTCAAGGTGTCAATCATAATTTACCAGACTTCAATCTTCCGTACCTTTTACTTGGCT
CCACCGAATCGGGTAAATTGTACATATGGGAGTTAAATTCAGGGATTTTATTGAACGTGA
AGCCTATGGCTCATTACCAAAGTATACCAAGATTAAGTCCATTTTAAACGGCAAGTATA
TTATTACTTCTGGTAACGATTCGAGAGTTATTATATGGCAAACCTGTTGACTTGGTATCAG
CGTCCAATGATGATCCTAAGCCTTTATGTATCCTTCACGATCATACTCTACCCGTGACAG
ATTTCCAAGTTTCTTCTAGTCAAGGAAAATTTTATCATGTACTGATACGAAACTCTTCA
CAGTATCTCAAGATGCTACCATTAGATGCTATGATTTGAGTTTAATAGGCAGCAAAAAGA
AGCAGAAGGCAAACGAAAATGACGTTAGTATTGGTAAGACCCAGTATTGCTTGCGACAT
TTACAACCTCCTTATTCTATCAAATCCATTGTACTGGATCCTGCTGACAGAGCATGCTATA
TTGGTACTGCGGAAGGTTGTTTTTTCATTGAATTTATTTTATAAACTAAAGGGTAATGCTA
TCGTTAATCTGCTACAGTCCGCCGGAGTAAACACAGTTCAAAAAGGTAGGGTTTTTTCCC
TAGTGCAACGTAACCTCACTAAGTGGCGGCGAAAATGAAGATTTGGATGCACTATATGCAA
TGGGCCAACTTGTCTGTGAGAATGTCCTAAATTCAAATGTGTATGCCTAGAAATATCAA
TGGATGGTACATTATTATTGATCGGTGATACGGAGGGGAAAGTTTCTATTGCGGAAATTT
ACTCAAAACAAATCATAGAACTATCCAACTTTAACTACATCACAGGATTCAGTTGGAG
AAGTGACCAATCTCTTAACCAACCTTACAGACTCGAACGTGGAAATTTACTTTTTGAAG
GAGAATCCAAAGGCAAACAACCTAGTAATAATAATGGTCACAATTTTATGAAGATACCAA
ACTTACAAAGAGTTATCTTTGATGGTAAAAACAAAGGCCATTTACACGATATTTGGTATC
AGATAGGAGAACCAGAAGCAGAGACAGATCCTAACCTCGCATTAACCTTAACGACTTTA
ATGCCTATTTGGAGCAGGTCAAAACGCAAGAATCGATATTTTCACATATCGGTAAGGTGT
CAAGCAATGTAAGAGTGAATGACAATAAAATCGACGCCACTTCATCTTTAGACAGCAATG
CCGCTAAAGATGAGGAAATTACAGAACTTAAGACCAACATAGAAGCATTAACCTCATGCCT
ACAAGGAGTTACGTGACATGCACGAAAAGCTGTACGAGGAACACCAACAGATGCTTGACA
AGCAATAA

YNL182C, 555 aa (SEQ ID NO 240)

MDEQVIFTTNTSGTIA SVHSFEQINLRQCSTQSRNSCVQVGNKYLFIAQAQKALINVYNL
SGSFKRESVEQRLPLPEILKCLEVVENDGVQYDRIQGVNHNLPDFNLPYLLLGSTESGKL
YIWELNSGILLNVKPMHYQSITKIKSILNGKYIITSND SRV I IWQTVDLVSASND DPK
PLCILHDHTLPVTD FQVSSSQGKFLSCTDTKLF TVSQDATIRCYDLSLIGSKKKQKANEN
DVSIGKTPVLLATFTTPYSIKSIVLDPADRACYIGTAEGCFSLNLFYKLKGNAIVNLLQS
AGVNTVQKGRVFSLVQRNSLTGGENEDLDALYAMGQLVCENVLNSNVSCLEISMDGTL LL
IGDTEGKVSIAEIIYSKQIIRTIQTLTTSQDSVGEVTNLLTNPYRLERGNLLFEGESK GKQ
PSNNNGHNFMKIPNLQRVIFDGKNKGHLHDIWYQIGEPEAETDPNLALPLNDFNAYLEQV
KTQESIFSHIGKVSSNVKVIDNKIDATSSLD SNAAKDEEITELKTNIEALTHAYKELRDM
HEKLYEEHQQMLDKQ

YNL190W, 1115 bp, CDS: 501-1115 (SEQ ID NO 241)

AATGCGCTCCCGTACGTCAGTGGCTGTTGCTGAAACGAGACAATTTCTCAATTCGTTTGT
TTGTGTACTGTATTTGTTATCTTTACTATATATATGTTGTTAAGTTTCTTTTACCAATTA
GTGCTCACTTCTCTCGTCTTTTATTAGGTGTGTGTGTTGTGCGTAATTTTCGTTTCGCTG
ATTACTTTATATAGTGTAGTTTGTTCCTGAATGTAATAAAGACTTCTGTTTTATTTTGT
TTGTTATTTAGAAACAGTCTATCTGGTTTAACTTAAACGAGTGAGCTTAAGATAATCTGA
CTACAAGAAAACCAAGCTTCTATTACTTTGTTTCTTCTCTTTTTTCTTTTTTGAATAAA
GAATTTTCTTTAAGGAGTAACTTAAAGCATTTAGCTGCACATTAACACTTTTTTTTTTA
CTTCTAACTCACACACTTTTGAAGAACATTTATTTTTTCGACCTTCTTTCCCAAATACC
CAGCGCTTTATAAATTGAAATATGAAGTTCTTCTGTTACTGCTATTACTCTAGCCACCG
TTGCCACCGTTGCCACTGCTAAGAAGGGTGAACATGATTTCACTACCACTTTAACTTTGT
CATCGGACGGTAGTTTAACTACTACCACCTCTACTCATACCACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACCCCAAACCACTGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
TCAACAAGACTTCCAAGTCCAAGACTCCAAACCATACCGGTACTCACAAGTACGGTAAGT
TCAACAAGACCTCCAAGTCTAAGACCCCAAACCATACCGGTACTCACAAGTATGGTAAGT
TCAACAAAACCAAACATGACACTACCACTTATGGTCCTGGTGAAAAGGCCCGTAAGAACA
ATGCCGCCCCCTGGTCCATCTAATTTCAACTCCATAAAATGTTTGGTGTACCGCTGGTA
GTGCTGCCGTAGCCGGTGCCTTATTACTATTATAA

YNL190W, 204 aa (SEQ ID NO 242)

MKFSSVTAITLATVATVATAKKGEHDFTTTLTLSSDGSLLTTTSTHTTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTSKS
KTPNHTGTHKYGKFNKTSKSKTPNHTGTHKYGKFNKTKHDTTTYGPGEKARKNNAAPGPS
NFNSIKLFGVTAGSAAVAGALLL

YNL208W, 1115 bp, CDS: 501-1115 (SEQ ID NO 243)

GGTTATACACATATATATATATTTTTCATTTTAAATGTCTTAGCTTTTGTATCTTAGATGAA
GTTTTAGTTCTGTATATCACGATCAAGATATCATAAATCAATTATTCTTCT
GTTTCCCCTCTTGAGGCATCAAACGAGTGTGACTGATACACACCAACATACTAAGGCA
ACTTTTCTGGCTGCCCAAAGCTGTGGCACGTATGAACTGCTTTTCGGCTGCATAAAACA
ACCATGTGGAGTTTTTACTGTATTTCGCATTTTCGCCCCGCTAGCATTCTTCGTTTCATGCTA
AAAATGAGGCGTGGGCTAATATTCAGTATTAATAATTCGGGCACCCGCACAGCCCATACC
GGAAAAGGGGCTGGCTGTTGGGCTTGGCAAAAACTCAATCTGAGCAGTCATTTATAAAG
AAAGACTTTAATTTGTCTTGCTAAACACTTGTAAGCCTTCCAAATATAGATCACTTAAGA
CAATCTAACAAGTGTCCAAAATGTCTGCAAACGAATCTACTCAAGTGGCCAACAAGGTC
AATATAACCAGCAAAACAACCAAGAAAGAACTGGTGCTCCAAACAACGGTCAATATGGTG
CCGACAATGGTAACCCCAACGGTGAACGTGGTTTATTTTCCACTATTGTAGGTGGCAGTG
CCGGTGCCTACGCTGGATCTAAGGTGTGCAACAACCATCTAAGTTGAGTGGTGTGCTGG
GCGCCATAGGTGGTGCATTCCTTGCCAACAAGATATCTGATGAGCGTAAAGAGCATAAGC
AACAAGAGCAATACGGCAACTCAAACCTCGGAGGTGCTCCTCAAGGTGGACACAACAACC
ATCACCGTCAGACAATAACAACAATAACGGTGGATTGCGCGTCCAGGCGGCCCTGGCGG
TCAAGGTTTCGGAAGACAAGGCCACAAGGATTTGGAGGTCCCTGGTCCACAAGAGTTTGG
TGGTCCAGGTGGCCAAGGATTCGGTGGTCCAAATCCTCAAGAATTCGGCGGCCAGGTGGC
CAAGGATTCGGTGGTCCAAACCCTCAGGAATTCGGGGGCCAAGGTGCTCAAGGATTCAAT
GGCGGTTACGTTGGTGAATGGCTCAACAGAGTGA

YNL208W, 204 aa (SEQ ID NO 244)

MSANEFYSSGQQGQYNQNNQERTGAPNNGQYGADNGNPNGERGLFSTIVGGSAGAYAGS
KVSNNHSLSGVLGAIGGAFLANKISDERKEHKQOEQYGNNSNFGGAPQGGHNNHHRQTIT
TITVDLAVQAALAVKVSEDKAHKDLEVLVHKSLLVQVAKDSVVQILKNSAARWPRIRWSK
PSGIRGPRSSRIQWRFTLVNGSTE

YNL210W, 1313 bp, CDS: 501-1313 (SEQ ID NO 245)

TCATAACGGGTTCTTTTCAAAAAACCGTAAAAATTTGAGGTCACACCAACTAAATACAAA
TTGTTTCATCACGGTGACTATATCAAGAACTTCGTAAGGAAACATTTAGAAAACCTCAATA
TAGTAAAGTTTCATCAGCAATCTTATCTGAGTAATATTATCTACGATCTAAATATAGGAT
GATCTGCCGATTTAGGAATCGTACTGTAGATTGCTCTTGGCGACAGATATAGTGAAATAC
CTTTTACAAAGTGGATACAGGTGCTTATCACTACCGCCATTTCACTAGCAAGTAGAGTA
TTGAGAAAACGGTAAACTTTGAAAGTTGCAGATGCAGAATATATATCTGGTTTTGTAGTT
CTATCCGCTAAACGGGACGATCGCATTTTAGCCGCCGACAGTGTTAATATAAGTAATGAA
CTTGGGTTAATTTGATTACGCGTCACAGCTACTAATAAAATAAGACCGAGAGTTTTAATC
AGCTAGTGCATACCAAAACAATGAGTAACCAACACAGCCCTCAGCCATTTTGTGTTGGACA
CCAAATTGGTGAAACTATTAGAAGAGCTCCAGGAGGGAAAGCAATTCAACAATAAAAACA
TATTCCCGGAAAAAGCATTATATTTGAAGCTCGCTCTTGATTATTCTTTCTTCAGAAAGA
ATTTACTAGAGTTTTGCGTCCACCTTGACAAGATAAAAGGAGTCATTAGACCAAACTATG
ACACTATATATATTTTGTGCCTGTTGGAGGTGGATCTCCTCAATCTGGTATTTACCGACA
ATATATTGGAAATATGTTTGCCAGGTTTGTGTTCAAGGGAGGACTTGAGGGTTTTTAATA
ATACTTTTTACACATATCACGATAACCGCCTACGTATTCTCCAAGAAGACTTTTCTCAAT
TGTTCAAAAAAATCAAAACTAAGGCTTCTGTACTATGTTTTACAGTTGAGGAAATTTTC
TGACAAACCAAGAAATTTTACCTCAAACTCAACAGTGGCAGAACTGCAAAAGAGCACTA
ATAAAGTACAGACAAATGGGCCGCAACGGCACGATTTTCATAGTCACTCTAGAAATAAAAC
TGAACAAAACACAAATCACTTTCCTCATTGGAGCTAAAGGAACGAGAATTGAAAGCTTGA
GGGAAAAATCAGGCGCCAGCATAAAAATAATACCTATTAGTGATAAAATGACTGCACATG
AAAGGAACCACCTGAATCTGTTCAACAAACAATACTAATTTCGGGTGACTTATACTCAA
TTGCATTAGCCGTCACCAGTATAGAGTCTGCATTAATTACTTTGGATTATAG

YNL210W, 270 aa (SEQ ID NO 246)

MSNQHSPQPFCLDTKLVLLEELQEGKQFNNKNIFPEKALYLKLALDYSFFRKNLLEFCV
HLDKIKGVIRPNYDTIYILCLLEVLLNLVFTDNILEICLPRFVSREDLRVFNNTFYTYH

DNRLRILQEDFSQLFKKIKTKASVLCFTVEEIFLTNQEILPQNSTVAELOKSTNKVQTNQ
PQRHDFIVTLEIKLNKTQITFLIGAKGTRIESLREKSGASIKIIPISDKMTAHERNHPES
VQQTILISGDLYSIALAVTSIESALITLDL

YOL031C, 1766 bp, CDS: 501-1766 (SEQ ID NO 247)

AGTTTTTTTTCTCGAGAAATTGTGAACAAAAGAAAGCAAAGACACAGAAGATGATAAGAG
AGAGAAACAACGAAGAAAGAAACAACAATGTTGGGGTTCACCCGAGAGATATTGACATACT
GACCTTAGAAAAGGCATTACTGAGGCTACTGACTAAAGCGCGTTACATAAATGCATAGTA
TATTTCTTGTGTATACGCAGCGGCCAACTAGTGGCAGCAAGAATGTAATGAACGATTCA
TCTGCAGGTTTGGAGGCCGCAACTAGATCAAAACGTAAATAGCGGGTGAAGTGTCTGGA
CGTTAGAAGTAACGTCCGCAGATCGAAGCTAAACACGAGATTAGATTTCTGGGTAAACGGAA
TTGTGATAATTAAGAAAGACCAGACTATGTGAAAAGGCCACGTAAATGATAGAGCACACA
TTAGCAACTATAATAGACTAGTTTTTCGCATCGCTGGAAGTTCTCGATATTGAATATCACT
TCCAAGAACGCAAACTTAGAATGGTCCGGATTCTTCCCATAATTTTGAGCGCCCTATCTT
CGAAATTAGTGGCGAGTACAATATTGCATTTCATCCATACACTCAGTGCCATCTGGAGGCG
AAATCATATCTGCAGAAGATCTTAAAGAACTTGAAATTTTCAGGGAATTCGATCTGCGTTG
ATAATCGTTGCTATCCTAAGATATTTGAACCAAGACACGATTGGCAGCCCATACTGCCAG
GTCAAGAACTCCCCGGTGGTTTGGACATTAGAATAAACATGGACACAGGTTTAAAAGAGG
CAAACTAAATGATGAGAAGAATGTCCGGTGATAATGGTAGCCATGAGTTAATTGTATCTT
CAGAAGACATGAAAGCATCGCCTGGTGACTATGAATTTTCCAGTGATTTCAAAGAAATGA
GAAACATCATAGATTTCTAACCCGACTTTATCTTCACAGGACATTGCCAGATTGGAGGATA
GTTTTGATAGAATAATGGAATTTGCGCATGATTACAAGCACGGCTACAAAATTATTACCC
ATGAATTCGCCCTCTTGGCCAACCTTAGTCTCAATGAAAATTTGCCGTTAACATTGAGAG
AGCTCAGTACTAGAGTCATTACCAGCTGCTTGAGAAACAATCCTCCTGTAGTCGAGTTCA
TTAATGAAAGTTTTCCAAATTTTAAAGCAAAATCATGGCCGCTCTGTCAAATTTGAATG
ATTCTAACCACAGATCCTCTAATATCCTAATAAAAAGATACTTGTCCATTTTAAACGAAT
TACCTGTACATCCGAAGATCTTCTATATACTCTACGGTTGTTTTACAAAATGTATATG
AAAGAAACAACAAGGACAAACAGTTACAAATAAAAGTCCTGGAGTTGATCAGCAAAATTT
TGAAGGCCGACATGTACGAAAATGACGATACAAATCTAATTTTGTTCAAAAGAAATGCTG
AGAATTGGTCGTCAAATCTGCAAGAGTGGGCAAACGAGTTCCAAGAGATGGTCCAGAACA
AAAGTATAGATGAACTACATACAAGAACGTTTTTTTGACACCCTTTACAACCTGAAGAAAA
TTTTTCAAAGTGACATCACGATCAACAAAGGGTTTTTTGAATTGGTTAGCGCAACAATGTA
AAGCCAGGCAATCTAACTTGGACAATGGGCTCCAAGAGAGAGATACTGAACAAGACTCAT
TTGATAAGAACTTATCGACAGCAGACACTTGATCTTTGGCAACCCCATGGCTCATAGAA
TAAAAAATTCAGAGATGAACTCTGA

YOL031C, 421 aa (SEQ ID NO 248)

MVRILPIILSALSSKLVASTITLHSSIHSVPSGGEIISAEDLKELEISGNSICVDNRCYPK
IFEPRHWDQPILPQGELPGGLDIRINMDTGLKEAKLNDEKNVGDNGSHELIVSSEDMKAS
PGDYEFSSDFKEMRNIIDSNPTLSSQDIARLEDSFDRIMEFAHDYKHGYKIITHEFALLA
NLNLNENLPLTLRELSTRVITSCLRNNPPVVEFINESFPNFKSKIMAALSNLNSNHRSS
NILIKRYLSILNELPVTSEDLPYISTVVLQNVYERNNKDKQLQIKVLELISKILKADMYE
NDDTNLILFKRNAENWSSNLQEWANEFQEMVQNKSIDELHTRTFDFTLYNLKKIFKSDIT
INKGFLNWLAAQQCKARQSNLDNGLQERDTEQDSFDKKLIDSRHLIFGNPMAHRIKNFRDE
L

YOL048C, 821 bp, CDS: 501-821 (SEQ ID NO 249)

TAAGTACATGATTTTTGTGTTGCATTGATATGACTTGTTTTATGACTAACATATTTAATTT
TTATTTGTTAACCGTAGGGGTTTTATGAAGTGCTGACGAATCCTGTTTATTGGAAGCATA
TTTTACTGTTTGCGGTTTGCTATGCCCTGATTTTTGTCACTATTGCTGGTCTCTTTTATG
TCACACTTGTACCGCTTTTAGTGACATGGGCCATACTGTTATTAGGGCCTCTTGGTGTGA
TACTGGTTCATATTCAATGGATTTTACAAACGAATGTCTTGACTGCCTTTGTTTGTAGAA
CACTGGTCCTGACCCATATTACGAATCAGATATTTGATATATCTTTGGTGTGCAAGACC
AAGATGAATTTCTAAACGAGGTGAAGGTATTGCCTAAACCACAAAAGCCACATAGAAAAA
TCGATGAACCTGATGCGGTGAGAAATTTCAACACAATAAAGGGAAGTCGGATTTTTAAGA
TTCCCAGATTACTATTGAGAAATGTTTTTAAAGTCTCCAATTTTACTTCACTAACATTAC
TGTCGCTAATTCCTATTGTAGGACCAATCTTGGCAAATCAACTAATGGCCCCAAAAGAA
CCTTTACCTATTTGCAGAGGTACTTTTTACTAAAGGGATTCAGTAAGAAACAGGCCAAAG
ATTTTCAGTACGAGCATTACGCAAGTTTCATATGTTTCGGTATGTCTGCCGGTCTACTAG
AGTTAATACCCTTCTTCACAATAGTCACCATATCTAGCAACACTGTTGGTGCAGCTAAAT

GGTGTACTTCGCTACTAAAGGGTGAAAGAAAGAAGGAATGA

YOL048C, 106 aa (SEQ ID NO 250)

MFFKVSNFTSLTLLSLIPIVGPILANQLMAPKRTFTYLQRYFLLKGFSKKQAKDFQYEHY
ASFICFGMSAGLLELIPFFFTIVTISSNTVGAANKWCTSLLKGERKKE

YOR010C, 1256 bp, CDS: 501-1256 (SEQ ID NO 251)

ACATTTCCCAAAAAAGACATTTCTGTCCAAAAGTAGAAGGCAAGAAAACCCCTGGAGGAAT
CATAGGCAAAGAAAGAAAAGAAGAAGTTCATCTTTAAACTACCTTTCAAGCCTTTATTC
GTTCTCGTAAAGGACACACGAAAAAATAAACAGTACCTTGCAGAAGGAGTGCAGAGTT
AGGTTCGAGGGAATCCTTGAAAGCCAAGAGTTTTTTTTCCGTAATGATCTCCCAAAGCAA
CCATCAACATTGTGGTGCAAAGTTTAGTGTAAGATGTTCTACTGAACTATCTTAATAGCT
GAGCATCATGTGAGTAAACGAGTAAGCAAGAAAACAACAAAGTAATGTTCAACTTTCGTA
ACTACGAAAATAATATATAAGTAGTTAACGAAATTCGAACAATGAGAGCTCTCACATAT
CATCTTCTTTTCCAGTTTAGCCATTATCAGCACAATAACAAAACACACTCGTACACTC
GCTTCAACTATAACAAAAAATGGCTTACATCAAGATCGCTTTATTAGCTGCTATCGCTG
CTTTGGCTTCTGCCCAAACCTCAGGAAGAAATTGACGAATTGAACGTTATTTTGAATGACG
TTAAGTCCAACCTTGCAAGAATATATTAGTTTGGCTGAAGATTCTTCATCTGGATTTTCCT
TAAGCAGTCTGCCATCTGGTGTTTTAGACATCGGTTTAGCTTTGGCTTCCGCCACTGATG
ACTCCTACACTACTTTGTACTCTGAGGTTGACTTTGCTGCTGTTAGCAAGATGTTGACCA
TGGTTCCATGGTATTCTTCCAGGCTTCTACCAGAATTGGAATCCTTGTTAGGAACCTCTA
CCACCGCTGCCTCTTCTACTGAAGCTTCTTCTGCTGCTACTTCTTCCGCTGTTGCTTCCT
CCAGTGAAACTACTTCTTCTGCCGTCGCTTCCCTCCAGTGAAGCTACTTCTTCTGCCGTCG
CTTCTTCCAGTGAAGCTTCTTCTTCTGCTGCTACTTCTTCTGCTGTCGCTTCTTCCAGTG
AGGCTACCTCTTCCACCGTCGCTTCCCTTACCAAGGCTGCCTCTTCCACTAAGGCTTCTT
CCTCTGCTGTTTCTTCCAGCTGTTGCTTCTTCCACCAAGCCTCCGCCATTCTCAAATCA
GTGATGGTCAAGTTCAAGCCACTAGCACTGTTTCCGAACAACTGAAAACGGTGCTGCCA
AGGCTGTCATCGGTATGGGTGCTGGTGTATGGCCGCTGCCGCCATGTTATTATAA

YOR010C, 251 aa (SEQ ID NO 252)

MAYIKIALLAIAALASAOQTQEEIDELNVILNDVKSNIQYISLAEDSSSGFSLSSLPSG
VLDIGLALASATDDSYTTLYSEVDFAAVSKMLTMVPWYSSRLPELESLLGTSTTAASST
EASSAATSSAVASSSETTSSAVASSSEATSSAVASSSEASSAATSSAVASSSEATSSSTV
ASSTKAASSTKASSSAVSSAVASSTKASAIQISDGQVQATSTVSEQTENGAAKAVIGMG
AGVMAAAAML

YOR019W, 2693 bp, CDS: 501-2693 (SEQ ID NO 253)

CATTGATCTCGAGCACAGCTGCTCTTTTCTCTCAATGAATTACGTTATATGTTAATCACA
CAAGCATCAGTTTTTCATCGCAAAGAAAATATTTAGAGTTCTTGCAATTCAGATGTACC
TCAATTAATAACTCAATCACCTCCTATGTTCTTGCTGGTAGTACTGCTTTTGTCTTAATT
ACTGCTGAATCAGCCTTCTAGAAGACCGTTCTGTTTTCAGCCGCTCGCCCTTTTCAAAGC
TTGCGCGGCTGAGTTTTATGAGGGGCGGCTTTTTTGTGAATGGCAATCTACCATTATTAG
TAGCAATATGATTTGCAGATAGATACATATATATCCTTCTGGGTTTCATGTCTCGTTACCA
TCCACACTAATGCATAGGACCAGAAAGAAAGGACATCGAATCCAACACGTATTAAAATAA
GGACTCCTCATTAATAAGGCTTTTAATATTCAACTTGCTATAGATCACGCACCCTTTTGG
CAAGTCAACCTTAAATTATTATGATTTCTGTTTGCCCAAAAATGACTTGCAAAAATGCT
ACAGAAGCCTCACATTTCGATGTTCCAGGACAACAATTCGAAGAGAGAAATGAACAAAACC
TTAAAAAACGGGCCAAAAGAAAGGCAGTTTCCAACCATCTGTTGCCTTTGACACAGTGC
CTTCCACCGCTGGTTATTCTTCTATAGACGACAGCAGGGAAGGATTCAAAGGTGTACCTG
TTCCCAACTATTACACGATGGAAGAGTGCTATGACGATGAAACAGACTCTTTTTCGCCAA
ATTTGCAATATTATTGAGAGATACATTCCAATCATCACCTTTTCTGAATACTAGAAAAG
AGAACAAATCTGAATCCAGTAGTTTCCAATGAGATCCTCAAAGTTGTTGGAAGAATTT
CTGACATCAAAAAATATTTCTTGGTATCCAAGAATGGAAAAATAGTGAGGAGAGACTATC
CAAGCACGCCAGTAATTGTCAACGAAACGTTGATGATAAACAGGTTTGAAAAGAACTGGA
TAAAGTTATGGCGCCAAAGAAAACATAAAATAAATGAAAGGCTGAATGACAAAAAAAT
GGTTTACTTACCCAGAACTTATCTTCTGGAAGAGCGTATTAAACCGTTATATAGAGGAG
ATGATAGTGCACCATGTACAAAAGAACAAAAAGAAAGCATAAATACTTCAACAAAAGG
TCGGATATCCCAATAACCTAAGACAATAGTTTGTACATTAAACGGAAAAAACATACGT
GGGTTGCCCTAGACTGGACAGTCTACAAGTTTGCACGAAATCTTGATCACATTGTTGTCA
TAACTACACTGCCAAAATGATTTCTAACAGGAAAAAACTGCAAAAGATGATACAGAAT

GGGCACCGGGATATCAAAAAGAAGTAATAGATCAAAAATTAAACGACATTTTTGATTATA
TTTTACAGCTAGTAAAAGTGGTCAAAATATCCGTCAAAATTACTTTAGAAATAATTGTAG
GCAAAATTAAAAAAGTCTGGTAGATGTCATTAATGTCCATACTCCAGATTTCTTAGTTC
TTGCTACTTTAAAGCACGAGCGAAATGAGAATCTTATTACATATAAATCCAAAAGCTGA
CAGATGTCTTTCCCTGTTAGTTATCCGATTTCCACATTTGTTGTTCCCTCGAAACGAATGT
ATTCGTTTCGAACCTGAATCTACAAAGAGAAGTAAATGAACATTATGTCTCAAAAAATCATA
TGAAGCACGAACACACTGACGTTGAGAGCATGAGCAGTTCAATGTTCAAAAAAATACAA
TATCAGATATTTCTTCACATATTTCCGTAGATTCGTACGCCGAAGATTTCAAAGGCAAG
GCTACATCAAAAAGCAGTTCAACACCTCTAATGATTCCATTCCAAGAAAATTGACCGGTC
TCGCCCAGCATTCAAGAAGGAAGATCACGGGTGATATAGAAAAATTACAAGACGATGAGA
AAGATAGAGAATGTACTAAGGAAAACTTTTGTGTAAGAAAATTGATATCATAATTAGAG
AGTCATTGAAGTCTTCTTTAGCGATAGAGACGTTGCCTGGTAAAAATGTATCGCAGTCCA
GTCACGGTGACCAAATTTCCAGCTTTAAGAATGCTTTGATAGGCAATGGGTCGAAAAACA
CAAAGTTTAGAAAATCTTTAATACCATATTTCTTCTCAGAGGAACAAAATACCACAACAA
CTATTAACTCAGTAGCTCGCTACGTCCCAAATCAAGTTTGCAACCTCTGTAAACACA
AAGATGGAAGAGCCGCCCTTGGCAAAGCCAGAAATCTGCCTGATATAAGGCACAGTATTT
CCTTCGACAAAGAAAATTCCTTTGATCCATCTGATAAAAGCAGTAGTGTGATAATAGCA
TTCCTTTGAGGAAAGTTAAAAGTGCCGGTGCGTTAAGAAAAGTCAAACTAATGACTCCT
CAAGTAGTGCAGGGTCAAAGAAAAGCTCGTCTAGTTTTAGTACTGTGAACACCTTCACTG
GGGGTGGAGTTGGGATTTTAAAGGTGTTTAAAAGTGGAAGTTCCTCTGGAAATAAATCAT
CCAGTAGAAGGAATAGTAGCAGTGGCGATGTTTTTGAAAGTGATGATCGTAACGACAAGA
AAAAGAAGAAGAAAAAAGAAGAAATCATTTGTTCTTATTCGGCAAAATATGA

YOR019W, 730 aa (SEQ ID NO 254)

MISVCPQNDLQKCYRSLTFDVPQQFEERNEQNLKKRAKKKGSFQPSVAFDTPVSTAGYS
SIDDSREGFKGVPPVNYTMEECYDDETDSPNLYLRDTFQSSPFLNTRKENKSESS
SFPMRSSKLLKNSDIKKYFLVSKNGKIVRRDYPSTPVIIVNETLMINRFEKNWIKLWRQR
KLQINERLNDKKKWFTYPELIFSEERIKPLYRGDDAPCTKEQKRKHKILQOKVGYPNP
KTIVCHINGKKHTWVALDWTVYKFARNLDHIVITTLPKMISNRKKTAKDDTEWAPGYQK
EVIDQKLNDIFDYILQLVKVKISVKITLEIIVGKIKKSLVDVINVHTPDFLVLATLKHE
RNENLITYKSKKLTDFVPVSYPIPTFVVP SKRMYSFELNLQREVNEHYVSKNHMKHEHTD
VESMSSSMFKNTISDISSHISVDSYAEDFKRQGYIKKQFNSTNDSIPRKLTLGLAQHSRR
KITGDIEKLQDDEKDIRECTKEKLLKIDIIRESLKS SLAIETLPKKNVSQSSSHGDQIS
SFKNALIGNGSKNTKFRKSLIPYSSSEEQNTTTTIKLSSSPTSQIKFATSVKHKDGRAAL
GKARNLPDIRHSISFDKENSFDPSDKSSSVDNSIPLRKVKSAGALRKVKTNDSSSSAGSK
KSSSFSTVNTFTGGGVGIFKVKSGSSSGNKSSSRNSSSGDVFESDDRNDKKKKKKKK
KKSFLFLGKI

YOR027W, 2270 bp, CDS: 501-2270 (SEQ ID NO 255)

AATTTTCCCCCGTCATAAGTTCCTATACACGGCTGGCTCTGATGGCATAATTTTCATGCT
GGAACCTACAAACCCGCAAGAAAATAAAAAATTTCCGCAAATTTAACGAAGACAGCGTGG
TTAAAATTGCTTGTTTCGGACAATATCTATGTCTGGCAACTTCTGATGATACTTTCAAGA
CAAACGCCGCAATTGACCAAATTTGAACATAACGCAAGTTCAATATACATAATATTTG
ACTATGAGAACTGATATCTTCGTGAAGATTTCGTGTAGTATGATAGAACATTCAGAAAAA
AAATTCAGATTCATCGCTCTCTCTTCGCTTCTCCTCCTTTAAGGAATAAAGAAAAAATCA
CATACATAGATTAAGTAAATAGGATCTGCTAGAAAAATTATATATAGATCAATCATCTTA
TTAAGGTATCTTGTTTAAGCCCAAAAGTCTGCTCCCAAATTCCTCACTGTAGCTACTAAA
ACAACCTATACGCAAGAAAGATGTCATTGACAGCCGATGAATACAAACAACAAGGTAACG
CTGCATTTACCGCTAAGGATTACGATAAAGCGATAGAGCTCTTCACTAAAGCTATTGAAG
TTTCTGAAACTCCAAACCATGTTTTATATTTCTAACAGGTCCGCCTGTTATACTTCTTTAA
AGAAATTTAGTGACGCATTGAATGATGCTAATGAATGTGTCAAATCAATCCATCTTGGT
CTAAGGGTTATAATAGACTCGGTGCCGCCCACTTAGGTCTTGGCGATCTCGACGAAGCTG
AAAGCAACTACAAAAAGCCTTGAGATTGGATGCCAGTAACAAGGCCGCCAAAGAAGGAT
TGGATCAGGTTTCATCGTACCCAACAGGCAAGACAGGCACAGCCTGATTTAGGGTTGACAC
AGTTGTTTGCTGACCCAAATTTAATTGAAAATTTAAAGAAGAACCCTAAACTAGCGAAA
TGATGAAGGACCTCAATTAGTGGCTAAACTGATTGGGTACAAACAAAATCCGCAAGCTA
TTGGCCAAGATCTGTTTACTGATCCAAGATTAATGACCATCATGGCTACATTGATGGGGG
TTGATTTAAACATGGATGATATAAACCAATCAAATCCATGCCAAAGGAACCGGAAACCA
GTAAAAGCACTGAACAAAAGAAAGATGCTGAACCACAAAGCGATTCCACTACGAGCAAGG
AAAATTCCTCTAAAGCACACAGAAAGAAGAAAGTAAGGAATCCGAGCCAATGGAAGTTG

ATGAAGATGACTCTAAAATTGAGGCCGACAAGGAAAAGGCCGAAGGTAACAAGTTTTACA
AGGCACGTCAATTCGATGAAGCTATAGAGCACTACAACAAGGCGTGGGAAGTGCATAAAG
ATATTACCTATTTAAACAACCGTGCTGCTGCTGAATACGAAAAAGGCGAATACGAGACAG
CTATTTCTACCTTGAATGATGCTGTTGAGCAAGGTAGAGAAATGAGAGCGGATTACAAGG
TCATTTCCAAATCATTGCGCGTATTGGTAATGCCTATCACAATTTGGGTGACTTGAAGA
AACTATAGAATACTACCAAAAATCATTGACCGAACATCGTACTGCTGACATTTTGACCA
AGTTAAGGAATGCTGAAAAAGAATTGAAGAAAGCTGAGGCGGAGGCGTATGTTAACCCTG
AAAAGGCGGAGGAAGCCCGTCTTGAAGGTAAGGAATATTTTACCAAGAGTGATTGGCCGA
ATGCTGTTAAGGCTTACACTGAAATGATCAAAAGGGCACCTGAAGATGCTAGAGGATATT
CTAATAGAGCTGCTGCACTAGCGAAGTTAATGTCTTTCCCTGAAGCTATCGCAGATTGTA
ACAAAGCCATTGAAAAAGATCCAAATTTCTGTGAGAGCTTATATCAGAAAGGCCACCGCAC
AAATTGCTGTTAAAGAATATGCTTCCGCTTTGGAAACACTAGATGCGGCCAGAACCAAAG
ATGCTGAAGTGAATAATGGTTCTAGTGCAAGGGAAATTGATCAACTGTACTACAAGGCAA
GCCAACAAAGATTCCAACCTGGTACCAGTAACGAAACCCAGAAAGAAACCTATCAAAGGG
CCATGAAAGATCCTGAAGTGGCTGCGATCATGCAAGATCCTGTTATGCAAAGTATTTTGC
AGCAGGCCCAACAGAATCCCGCTGCTTTACAAGAACACATGAAAAATCCAGAAGTATTCA
AAAAGATTCAGACGTTGATCGCTGCTGGTATCATCCGGAAGTGGCCGCTAA

YOR027W, 589 aa (SEQ ID NO 256)

MSLTAD EYKQQGNAAFTAKDYDKAIELFTKAIEVSETPNHVLYSNRSACYTSLKKFSDAL
NDANECVKINPSWSKGYNRLGAAHLGLGLDLEAESNYKKALELDASNKAAKEGLDQVHRT
QQARQAQPDGLTLQLFADPNLIENLKNPKTSEMMKDPQLVAKLIGYKQNPQAIGQDLFT
DPRLMTIMATLMGVDLNMDINQSNMPKEPETSKESTEQKKDAEPQSDSTTSKENS SKAP
QKEESKESEPMEVDEDDSKIEADKEKAEGNKFYKARQFDEAIEHYNKAWELHKDITYLNN
RAAAEYKGEYETAISTLNDAVEQGREMRADYKVISKSFARIGNAYHKLGLDLKKTIEYYQ
KSLTEHRTADILTKLRNAEKELKKAEEAYVNPKEAEEARLEGKEYFTKSDWPNAVKEY
EMIKRAPEDARGYSNRAAALAKLSFPEAIADCNKAIEKDPNFVRAYIRKATAQIAVKEY
ASALETLDAARTKDAEVNNGSSAREIDQLYKASQORFQPGTSNETPEETYQRAMKDPEV
AAIMQDPVMQSILOQAQONPAALQEHMKNPEVFKKIQTILIAAGIIRTGR

YOR031W, 710 bp, CDS: 501-710 (SEQ ID NO 257)

CTGCAGAAGTACAGCTGCCTTTATTTCTTGTGGTCATTTATTGCTTTTATTTTCAAGTCA
GATATACAAGAAAATCAAATCCCATCGTCAACGTCACGTATAAACGATTAATTTACAGTA
ATACCATACTCTACCAACATTATTTTAGTCCGACGTTCAAGTCTGTAGGTGTTCCAAATC
CTTCTGGCATTGACTTCTGTGCAGAAACCTTCAAATGAGTTCACCTTTACGTCAGATC
GCATAACAACCGGTCATATATTTTTTTCTTTTGCTAAACCCCTACTGCAAGCACTTTTA
AGAAAAAGACAATAAATGCGTCTTTATTGCTGTGTGGAAGTGATTTTGTCTTTCCGGAC
AAAAAAAGGATAGGGATGCGAGAGGGCTGTGAAGTAGTGATCAAGCGGGGCTATATAAG
AAGGGCGCACATCGTCCCCCTAAGAATAGCGAAGCGATATTACACTGAACACTACAATG
TCAAATAGTACTCAATAAATATGACTGTAAAAATATGTGACTGTGAAGGCGAATGTTGTA
AGGACTCTTGTCAATTGTGGGAGCACCTGCCTTCCAAGCTGTTCTGGCGGTGAAAAGTGCA
AATGTGATCACAGCACCGGAAGCCCTCAATGTAAGAGTTGTGGTGAAAAATGCAAATGCG
AAACCACGTGCACTTGTGAAAAGAGTAAATGCAATTGTGAAAAATGTTAG

YOR031W, 69 aa (SEQ ID NO 258)

MTVKICDCEGECKDSCHCGSTCLPSCSGGEKCKCDHSTGSPQCKSCGEKCKCETTCTCE
KSKCNCEKC

YOR096W, 1474 bp, exon1: 501-644, intron1: 645-1045, exon2:
1046-1474 (SEQ ID NO 259)

AAACCCATACACAATGAACCTTATCACACCCAAACATATGATATGGTATTAAAAAATGAA
AAAAATTCAATTATCTTTAGCGTAATTATTGAAGAAAAACAGTGCGCGCGGTAAATTTT
TGTCACCTCAGTAAGTACAGAGAGAAGCCGAATGTACTCCCCCGGCTAGCTGGAGACCATGGC
TCTGCCTAGGATTTCTCTTATGCTTTCTTTTACCAATCACTTTGTTCCGGCGAGGCCCG
CGAAGCTCGCTTTCTTTTCAAGCTAGCAATCATGTTCTTGCCAGCGTCGTAGACTACTGTA
TGGCAGTTGCTGCACTTGCCATGAATATCCTAGTGAAGCCTCTATGCAATAATCCAGTTA
CTGCGTTAGAATCCTGGTAAATGTCTAATCTTATTACATTACAGCAACGTATTAGATTT
TGATTGAAAATTAGTCCTTGCGACTTGGTATATATCTTATTTTAAGAAAGCTGAAAGGAA
GAAAGATCATCACGAACAACATGTCTGCTCCACAAGCCAAGATTTTGTCTCAAGCTCCAA
CTGAATTGGAATTACAAGTTGCTCAAGCTTTCGTTGAATTGGAAAATTCTTCTCCAGAAT

TGAAAGCTGAGTTGAGACCTTTGCAATTCAAGTCCATCAGAGAAGTATGTTATTAATTTG
AATCTAAACTTAAGAATAATGGAGAGTAACAAAGGAAAAAAGTGTGAACGGGACGATACC
AGAATGTTTCAATCTAGAAAAGTATAAAAGATAAGGACTAGGACTCAAATGTATTTGGCT
GACTATCGCCTGAACCTTGATGCTAAGCAAATACCATATCTTCAAGAAAAAGCCTACTCC
AGTGTTTAAGAAGAAGGGAACGATTTACTAGATCATGCTATACGCAGTAAGGTTCTGATA
GTTAATTACAATCGGTCCAAGTTCTAAGCGGTGTCGTCCATGCATATATCATTTACAAGT
TACTGGCGTCAACTCTTCAAATATTTCAAAATATCACCTAATCAAACCTTACTAACATTTTC
CTTTTTTGTTCCTTCTTTTATAGATCGACGTTGCTGGTGGTAAGAAGGCTTTGGCCAT
TTTTGTTCAGTCCCATCTTTGGCTGGTTTCCACAAGGTTCAAACCTAAGTTGACCCGTGA
ATTGGAAGAAGAAATTTCCAAGACCGTTCATGTCATCTTCTTGGCTGAAAGAAGAATCTTGCC
AAAGCCATCTAGAACATCTAGACAAGTCCAAAAGAGACCAAGATCCAGAACCTTGACTGC
TGTTTCATGACAAGATCTTGGAAGACTTAGTCTTCCCAACTGAAATCGTTGGTAAGAGAGT
TAGATATTTGGTTGGTGGTAACAAGATCCAAAAGGTTTGTAGACTCAAAGGATGTCCA
ACAAATCGACTACAAATTGGAATCTTTCCAAGCTGTTTACAACAAATTGACTGGTAAGCA
AATTGTTTTCGAAATTCCAAGTGAACTCATTAG

YOR096W, 190 aa (SEQ ID NO 260)

MSAPQAKILSQAPTELELQVAQAFVELENSPELKAELRPLQFKSIREIDVAGGKKALAI
FVPVPSLAGFHKVQTKLTRELEKKFQDRHVIFLAERRILPKPSRTSRQVQKRPRSRTLTA
VHDKILEDLVFPTEIVGKRVRYLVGGNKIQKVLDSKDVQQIDYKLESFQAVYNKLTGKQ
IVFEIPSETH

YOR248W, 803 bp, CDS: 501-803 (SEQ ID NO 261)

ACCCATTTTACAAATTTTTTTTGCTATTTGAGCCATAGTACCCATTAATAGGTCTCGTCC
ATTCCTTGTTTTTTTTTTTATTGTTTCAATTACACTACATAATTAATAATCACATCACTT
TCACTCTCACCTTAGTCGTTCTTTATCAACCAAAAATAAAAAAATGCTTCAATCCGTTGT
CTTTTTTCGCTCTTTTAACCTTCGCAAGTTCTGTGTCAGCGATTTATTCAAACAATACTGT
TTCTACAACCTACCCTTTAGCGCCCGAGTACTCCTTGGTGCCCCAAGAGACTACCATATC
GTACGCCGACGACACCACTACCTTTTTTGTACCTCAACGGTCTACTCCACGAGCTGGTT
CACCTCAACTTCAGCCACCATTACCAATGCGGCCCTCCTCCTCCTTGTCACCTCTTCGGC
CTCTGGATCTGTAACCCCAAGATCCACCCATGAAATTACCTCCACCTCGACTATCACGTC
CACTTTGCTGCTAACCCTTCATGACTCCACTACTTTGTCTCCATCATCTACTGCAGCAAG
TGTCAGTGACGAAGATTCAAACAACAAAGATGCAAAGGTCAAGTCCTTTGAACAGGCTTC
AACTTCCAATGGTTGCGTCCCAATCACAAAGTTTGTCACTGTACCAATGAGCCCGTTAC
CCAGTACGTTACAGTACCCCCAAATACGACTACACAATACGTTACTGTACCCGGTGCACC
TTCTGTTACCACTACCTCTCCAGGTAACGTACAATGGTACAACACCACTTCGATTACTAA
TTCGACCAGTTGGTGAATTATGA

YOR248W, 100 aa (SEQ ID NO 262)

MTPLLCLHLLQQVSVTKIQTTKMQRSSPLNRLQLPMVASQSQSLSLSPMSPLPSTLQSP
QIRLHNTLLSPVHLLPLPLQVTYNGTTPLRLLIRPVGEL

YOR293W, 1255 bp, exon1: 501-552, intron1: 553-989, exon2:
990-1255 (SEQ ID NO 263)

AACTTTCGAAATATATACTCTGAGTTCTTGCTCCCCGTTTTGTACGATGTTCTTAATGCA
AACACACGTCCTTTAAAGATCCCCGTAGAGTTTCATTAAAGGCAACTTCCATACACGTT
GAAGTGCCAATTTTTTCCCTACATCCAAGCATTTCTGGGTTTGTATGGGTGTTACACCGGT
TTTTCTTTTTTATTTCCAGAGAAGTACAATTTTAGGCGGGTTTCAAATTTCCCTGTGTG
CGAGAAACGCTCCGGTACGCCTAGGCTCACTCCGGTCTTCTCCCCATTTCTATCAGCGC
GATAGGCATACTGTGGGAGAGCGGCACTAGGGAGACCGGTGGGAAGCACCGTATCTAGTA
ACGCACGCTCTTTTGCAAAAATATCCATTAATTGCATGTAACCTTAGATTAACACTGGTAT
TAAGATTTTCGCAATTTTGGGCTGGATTATTAAGGTGAGTAGCAAAGTTTAGCAAGAACA
GTACGAACCTAAGTAGCCAAGATGTTGATGCCAAAGGAAGACAGAAACAAGATCCACCAAT
ACTTATTTCCAAGGTATGTTTTAGAATAACTTTCAGAAAGCATGAAGATACACGGAAAGTC
AAGCGAGGGAAGTTATGCGTATACACAGTAGCGGTAGTGTGCATTACATACACGATGTT
TCAAACACACAGATGGATACCATGCATATGAGGTTAAAGGATTTCTTATGAATATATTAG
TGGATTACATAGAAGAAATTACAAGGAACCGTGTGACGACATTTTCGAAAGGACAGCACA
AGGCCATCGACCCTGGAGACGTATGAAATATGGTATACGTCCTATATTTGGGCAAGAAAA

CGGTAAAACTGTTTTACGCGGAGATCCAACCTTTTGATCCTTACCGAGTACCACGAATCAT
CTATATGATCTTTTTACTAAGTTATCTTCAATTTCAACGGAGAGATGTAAACATCATTCT
CTCCTATGATAATTTCTTTTTTTTATACAGAAGGTGTTGTTGTCGCCAAGAAGGATTTCAA
CCAAGCCAAGCACGAAGAAATTGACACCAAGAACTTGTATGTCATTAAGGCTTTACAATC
CTTGACTTCTAAGGGTTACGTCAAGACTCAATTCTCATGGCAATACTACTACTACACCTT
GACTGAAGAAGGTGTTGAATACTTGAGAGAATACTTGAAGTTGCCAGAACACATTGTTCC
AGGTACCTACATTCAAGAAAGAAACCCAACCTCAAAGACCACAAAGAAGATATTAA

YOR293W, 105 aa (SEQ ID NO 264)

MLMPKEDRNKIHQYLFQEGVVVAKKDFNQAKHEEIDTKNLYVIKALQSLTSKGYVKTQFS
WQYYYYTLTEEGVEYLR EYLNLP EHVPGTYIQERNPTQRPQRRY

YOR312C, 1432 bp, exon1: 501-507, intron1: 508-914, exon2:
915-1432 (SEQ ID NO 265)

TATTTACAAGCTAGATAAAAAAAAAAATCAAATAGCAAGCTATTCTGTCATATCTTAAGGT
GCTGATTGTTTGTAGGCACGAAGTAAACAAGCTCTTCCCCAAAACAATAAATACGGTTTTT
CGGGACTGTTACCCGTACATTTTACGTTTCCGACGGCGCGATGCTATCTTTGAATTTTT
ATCTCTTTCAGGTAACCCCATGACCAGTAGGGCGGCTTACTACCGAAGAGAAAAATGTCC
GCGGCCTAGACAGTTACTTCCCAGGCCAGGGCCAGGCCACACGGACAGAGGCAGATTCCA
AGTTGTTCCGCATAGTCTGTCTAGCTCTTTCTCAATTTTCCGCCAGATTCTGTCTAATTT
CTTTCGCTCGAGTTGGCAACAGTACGAAGAAGTAACTCTAATAGATAGATATAACCGTT
TTTGAGGGCATTATTTTTGCAGAAGATAATAGAAGAGAACCGTAACAAAGGAATCAAGCA
AAGAAAAAGTATGTAATAGAATGTATTGTATGCTTGTGGAATGAATGTCAATGTAGCTAT
TTTATATGGTGAGCTCAAATTGAATGAACATATCGTGGAATTTAAAAATACTGAAGAATA
CCCAATAAGTCAATGCAACCTGTGAATGTTTTCTGAAATACGCCGAATACTGAATACG
ATTATTACCATAAATTGCTTCTAGAAGGAAGGCGGTGTACCATTTAATACTGATGATATG
GTTAATATCATTTGAGAAGTCTTCACATGAGGACTATAGAATACTACCATCCAGGAATTATA
GAGGAAATTAAGTGAATCAGAGATCTATTTTGAACATTCATTTACATGTAATTGTCTGC
AATAAAGCAATATTTTTGAAATATGCAAGTTTACTAACAAGAATAAATCTTTTTTTGATT
TTTATCTTTAACAGTGGCTCATTTCAAAGAATACCAAGTCATTGGTCGTCGTTTACCAAC
TGAATCCGTTCCAGAACC AAGTTGTT CAGAATGAGAATTTTGTCTTCAAATGAAGTCAT
CGCCAAGTCTCGTTACTGGTATTTCTTGCAAAAATTGCACAAGGTTAAGAAGGCTTCTGG
TGAAATTGTTTCCATCAACCAAATCAACGAAGCTCACCCAACCAAGGTCAAGAACTTCGG
TGTTTGGGTTAGATACGATTCCAGATCTGGTACTCACAACATGTACAAGGAAATCAGAGA
CGTATCCAGAGTTGCTGCCGTCGAAACCTTATACCAAGACATGGCTGCTAGACACAGAGC
TAGATTTAGATCTATTCACATCTTGAAGGTTGCTGAAATTGAAAAGACTGCTGATGTCAA
GAGACAATACGTCAAGCAATTCTTGACCAAGGATTTAAAATTCCCATTACCTCACAGAGT
CCAAAAATCTACCAAGACTTTCTCTTACAAGAGACCATCAACCTTCTACTAA

YOR312C, 174 aa (SEQ ID NO 266)

MYLAHFKEYQVIGRRLPTESVPEPKLFRMRIFASNEVIAKSRWYFLQKLHKVKKASGEI
VSINQINEAHPTKVKNFGVWVRYDSRSGTHNMYKEIRDVSRVA AVETLYQDMAARHRARF
RSIHILKVAEIEKTADV KRYVKQFLTKDLKFPLPHRVQKSTKTF SYKRPSTFY

YOR369C, 932 bp, CDS: 501-932 (SEQ ID NO 267)

CTTCTTACAAGTTAATGAATAGTATATATATGTAAAAAAATTTCTGCTTCATGTATATA
CGCACCTCGTTATTGAGGTATTGCGAATGTAGCAGTTGAATAAGCAAAGACGAGGTTTGT
ACATCTTGGCATATTAAATGGTTATTTCCGGGGTTTGTTCGGCTCAACGGTGATATAAAA
AGAAATCCAGTACTGTTTACCATTGTGCATCCGTACATTTGATTTGTTTACAACATCTTC
ACATTTCCATTGTGGAATCATTTTATTTTTTTTTCAGAATACCTTACCCGCAAGCAAATTT
CAAGCAAATTTACAATTTGCAAAATTTTCATCGAATTTCTCCGCAGGACATATTATAAAAGT
TATGTCATCTCTTATCACAACAGGTCTATAAGTGTTCCTTGTTC AATTGTTTTTCCCAAT
TCAAACTCTTCACGGAGCAGTTTAATTATCTTACTGTGCAAGAAGTCAAAACTAGACT
ATATATTATTGAGAAGAAAAATGTCTGACGTTGAAGAAGTCGTTGAAGTTCAAGAAGAAA
CTGTTGTTGAACAACTGCCGAAGTTACTATCGAAGATGCTTTGAAGGTTGTTTTGAGAA
CCGCTTTGGTTCACGATGGTCTAGCTAGAGGTTTGAGAGAATCTACCAAGGCTTTAACCA
GAGGTGAAGCTTTATTGGTTGTTTTGGTTCAGCTCTGTTACTGAAGCTAACATTATCAAGT
TGGTTGAAGGTTTGGCTAACGACCCAGAAAACAAGGTTCCATTGATCAAGGTTGCTGATG
CTAAGCAATTAGGTGAATGGGCTGGTTTGGGTAAAGATCGACCGTGAAGGTAACGCCAGAA
AGGTTGTCGGTGCCCTCCGTTGTTGTTGTCAAGAACTGGGGTGCTGAAACTGATGAATTGT

CCATGATCATGGAACACTTCTCCCAACAATAA

YOR369C, 143 aa (SEQ ID NO 268)

MSDVVEVVEVQEETVVEQTAEVTIEDALKVVLRTALVHDGLARGLRESTKALTRGEALLV
VLVSSVTEANI IKLVEGLANDPENKVPLIKVADAKQLGEWAGLGKIDREGNARKVVGASV
VVVKNWGAETDELSMIMEHFSQQ

YPL047W, 800 bp, CDS: 501-800 (SEQ ID NO 269)

GGTTAGGGGCCAAGATTACGTTCCAGCTTTCGATGTCGCACCAGATTGGGAATCTTACGA
CTATGCAAAGTTGGATCCAAC TAACGACGACGACAAAGAATTCATCAATAACATGTGGGC
CTGGGATAAGCCAGTTTCCGTCAATGGCGAACC AAAGGAAATTGTTGACGGTAAGGTCTT
AAAATAATCTCTTCGTACTATCCTTCATGTCGCCTTTTATTATAAAGTATGCTAGGTAGT
TTTATCTATATCTTATTTATGACGCAATATAGGGTAACAGAGTTTTTCTGCTCTGAAACT
TCCGCAGAAAAAAATCAAGTTTTCTTTTCGTATCTTGGATTATTGTTATATAATAGAT
GCATGTATTATATGTATAGCAGTGATTGCTTATTTTCTTGATTCTGAGGAATCGAAGAA
GTAAC TTAGCGTTTCTTCCGTTGAGCAGAGCAGTATAATAATCCTTCAAATTCTTTAGGT
TACGGGGTTTTCTGTTGCGATGACCGAAGAACTATTACTATAGATTCTATTTCAAATG
GGATACTGAATAACCTGTTAACCACATTGATCCAGGACATTGTAGCTCGGGAAACCACTC
AACAACAATTGCTGAAGACAAGATATCCGGATCTTCGCAGTTATTATTTTCGACCCGAACG
GATCTCTCGATATTAATGGACTACAGAAGCAACAAGAGTCCTCTCAGTATATTTCACTGTG
AGAATTGTGGCAGGGATGTGTCCGCAACAGACTAGCAGCTCATTTACAGAGATGTTTGA
GTAGGGGTGCTAGACGTTGA

YPL047W, 99 aa (SEQ ID NO 270)

MTEETITIDSISNGILNNLLTTLIQDIVARETTQQQLLKTRYPD LRSYFDPNGSLDING
LQKQQESSQYIHCENCGRDVSANRLAAHLQRCLSRGARR

YPL090C, 1605 bp, exon1: 501-506, intron1: 507-900, exon2:
901-1605 (SEQ ID NO 271)

GTAAGCAGAAGCCGGAAGAAGACAAGAGGTTCAATTCAGAGAAAACATCCGTACATTCGAG
TTCTCATTTGAACCCATACATTTCAACTATTTTACATAGTTTCGTTTTTCATGTGTAAAT
TGTCATCGACGCGCCGGAGCATCGGAAAGTTGGAACGTGCGCGATTGCACCAATCCCCT
GGGGCCGTGCATTCTGTAGGCAGGAAGCCACTGGACACTCTGCCCCGTCCCCTTGGAAAG
ATTGGCGTAATTCACGCTCCTCTATCGATTCTAGCGGGAAGTTATCTCTCCTGGTAAG
CGTTGGAGGAATGCCGCTACCTAGGTAAGTCTACTGGGTGGGAATTCCAGTACCGACGTC
TAGGAACATCATGATGCTGCAGTTTCTTTGAAATTTTCATATACAGTGTTACCAAGGATAA
AGTGGTTAATGCTTATTCGTCATTGAATTTTATATTTGCTTAAGAGAAGTGACAAAAGA
GTGAAGACAGACTATACATCATGAAGGTATGATTTATGATACTATTATTGAGGGGCAACA
GAGAACTTTATATGTGGAAAAATGGCATGAAAGTTTGAAAGTGAGAAAGAACTAAACAGA
ACCAGACGTCGTAAAGATTTTAGAAATTTTATGGAAGAAGCAGGAAGACTACCATAT
ACTAATTGATGCGTTTGTGGCGTTATTTTAAACAAACAGAGCGGGTTTACATATACTGT
TACTACAAACCGTGAAATTGAAGCAGTTTCATATACTTGGAGTATAGTCAATAAAAGACAA
GCTTTTTTCATCTTCCACTTAATAATTTCTCTAGAGTAATAAACTTCACCCTATTCAAACA
TTAATTTTGCAATAGTATACTAACAATTTTCTTAATAACCTGTTGAAAATTTAAATAG
TTGAACATTTCTTACCCAGTTAACGGGTCTCAAAGACCTTCGAAATTGATGATGAACAC
CGTATTCGTGTTTCTTCGACAAGAGAATCGGTCAAGAAGTCGATGGTGAAGCCGTTGGT
GACGAATTCAAGGGTTACGTCTTCAAGATCTCTGGTGGTAACGACAAACAAGGTTTCCCA
ATGAAGCAAGGTGTTTGTGTTGCCAACTAGAATCAAGTTGTTGTTGACCAAGAAGCGTTTCT
TGTTACAGACCAAGACGTGATGGTGAAAGAAAGAGAAAGTCCGTCAGAGGTGCCATTGTT
GGTCCAGATTTGGCTGTCTTGGCTTTGGTCAATTGTCAAGAAGGGTGAGCAAGAATTGGAA
GGTCTAACTGACACTACTGTTCCAAAGAGATTGGGTCCAAAGAGAGCTAACAACATCAGA
AAGTTCTTCCGTTTGTCCAAGGAAGATGACGTTTCGTGATTTTCGTCATCAGAAGAGAAGTC
ACCAAGGGTGAAAAGACTTACACCAAGGCTCCAAAGATCCAAAGATTGGTTACTCCTCAA
AGATTGCAAAGAAAGAGACACCAAGAGCTTTGAAGGTCAGAAACGCTCAAGCTCAAAGA
GAAGCTGCTGCCGAATACGCTCAATTGTTGGCTAAGAGATTGTCTGAAAGAAAGGCTGAG
AAGGCTGAAATCAGAAAGAGAAGAGCTTCTTCTTTGAAGGCTTAA

YPL090C, 236 aa (SEQ ID NO 272)

MKLNISYPVNGSQKTFEIDDEHRIRVFFDKRIGQEVDGEAVGDEFKGYVFKISGGNDKQG
FPMKQGVLLPTRIKLLLTKNVSCYRPRRDGERKRKSVRGAI VGPDLAVLALVIVKKGEQE

LEGLTDTTVPKRLGPKRANNIRKFFGLSKEDDVRDFVIRREVTKGEKTYTKAPKIQRLVT
PQRLQKRHRQALKVRNAQAQREAAAQYLAQLAKRLSERKAEKAEIRKRRASSLKA

YPL137C, 4331 bp, CDS: 501-4331 (SEQ ID NO 273)

GTCTCAGTGATGCAATCATCATGGCACGGGCATTAATTAAGGTTAAGGAACCACTTCTCT
ACGCCATACTCCAAACAATAACAATATTAGACCTAGCCAATTGATACCCATGAGCGTGCA
GTCATTGCCATGGATTATTCATCTCTTTTCGCTGTTCTCTTTCTTTCAAGTTTGTCTATC
ATCATGCCTTCACTTTTGCCTTTCCATCTTTCTTTTGTCTGCAAAATAAAGGGAAGAGGG
GTAAAAACGCAAGGAAGAACAAGAAGAAGAGGGTAGTGCAAGAAAAAGAAAAGAAGAAAA
AAAAAAAAAAGTAATCTTGATACCGTGAGCAATAAGCTAACGGAAGCGTAAGAAAGAA
GAGCGTGTTTTGGGAAATAACACCACAGCATAAAGCTAAAATTCAGTTTATATAATCTAT
AGTAGTCCTATAGAAATTGCGAATAACGGAACAATAGTCCACCAAAGCAAGCATAGGGA
GTGGAGATAGCATCTAGGTTATGATAACTAACACCGAGTTTCGATGTGCCCGTAGATTGGT
TGTATAAAGGTAAGAGTAGACGGAAGACAAATACGAAGCCATCGAGGCCTTCTACGTCTGC
CAGCCTCCTCTTCATCTACGTCTCTTCGAAAAACGGAGACAATAGCACGAGTGGTAACA
GGTCTAGCAATGATAAGCCTCGTGCGAGGTCGTCTATCTGATCCAATGCAGCACTTTGTA
ATACTGAGAAACCAGATTTGAAGAGGAACGATGGTAATACCTCTGCATCAGACACTGATA
ACATACCGCTACTTACTCCTATTAATAGCGGTAACCGGAGCGATTCCGCTGACATTGATA
ATCCGGCTACCGTAGACGCCATAGACCTTATAGATAATGATGACAACGGCTCAAGTACTC
AATTTGTAAGGAAAAACGTTCCACTTCTATATCCAATGCTGTGGTCTCGTCCAAACCAA
GACTGGCCAGTTCTGCCATAAACGCCACCGCATCTTCTTCTGTTGGCAAGGGAAAGCACC
CGCCAATTTCTTCAACCATCTAATGCTACTCTCAAGAGAAGCAACTCGACTAGTGGAGAAA
AGACTAAAAGGTCGATTTTTGGATCTTTGTTTAGCAAACGGTCTACCTCTTCTTCAGCTT
CCACTGCCAAGAAACCATTACCTGTTGTTAATACTAGCACGACTGAGAATGAGTCTGGTG
GCATTAAAGCAGTTGCGACTCCTGATCCACGGGTGAAGGAGATATCATCACCATGAGAG
GAGTGGCACCAACAGCTAGCAAGCCACAGACACCTATACTCCCCCTCCCCCTGCACTTGCAG
TAAAAGACCTATCTACAGTTTCATTGAAAAGGGTCTCGTTTGCCGTCGATAAATTCGAAT
CCGATCCTCCCCAACAACTTCTTCAAGAACCCCAAAAAAGGGAAACATCCTTATCCCTG
ATGACATGATAAGCGAGGTTCTTCTATTTCCGTGGGTATTTCCAGTAGCAACCAATCGG
CCAAGTCAACCAATTCCAACATTAAGGGACCGTTGTACACTAAGAAGTCTAAAGAATATA
TACTCGCCCTGGAAAATCAAAAGTTGGCTTTAAGGGAGGCTGCTAAGCATCAGCAAGAAG
CTCATTTTGCTGCTAATAGAATAGCCTTTGAAGTAGCCAATTTTAAGACTGCTTCGGATG
CAGGCGGTAAGCTTACTGAAAAGTCATCAGAAGGCACCATTACGAAGCAAAGAGAAGAGG
TGTCACCTCCAAATGTTGAAGCTGATCGGGAGCTTGAGAATAATAAACTTGCAGAAAACC
TCTCAAAAGCCGGCATTGATAAGCCCATTCATATGCATGAGCACTATTTCAAGGAACCTG
ATCAAGATAAGTACCAAGACGGTCATTCTATTGAAAATAACGAAGTTACGCTGGATGTTA
TTTACACAAGATGCTGCCATTTAAGGGAAATTTTACCCATTCCGTCTACCCTAAGACAAG
TAAAGGACAAGACAGCTCCCTTGCAAATATTGAAGTTTTTGAACCCTAAGCCTACCTTGA
TCGATATTCTTTCTTTTGTGATTTTCATCACCATTGCTCCCATTCACACGATTGTTTTCG
ACAATGTAGCTTTAAACCAGGATATGTTTCAATAAATTATTTCTGCTTTGGTAAACTCCA
CAGTTTTGGACAAATTGAGTTTAAGAAATGTACGAATCGACCAAGATGGATGGAAATTAC
TATGTAAGTTCTTTTGCTAAACAAATCACTGAACAAGCTCGACATTTCCCAAACGAAAA
TCAAATCTGACCTTGCTGAATCACTATATCGCCATAACATGGATTGGAACCTGTTTACTG
ACGTCTTGCTCTCAGAGATCTCACAACCTATAGAAGAATTGTTATTCAATGGTATTCAAT
TTAGCAAAATTCCTTACTCATGCTTTGCACGTTTACTGACATCCTTTGCTACCCAAAAAA
ACTTTCCAGAATCGGGCATCAGGCTTGGTTTAGCAGGTGCCACTACTTCCAATATCTCTC
AGGATTGTCTGAAATTTATCTTCAATTGGATGTCTCAATATAACGTCCAGGGTGTGGATC
TAGCGTTTAATGATCTGTCCACTATGATTAAGCCAATGGTTGGTAAACTATCTGCTCTAT
CATATGATAACTTAAGATATTTCAATTTTGAACAGCACTAATATTTGACTTCTTATGATT
TAGCTTTGCTCTTGAAATATCTTTCTAAGTTGCCTAACTTGATTTTTTTGGATTGAGTA
ATTTGTGCAATGCTTTCTTGACATTTTACCCTACATGTACAAGTATTTACCAAGATTTT
CGAACCTGAAGAGGATACATTTGGATAGCAATAATTTGACATTAAAGGAAGTACCTGTCTG
TTTGTAATATTTTGATTAAAGTGCAAATCGCTCTCGCATGTGTCAATGACTAATCAAACG
TTGAAAACCTTCTATCTAATGAACGGCACAGATTCTCCCGTTCAACAACTAACACAGACG
GCGACTTGGATAGTTTCGAGCACATTGGACGTTAAGGGCCAATTTGCTAAAAATAGTTTTT
CATCCACACTTTACGCATTTGCTAGAGACTCTCCAACTTGATTGGTTTAGATTTTGACT
ATGATTTGATATCAGAAGAGATTCAATCAAGAATAGCACTGTGCTTGATGAGAAATATGA
AACGGACCATGGATTTCGACTTTCCAGTTAGATGAATTGGATTTCGAAGATGATTTGCTAT
TCGATGGCTCTTTAGTAACTATGACCGCTGAAAGTGTTTTAGAAAACTGAACTTGTTAA
GCGATAAGAGTACAAAGGTCAAAAAAGACACCACGAAGAGATATTTGCTGAAAAAATATA

TTGAAAAGTTCCATATCTTGCACCATAATGTTTCAGCATACAATAGATACTATGTTTCGAAA
AAAGGAAATCAGGTGAATTGCCATTGCAAGAAAAAGAAAACCTTGTAAGATTACTCCTTT
TGGAACAAAACCTTATGCAATATACTAGAATTGTTTTTCGCATAATCCGAATCTGAATGATG
TCCTTGATCCAGCAGGGATGATTCGAAGGAAAGTGTTGACTCCAGCGAAGATTCAAAAT
TACCAGCATTGAAGCACGTTGAATCCGGATACCATGTTCCCGAAGAAAAAATACAACCTG
AGAATGATGTAATTACAGCAAGACCACATTTAATGGCCACCGATTCTGGTAAACTATTG
ACGTTTTTCACAGGCAAACCATTTGGTGTTCAGCATACATCATCTAGTACTTCTGTAGGTT
GTAAAAAGCAGGAAGAAGAAGAAGGTGAACTACATAAATGGGGTTTCTTCGTTTCAGCAGC
AGAGGTCTTTATACCCTGAAAATGAATCAACAAGGCAGACACCTTTTGCATCAGGTGATA
CGCCTATCAACACAGAAACAGCTGGTAAGTCAACTTCATCTCCTTCAGTTTCAACTTCTA
ACAATGAACTGCTACCACCTAGTTTATTTAGCCCAGCTAATCCTAAGATTTTACCAAAAA
TTCCATCCGGTGCTGTCTTAAGATCGGCAATCATGAAGGCTAAAGGTATTGATTCTATCG
ATGATTTGATTTCAGAACGTTAACTCCAACAACATAGAATTGGAGAACATTTATGGTGAAT
CCATTCAGAATAGCGCTTCGACATTTACACCAGGCGTGGATTCTGATGTATCTGCGCCCA
ATACCGATAAAGGATCCGTAGAAACATTGCCTGCAGTCTCAACTGACGACCCAAATTGTG
AAGTCAAAGTCACTGCTACCTATGACAACTATTAAATAATTTGTTCGATGGAGAGGTCAA
TCAGACTTTGA

YPL137C, 1276 aa (SEQ ID NO 274)

MITNTEFDVPVDWLYKGKSRRKTNTKPSRPSTSPASSSTSSSKNGDNSTSGNRSSNDKP
RARSSSVSNAALCNTEKPD LKRNDGNTSASDTDNIPLLTPINSGNRSDSADIDNPATVDA
IDLIDNDDNGSSTQFVRKKRSTSI SNAVSSKPR LASSAINATASSSVGKGKHPPISSPS
NATLKRSNSTSGEKT KRSIFGSLFSKRSTSSSASTAKKPLPVVNTSTTENESGGIKAVAT
PDPRVKEISSPMRGVAPTAS KPQTPI LPSPALAVKDLSTVSLKRVSFVDFKFESDPPQQL
PSRTPKKGNILIPDDMI SEVPSISVGISSNQSAKSTNSNIKGPLYTKKSKEYILALENQ
KLALREAAKHQQEAHFAANRIAFEVANFKTASDAGGKLTEKSSEGTITKQREEVSPNVE
ADRELENNKLAENLSKAGIDKPIHMEHYFKEPDQDKYQDGH SIENNEVTLDVIYTRCCH
LREILPI PSTLRQVKDKTAPLQILKFLNPKPTLIDILSFCDFIT IAPIHTIVFDNVALNQ
DMFRIIISALVNSTVLDKLSLRNVRIDQDGWKL LCKFLLNKS LNKLDISQTKIKSDLAE
SLYRHNMDWNLF TDVLSQRSHKPIEELFNGIQFSKIPYSCFARLLTSFATQKNFPESGI
RLGLAGATTSNISQDCLKFIFNWMSQYNVQGVDLAFNDLSTMIKPMVGKLSALSYDNLRY
FILNSTNISTSYDLALLLKYLSKLPNLIFLDLSNLSQCFDILPYMYKYLPRFPNLKRIH
LDSNNLT LKELAVVCNILIKCKSLSHVSMTNQNVENFYLMNGTDS PVQQTNTDGDLDSSS
TLDVKGQFAKNSFSSTLYAFARDSPNLIGLDFDYDLISEEIQSRIALCLMRNMKRTMDST
FQDELDSQDDLLFDGSLVTMTAESVLEKLNLLSDKSTKVKKD TTKRYLLK KYIEKFHIL
HHNVQHTIDTMFEKRKSGELPLQEKENLVRL LLLLEQNLCNILELFSHNP NLNDVLGSSRD
DSKESVDSSEDSKLPALKHVESGYHVPEEKIQPEN DVITARPHLMATDSGKTIDVFTGKP
LVFKHTSSSTSVGCKKQEEEEGELHKWGFFVQQQ RSLYPENESTRQTPFASGDTPI NTET
AGKSTSSPSVSTSNNETATTS LFSPANPKILPKIPSGAVLRS AIMKAKGIDSIDDLIQNV
NSNNIELENIYGESIQNSASTFTPGVDS DVSAPNTDKGSVETLP AVSTDDPNCEVKVTAT
YDKLLNNLSMERSIRL

YPL159C, 1262 bp, CDS: 501-1262 (SEQ ID NO 275)

AAACAAAGCGATTTGAGTATTACGTTAAGATCTCCATTTGCTATGCTAAATCCTGCCTAC
TCAACAGCATTATATCGCTACCAACAGGTGTGGTCAAGAGGTCATTGACTCTTCCTGTC
GGTATGAAAATTTAAAAATATATAATAACATAAGTTTGCATTCATTAATATTAATATAAA
TCAACGTATCAACCATAAGAACCATAATCATAATAATTGTTTACCTTAATGGCGATATCG
CCTTTTATCACCATCGACGATAACAAACGCCTATTCTGTCTACCGTTTCTTTTTTTTCGCT
CGCAATATCAGAATCGTTTATCCCAAAGGGTAGTTATAGCAACTATTTAAATAACTTAGA
TGTTTCTTTAACTTATTCCGTCATACGTACACAAACACCCGCTAGATATAGCACTCCTTG
CTGTGCAACATTATAAAGGTGCTTTTAAACTACTAATCGTATATTCAGCAGGTCAGAAC
GCAAAGTCGGACGATAAACTATGTTGAAGCTAGCTCGTCCATTTATTCCGCCTTTATCAA
GGAACAATGCCATTTCTTCAGGAATAGTTCTCACTTCTAGAAGATTTTCAGTCTTCCTTTA
CGTTCTTAAGTAACCAGTCTTTACTATCTAAAAATCAAATGAAATCCAAAAGAAAAAAGG
GCAGTAAAAAGGCAGCGTACCATCGTCAACCCCCGGAACACGAACATACTGCACCACTTA
TAAAGCAAAACAAGACAATCACAAAGAAAGAACATAGCGATGTGAGAGGTTCTCATTTAA
AAAAGAAAAGAAGCGATTTTTTCGTGGCTACCAAGAGTACCATCCACCTCACATTTAAAGC
AGAGTGACATGACCACAAATGTACTCTATTCTGGATATAGACCCTTATTCATCAATCCCA
ATGACCCGAAGCTAAAGGAAGACACCGGAAGTACGTTATACGAATTTGCGATGAAGCTTG
AAGATTTAAATGAACCTCTATCACCATGGATTTCTCTGCCACTGGACTTGAATTCCTTTT

CAGAGTGGGAGAATATACCTAGTGAAC TACTGAAAAATTTGAAGCCTTTTCATCCACCTA
AGGAAAAATCAATGAACACAAATGAGCTTATTCATGTAAGTGCTAAGAGAAATACATTAG
TTGACAATAAAACAAGTGAGACGCTTCAGCGGAAAAATGGATGAATTTTCAAAGAGAAGAG
GAAAGGGGAGAAAAAAGTCAGTAGTGACGTTGCTCCAAATGAAGAAAAAACTTGAGGGAT
GA

YPL159C, 253 aa (SEQ ID NO 276)

MLKLARPFIPPLSRNNAISSGIVLTSRRFQSSFTFLSNQSLLSKNQMKSRRKKGSKKAAY
HRQPPEHEHTAPLIKQNKITITKKEHSDVRGSHLKKRSDFSWLPRVPSTSHLKQSDMTTN
VLYSGYRPLFINPNDPKLKEDTGSTLYEFAMKLEDLNEPLSPWISSATGLEFFSEWENIP
SELLKNLKPFFHPPKEKSMNTNELIHVSAKRNTLVDNKTSETLQRKMDEF SKRRGKGRKKS
VVTLLQMKKKLEG

YPL175W, 1940 bp, exon1: 501-514, intron1: 515-568, exon2:
569-1940 (SEQ ID NO 277)

ACGTTATTTTCAAAACACATACGAAATCGCTGGACTTTCTCACTAAAGGCTTCCGGAGCC
TGCGGTTCTTCCATCCCCATCTCTTCCACATATACCGGGGGTTCTGATGGCATTCTCTATA
GCTTGCTCAAAGTCCTGCGAGTTTAGCTCATCTTGTGAGTTATTTGCTGGTTCTTCAACA
TTCGGAAGAGTAGTGTAGCCCCTAGTATTCACCATATCCTTTGTATACTCATATGCGAAC
TTGTCTAATAACAATGTATACCAAAAATAACAGCTTGAAAAAAATCTCAGGGTCTTTTCAT
TGAATAATCTCATTCTGCTATTTTAAAGTTTTTCGTTTGCAACCCGAGACTGTCGAGCTAG
AAAATTTTCATTGATACGATTTAAAAATAATCGATGCCAGTAATAGCCTCAAAAAACTTAT
GCAAAAATACGAGATACTATAAACTACAGCTTAGCTAACTCTAACATTATTATATAAAAC
AATGGGCTTCAATATAGCGTATGTCTAGCTCACAGCATGTGTTCCAAATACATTAAAGAA
GATCTCTTTTGTGTTGATACTAACCAGTAAAGTTGAGAGTTATAACAATGAAAATAGGA
TGCTGTGCGACTTTTTTTTATCCACAGTTAGGTGGAGTCGAATTCATATATATCATTTAT
CGCAGAACTAATCGATTTGGGCCATTCTGTCTCATTATAACTCACGCTTACAAAGATC
GAGTCGGCGTACGACATCTTACCAACGGTCTAAAGGTCTATCACGTACCATTTTTTGTGA
TTTTTCAGAGAAACCACTTTCCCCACTGTTTTTTCAACATTTCCAATAATAAGGAATATTC
TTCTCAGAGAGCAGATCCAAATTGTTTCATTCTCATGGTAGCGCTTCCACGTTTCGCTCACG
AGGGAATTCTTCATGCTAATACTATGGGATTGAGAAGTGTGTTACGGACCATTCACTCT
ACGGTTTTTAATAACTTAACGTCGATTTGGGTGAATAAGTTGCTAACATTTACCTTGACAA
ACATAGATCGGGTTATATGTGTTTCTAATACATGCAAAGAAAATATGATTGTTAGAACAG
AATTAAGTCCTGATATAATCTCAGTAATTCCCAACGCAGTGGTGAGCGAAGATTTCAAAC
CAAGGGATCCTACTGGTGGCACCAGAGAGAAAACAAAGTAGGGATAAGATAGTGATCGTGG
TCATCGGAAGGCTCTTTCCAAACAAAGGGTCCGATTTACTTACTCGCATAATTCCGAAAG
TTTGTTCCCTCACATGAAGATGTCGAATTTATAGTAGCGGGCGATGGTCCAAAGTTCATAG
ATTTTCAACAAATGATTGAAAGTCATAGACTACAAAAACGTGTGCAACTCTTAGGCTCTG
TTCCACATGAGAAAGTCAGGGATGTATTATGTCAAGGTGACATATATTTACACGCTAGTT
TAACAGAAGCATTGTTGTAATTTCTAGTTGAGGCCGCATCTTGTAATTTGCTAATTGTAA
CGACACAAGTCGGAGGAATTTCCGAAGTGTTACCAAATGAGATGACTGTTTATGCAGAAC
AGACATCCGTTTCTGACCTTGTTCAAGCAACAAATAAAGCTATCAATATCATAAGAAGTA
AAGCTTTGGACACTTCCTCTTTTCATGATAGCGTGTCTAAAATGTACGACTGGATGGACG
TAGCCAAAAGGACAGTAGAGATATATACTAATATATCTTCTACTTCTTCCGCTGATGATA
AAGATTGGATGAAAATGGTAGCAAATCTTTACAAAAGAGATGGAATCTGGGCTAAACATC
TTTATCTGTTATGTGGAATTGTAGAGTACATGCTTTTTTTTCTCTTAGAGTGGCTATACC
CCAGGGATGAAATCGATCTAGCTCCAAATGGCCCAAGAAAACAGTGTCTAACGAGACGA
AGGAAGCAAGAGAACTTAA

YPL175W, 461 aa (SEQ ID NO 278)

MSSSHKVESYNNENRMLCDDFFYPQLGGVEFHIYHLSQKLIDLGHSVVIITHAYKDRVGV
HLTNGLKVYHVPFFVIFRETFPTVFSFPIIRNILLREIQIVHSHGSASTFAHEGILH
ANTMGLRTVFTDHSLYGFNNLTSIWVNKLLTFTLTNIDRVICVSNNTCKENMIVRTELS
PD IISVIPNAVVSDFKPRDPTGGTKRKQSRDKIVIVVIGRLF PNKGSDDLTRIIPKVCSS
H EDVEFIVAGDGPKFIDFQQMIESHRLQKRVLGSPHEKVRDVLCOGDIYLHASLTEAF
GTILVEAASCNLLIVTTQVGGIPEVLNEMTVYAEQTSVSDLVQATNKAINIIRSKALDT
SSFHDSVSKMYDWM DVAKRTVEIYTNISSTSSADDKDWMMKMANLYKRDGIWAKHLYLLC
GIVEYMLFFLLEWLYPRDEIDLAPKWPKKTVSNETKEARET

YPL180W, 2900 bp, CDS: 501-2900 (SEQ ID NO 279)

CTCAATGGGAATTGAGTGAAGATCAGTCTGATCGAGAGGAATTTGTACGATTCGTGGAAA
ACCAGCATTTCGTAGAAAAAGTTGATACGATTTACAACGGTTATAATGAAAGTCTATCAA
TGATGGACGACCTGACTAGAGAGTTACTACTATGGGAGAAAAAATATTCAAATAACACTA
ATGCCATTCAATAAACGCAAAACACTGCAATATTATTCTCAACCAAAGTATAACTGTAAT
GAGGCGAACAAACACATCTATACATATATATACATCTATATGGATATAAAAACGACTAAT
TCAACGTTGTTTTTATCAACCGAGCTTACTCTTGACGGGTAACCGCAAGGATAGCTAGT
TGCGGATGGTATAGCGATTTGGCTGGCAGCATGATTAAGGAATCCAAACATCTAATGGAC
TAGCACATTCTATCGATTTACGGGTCAGGTAAACATAGATATTGGGATATATCATATATC
CTTACTGAGTAACTATAATTATGGTTCATCGAGGAAGGACTTTGAAGTCAGACACTGATG
TAACATCTCTTAATGCGTCAACAGTATCACACCAGTCAAAGCCATTTAGACAGTTTTCGA
CTAGGTCGAGAGCAAAGAGTAACGCAAGCTTCAAAGGTTTTCGCTAGAGTTTAAACACATG
ATGGCACCTGGATAATGATTATTTTAATAAGCACAAACGTTTCTCAGAAATGCAAGAGTT
CTGATGCACTTTTTCAGAAAGCGAACGATTAGTGGGTTGAATATGACAGCTTTAACAAGAG
TAAAGTCCAATCAAGGAAAAAGATCAGCATCCTTTCATAGTCCGGTGCATAATACGCTGC
TCAGTCCAAAGAACAGCAGTCATTCTAATACTGGAAGTCTGCTGGTTTCGGCCTGAAACCAC
GAAGAAGTAAAAGTACCCAATCTGTTCTGAGTCTTCGAGATGCGCAAGAATCTAAAAAGA
GTGAATCTACTACTGACGAGGAGGTGGAATGTTTTTCGGAAGACAACATTGAAGATGGAA
AGGTGAATAATGATAAAGTAATAGCCGAGCATGTTATGCCTGAAGAAAAAAGAATGTGC
AGCAATTAAATCAGAATGAATTACAATCCCCGGATTCAATAGATGAACAAGAAGAAGATA
AATCAGGTACTGATGGAAAGGAAAATCATAGAGCTGTATCCTTACCATTACCTCATTTAT
CTTCCAATAACTATTTTCGGAGAATCAAGCCATTCTATAGAACATCAGAAAGATGGAGAAA
CATCTCCAAGCTCAATTGAAACAAAACCTGAATGCAACAAGTGAATCAATGAAGAGGGGC
AATCAAAGGTGACGAAGGAAGCTGATATTGATGACTTGTCCAGCCATTCTCAAAATTTGA
GGCCTCATTGGTTAAAGCGGGCGATAATATATCAGAAGCACCATATGATAAAGAAAAAA
AAATTCTTGATGTTGGTAATACCTTAGCTGCACATAAAAGTAATCAAAAACCAAGTCATT
CAGATGAACAGTTTGATCAGGAAGATCACATTGATGCCCCTAGGAGTAATTCATCAAGAA
AAAGCGACTCGAGCTTTATGTCTCTTAGGAGACAAAGTTCTAAACAACACAAATTATTAA
ACGAAGAAGAAGATCTAATCAAGCCTGATGATATTTCTTCCGCTGGTACCAAGGATATTG
AAGGGCATAGCTTACTGGAAAATTATGCGCCTAATATGATTCTCTCCAGTCGACTGGAG
TTGAACGTAGATTTGAAAATTCATCATCCATCCAAAATTCGCTTGGAATGAAATTCATG
ACTCGGGTGAGCATATGGCTTCAGGTGATACTTTTAATGAACTGGATGATGGCAAATTGC
GCAAGAGCAAGAAAAATGGTGAAGATCTCAACTTGGCCAAAATATACCGAACTCTCAGT
CTACTTTCCCCACCATTGCTAACATCGGTAGTAAAGATAATAATGTACCACAGCACAACT
TTTCGACCTCCATATCGAGTTTAACCAATAATTTGAGGAGAGCTGCTCCTGAAAGCTTCC
ATGGTTCAAGAATGAATAATTTTTTCAACAAGAAAGGTAATCAGAATCTACTTCTGAGAT
CCAACGATCTCAACAAAAATTCGAGCCCCGGCCTCTCCATTGTCCAACGAACATATTA
CATCTAGTACGAACTCCGGTAGCGATGCAAACAGACAATCCAACCTCAGGTGCCAAATTTA
ATAGCTTCGCCCAGTTCCTTAAATCAGATGGGATTGATGCAGAAATCAAGAACACAAAGAA
AATTATGGTTGCAGAGGGAGAATTCTATTATGGACTTAAGTTCACAAAATGACGGTAGTG
ACTCTATCTTTATGGCAGGAAACATTGATGCGAAAAGGGAGTTTGAGAGAATATCCCATG
AATACTCTAATGTAAAAAGATTTTACAACCCATTAGATGAAGCATTGTTGAGAGTACAAC
CTATAATAACGGGAAATGCAAATAATATCAGGAAAAAAGCCATAACGATGCTCAGTCAA
TCGCACATTCTAGCAGTGATACAGATCATAAGGATGAGGACGATTTGCTCTTTACTAACT
ATGACAAAAAATTTGATGATCTTTATCCACATCTTGCAAGTGCAAAGATTCAGGCAGTGT
TGTCGGTATATGGAAAAGCGAAAGTTACTTATTTAACAAGGATGTTAATCCAATCAACA
AGAATAGGACAACGAGTACAAACCACAGCGTTGGCCCACTGCTTCACAGAATGCACGTA
ACTTGCTGAGGGGGCCGATGGGTTCAGCACGACTTTGCAACCACCAACGCGTCATTAAC
CTCTGCAGCCGACTACGAGGGCAGTGAATCGCAGGATGGAAAATGTGGGCTACATGCATA
CACAGCCACAACAAAGGTGA

YPL180W, 799 aa (SEQ ID NO 280)

MVHRGRTLKSDTDVTSLNASTVSHQSKPFRQFSTRSRAKSNASFKGLRRVLTHDGTLDND
YFNKHNVSQKCKSSDALFRKRTISGLNMTALTRVKSNOGKRSASFHSPVHNTLLSPKNSS
HSNTGTAGFGLKPRRSKSTQSVLSLRDAQESKSESTTDEEVECFSEDNIEDGKVNDKV
IAEHVMPEEKKNVQQLNQNELQSPDSIDEQEEDKSGTDGKENHRAVSLPLPHLSSNNYFG
ESSHSIEHQKDGETSPSSIETKLNATSVINEEGQSKVTKEADIDDLSSHQNLRLASLVKA
GDNISEAPYDKEKKILDVGNLTAHKSNOQKPSHSDEQFDQEDHIDAPRSNSSRKSDSSFM
SLRRQSSKQHKLLNEEEDLIKPD DISSAGTKDIEGHSLLENYAPNMILSQSTGVERRFEN
SSSIQNSLGNIEHDSGEHMASGDTFNELDGKLRSKKNNGRSQLGQNPNSQSTFPTIA
NIGSKDNNVPQHNFSTSISSLTNNLRRAPESFHGSRMNNIFHKKGNQNLNLLRSNDLNKN

SAAPASPLSNEHITSSTNSGSDANRQNSNGAKFNSFAQFLKSDGIDAESRTQRKLWLQRE
NSIMDLSSQNDGSDSIFMAGNIDAKREFERISHEYSNVKRFYNPLDEALLRVQPIITGNA
NNIRKKSHNDAQSIAHSSSDTDHKDEDDLFTNYDKKFDDLYPHLASAKIQAVLSGIWKS
ESYLFNKDVNPINKNRTTSTNHSVGHTASQNARNLLRGPMGSSTTLHHQRVINSLOPTTR
AVNRRMENVGYMHTQPQQR

YPL218W, 1212 bp, exon1: 501-528, intron1: 529-667, exon2:
668-1212 (SEQ ID NO 281)

TGATACAAGACAGGCATTAGGAAACACATGAGTTTTGCATATGTATTATGCAGGTTTCATT
TGTTCCCTTCCCTTATTTCTTTTCATAGTATTTATTTTATTTATTTATTTTATTTT
GGATTTTATTTTATTTCTTTTAAATGCTAAGAAAGTAATCCGCATAATTAAACGTGTG
CTGGCCTCGATAGGTACCTATAGTATACAGAAGCTTACGAAAAGCTCCTGCAGGATGGCA
CTTCTAAAATTTCGCGCTCAACATGGCCGTATTGTACATTATATCGTTCTATCATTATATC
GTATACGCCCGCATTACCCGACAACCTCCGTCTGCAACGCGTTGACCAGAAAACCTCGAACA
AGAGATCGCATAAAAAACCAAAGGAAACGAATTACTTGTCAAATAGTTATTGTAATGGA
TCCTCTAGAAAGGCAAACAGTAGATTTATTTCCCTTCTTTCTAGAAACATCATTATAACT
AACAAATATATAATTGGAATAATGGCTGGTTGGGATATTTTGGTTGGTGTATGTTATCAC
CCTGTTTACGTTTTTTCGGATACTTAGTTTTATTCAATGTGGTAAACATTGAATGTTTTCA
GCTTAAGATCTATTTTTTTTTTCTAGAAGAAATTGCGTCCCTTACTAACTTTATTTTAC
TGTACAGTCAGAGATGTGTTGGCTTCCCTTGGTCTGTGGAACAAACATGGTAAACTACTT
TTCTTGGGTTTGGATAATGCCGTAAGACCACATTGCTACATATGTTAAAGAACGATAGA
TTGGCAACCTTACAACCAACATGGCATCCAACCTTCTGAAGAACTGGCTATTGGTAACATT
AAGTTTACAACCTTTCGATTTGGGTGGTCATATTCAAGCTCGTCGTTTATGGAAGGATTAT
TTCCCAAGTAAATGGTATCGTCTTTTGTAGTCGATGCTGCTGACCCTGAAAGATTTGAT
GAAGCACGTGTCGAATTAGATGCTTTATTCAACATTGCCGAATTGAAGGACGTTCCCTTTT
GTAATTCTTGGTAACAAGATCGATGCTCCAAACGCCGTTTCTGAAGCGGAGCTACGTTCT
GCTTTAGGATTATTGAATACCACTGGCTCTCAAAGAATTGAAGGTCAAAGACCAGTTGAA
GTTTTCATGTGTTCCGTTGTTATGAGAAATGGTTATTTAGAGGCGTTCCAATGGTTATCT
CAATATATTTAA

YPL218W, 190 aa (SEQ ID NO 282)

MAGWDIFGWFRDVLASLGLWNKHGKLLFLGLDNAGKTTLLHMLKNDRLATLQPTWHPTSE
ELAIGNIKFTTFDLGGHIQARRLWKDYFPEVNGIVFLVDAADPERFDEARVELDALFNIA
ELKDVPFVILGNKIDAPNAVSEAEELRSALGLLNTTGSQRIEGQRPVEVFMCSVVMRNGYL
EAFQWLSQYI

YPR102C, 1025 bp, CDS: 501-1025 (SEQ ID NO 283)

TTCTTTACAATTCACCTTGCATTATTGAAGGAGTGCTATTCTTCGTTTTGCCACCCTTTT
GCTGTTTTCCCTCATATCACATAATACCCGGAGAGGCTCTTTCCTGCGACAGCGCAACAT
CCAACCATCCTAAAGGTATGGGTGTAAGTACGATGCGATTATTTTATTAAAGTTCTGTCTT
TTTTGTATAAATGAAAAAGAACGGTGAAATCCATAGAAATACAGAGAGCGACGCAACA
GCGCGCAGACTCTACGGGTAATAGACTCACATCCACGTGACCAGTTTCCAATCGAACTTT
TTCACCTTTGCAGGGAATTATTGTTTCACTAGCAAAGGTAGCCCACTTACCACTCAGCTAT
GCGAAAGTTTCATTGTTTGATACATCTTGATAGTAACCGCAGGCTTCTTTCTTAGTTTCAT
ATTTTATTGTATTTCAACTAATATTATTTTTTTTTTTCAGTGGAAGGGAAGGTGAACCAAGA
ACATACAAACATAGCCAAAGATGTCTGCCAAAGCTCAAACCCCTATGCGTGATTTGAAGA
TCGAAAAGTTGGTCTTAAACATTTCTGTTGGTGAATCTGGTGACAGATTGACCAGAGCCT
CCAAGGTTTTAGAGCAATTATCTGGTCAAACCTCCAGTTCAATCCAAGGCCAGATACACTG
TCAGAACTTTCGGTATCAGAAAGAAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTC
CAAAGGCTGAAGAAATTTTGAAAGAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACA
GAACTTCTCTGCTACCGGTAACCTTCGGTTTCGGTATTGACGAACACATTGACTTGGGTA
TCAAGTATGACCCATCCATCGGTATTTTCGGTATGGATTTCTATGTCGTCATGAACAGAC
CAGGTGCTAGAGTCACTAGAAGAAAGAGATGTAAGGGTACCGTTGGTAACTCCCACAAGA
CAACTAAGGAAGACACCGTCTCTTGGTTCAAGCAAAGTACGATGCTGATGTTTTGGACA
AATAA

YPR102C, 174 aa (SEQ ID NO 284)

MSAKQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIR
RNEKIAVHVTVRGPKEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSI
GIFGMDFYVVMNRPGARVTRRKRCRGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YBL003C, 899 bp, CDS: 501-899 (SEQ ID NO 457)

TATATGACGGCAAGTGTCTCACTGTTGCATTACGCGATGTTTCTTTTCTTTGTTCTTGTAAG
CGCGATTTTACCAGAACTAGATGGCGCTCGTGATCCTGAAAACGGGGAGAAATTTTGAGAAC
ACCGCTTTATTAGGCGAAGCGGTGGGCACAGCTCACGCGTAAGGTGTTCCCATTTATTTCTCA
AAGTGATGCGAATTTTCAGAGAACACATTAACCTGGGGGCCATAAACGCGACGTGCTACCATT
TTCGTTACGTATACTTAGGCCAGAGATTACAACATGACTACTAATATCAAACATAACTCTAT
ATATAAGGGATGAAGATGTATGCTTTCTTAGAATTTCAAACATGTTCCGTTAAAGTTTTACT
TTTCGATTTCAATTTTCGACTGCATGATGCTTTTCTTAGGTAGTTTTTTGTTATTAAATAGTA
TCATAAATTCCTTGTCTTTTACATAAGAATTAGGAAAGTACAGAACAAAGAGCAAATTTAATA
TATAATGTCCGGTGGTAAAGGTGGTAAAGCTGGTTCAGCTGCTAAAGCTTCTCAATCTAGAT
CTGCTAAAGCTGGTTTAACATTCCCAGTTGGTAGAGTGCACAGATTGCTAAGAAGAGGTAAC
TACGCCCAGAGAATTGGTCTGGTGCTCCAGTCTATCTAACTGCTGTCTTAGAATATTTGGC
TGCTGAAATTTTAGAATTGGCTGGTAATGCTGCTAGAGATAACAAAAAACAGAAATTTATTC
CAAGACATTTACAATTGGCCATCAGAAATGATGATGAATTGAACAAGCTATTGGGTAATGTT
ACCATCGCCCAAGGTGGTGTTTTGCCAAACATTCACCAAACCTTGTTGCCAAAGAAGTCTGC
CAAGACTGCCAAAGCTTCTCAAGAAGTGTAA

YBL003C, 132 aa (SEQ ID NO 458)

MSGGKGGKAGSAAKASQSRSAKAGLTFPVGRVHRLRRGNYAQRIGSGAPVYLTAVLEYLAA
EILELAGNAARDNKKTRIIPRHLQLAIRNDDELNKLGNVTIAQGGVLPNIHQNLKPKSAK
TAKASQEL

YDR442W, 893 bp, CDS: 501-893 (SEQ ID NO 459)

TGAACGGGTGCAAAATTTACTTTAACACCCAAAAAGTATATGCGTATATATATATATTTATC
CTTGTTATTTTTGTAAATTGAGCTATGCAACATAAGATTCCCTGCGATGTAAGAACTACTTGC
TAATCAAGAGAACTTCAACAATTTTCCATCGCAGAGACGAAAAAACTGGAAAAAATAAAAA
GAAAAAATTGAAAAAGAAATCGCGACTTCCGATTACATAACCTTATACGGAGTATGATACCAT
TCTTGACATCATCAACACACCATCGCAGACCCACGTGGCCGCTTCGTGTGCCTTGAAAATAC
AGCCTTAAACGCAATCTCATTTCGCGTTCTGTGGAAATTGTCTCGGACTACACGCTGGGCGTG
CATCACCAGTGAAAATGCCGTACCGCCCCGCTTCCGGTTTTGTTTTTATAAATCCGACTGGA
GAAATAGACTTCTGGGTTTACACCCCGGAATAATACTAAAACCAAACCTGGTAAATAGGGCT
ACAGATGAGCAGGAAAACGTTGCCGGAAAAAGTTTATTTATCCGAGAGAATAATTGATGAAG
AAGTAGCGGTATGCACAGTAGCGGCGGAAGTATTAGCAATTTTTACTCTGGTGTGCACAAGA
GTGTTTCATCATTTTTTTTACCGGCTAGGATATGCCATGGAATATGGCCATCTTCGCCATCAGA
GAGACCGTACCACACGTTTAGAGCAGCCAGGTTCGGAACCTCTTCTAAGATGGTTTCCAGCA
ATTGTGTACTATCAGAATGTGGACAGTTTAAAAGGTTGACTGCGAATTTGTCCCAAACCGTA
TCACCGTCGCATTTTTTTGAATTTGATCAAAGCACCCTCCTAATAGCACAGCGATGCTGTGA
GTGTGCCAGTGGGAACGGGTGCTGA

YDR442W, 130 aa (SEQ ID NO 460)

MSRKTLPKVVYLSERIIDEVAVCTVAAEVLAIFTLVCTRVIIFFTARICHGIWPSSPSE
PYHTFRAARLRNSSKMVSSNCVLSECGQFKRLTANLSQTVSPSHFLNLIKAPLLIAQRCCEC
ASGNGC

YDR529C, 884 bp, CDS: 501-884 (SEQ ID NO 461)

GAGTCTCCGGAGTTGACCAAGTCATACAATGTGCTACTGACCAAGAAATGGATCTGTGTAGT
TCCAAGATCGCATGCCAAGAGTGGACCGCCATTGATGTTAAACATTAACCTCCACGGGGTACT
GTGGTATGATCCTCGTTAAAGACAGAGAAAACTAGAGAACCTCACTGAAGATCCTCATCTT
GTGGACAAGTCGTTACTGCAATGCGGTTTCCCCAACACAGCAGGCCAAAAACCAACAGAGTA
TCACTATTAAGGTCTATTAGCCATATGTACATTGTCTATAGATGTGTAACCTGCGCTGTGATC
TTGTTTTGACCAATCAGGAGCGACGCGCTTTTTATCGGGTCACCCCGCGGGGGGCGCTGACA
ATTTACTTTTCATAGAGCAGTAATAAAAGGGAAGAGATGTAAGCTTGGAATAATAGCAGTA
AAGGTTGTTGTTGGACAATTTATCAGAAATTTAGTAACCTGTAATTAACGTTCCAGAAAGAA
CAAAATGCCACAGTCTTTTACGTCTATTGCGAGAAATTGGTGACTATATTTTGAAGTCACCCG
TCCTCTCCAAGTTATGTGTTCCAGTTGCCAATCAGTTTCAATTAACCTCGCAGGTTACAAGAAG
TTAGGGCTCAAATTTGACGACTTAATTGCAGAGGAAATCCCATCATGCAGACCGCTTTAAG
AAGACTCCCTGAAGATGAATCTTATGCCAGAGCATATAGAATAATCAGGGCTCATCAAACCG
AGTTGACTCATCATTTACTGCCAAGAAACGAATGGATCAAAGCCCAAGAGGATGTTCTTAC

CTGTTGCCATACATATTAGAAGCTGAAGCTGCAGCTAAGGAGAAGGACGAGTTAGACAACAT
AGAGGTCTCCAAATGA

YDR529C, 127 aa (SEQ ID NO 462)

MPQSFTSIARIGDYILKSPVLSKLCVPVANQFINLAGYKKLGLKFDDLIAEENPIMQTALRR
LPEDESYARAYRIIRAHQTELTTHLLPRNEWIKAQEDVPYLLPYILEAEAAAKEKDELDNIE
VSK

YGR085C, 1025 bp, CDS: 501-1025 (SEQ ID NO 463)

TCCTTACTTTAGTCTATTATCAATATCTCTTCCCCCTCCTAAATATGTACTCTTTTATTTTT
TTTAATTGTGAAGGAACAATTCAAGTTAGAACTCTTTTGATAGGAAACATTATTTCTGTGT
AGCCTAATGTTTAATGCCTAATTTTTTTCTAAAATGCAGCAACATACATATGTTGAGTCGTA
TAGACATCTATATATAACAAGCACAGAACCGTCTAATTGGTATTTTTTCAGGACATTTTAAAC
ATCCGTACAACGAGAACCCATACATTACTTTTTTTTAATATTCTTTTTTGTTCACCGCCTTC
TTTTTATTTTTATCCGAAGATCTTTTGGAACCCGCTCTGCGAATAGCGAAGCTAGGATACCA
AATTGAACTTGGACATAACTCATCATTAAGAAGTATACTGTTAAGAGAGGCATTCATTTTC
GTGTATTATAACGTTTAGCATCAGTTACCCTTGAAAGCCCAACATATACAAAATACGCGTC
CAAGATGTCTACTAAAGCCCAAACCCCTATGCGTGATTTGAAGATCGAGAAATTGGTCTTGA
ACATCTCCGTTGGTGAATCTGGTGACAGATTAACCAGAGCCTCCAAGGTTTTAGAACAAATTA
TCTGGTCAAACCTCAGTTCAATCCAAGGCCAGATACACTGTCAGAACTTTCGGTATCAGAAG
AAACGAAAAAATTGCTGTTACGTTACCGTCAGAGGTCCAAAGGCTGAAGAAATTTTGGA
GAGGTTTGAAGGTCAAGGAATACCAATTGAGAGACAGAACTTCTCTGCTACCGGTAACCTTC
GGTTTCGGTATTGACGAACACATTGACTTGGGTATCAAGTATGACCCATCCATCGGTATTTT
CGGTATGGATTTCTATGTCGTCATGAACAGACCAGGTGCTAGAGTCACTAGAAGAAAGAGAT
GTAAGGGTACTGTTGGTAACTCCCAAGACAACCTAAGGAAGACACCGTCTCTTGGTTCAAG
CAAAAGTACGACGCTGATGTGCTCGATAAATAA

YGR085C, 174 aa (SEQ ID NO 464)

MSTKAQNPMRDLKIEKLVLNISVGESGDRLTRASKVLEQLSGQTPVQSKARYTVRTFGIRRN
EKIAVHVTVRGPKAEEILERGLKVKEYQLRDRNFSATGNFGFGIDEHIDLGIKYDPSIGIFG
MDFYVVMNRPGARVTRRKRCRGTVGNSHKTTKEDTVSWFKQKYDADVLDK

YGR106C, 1298 bp, CDS: 501-1298 (SEQ ID NO 465)

GCAACATTACCACCTTGTACGGAGCGTCAGAAAGAACGCACCTCATCATTATTATGAGAAC
GTACGATAACTTCTGTCTGAGATACGCTTCGTTGTTATAATACAAGTGAAACCGCCACGGAT
AATTAGCAGCAATTGAACACAAGGGATATCATTGTGTGACCTTTGTTCTCTCATAGTTGC
TGTGAACCCCTTAGTAACCTATTAATGTTTATTTTCATGAGACTAGTCAAAACATTCAATAACA
GTTTTTCTATATGAGAAAAAAGCAACAGTACGATTATT
ACACTGACTATGCTGCAGTTTCCGCAATAGCAAAATTGTGTACATTACACGAAAGAAAGAA
AGAACGCTATTTCTTATAAGAGCAAACCTGTTGATAAGTTTATAGCAAGAATAAAAAGGGTAA
AAAGTCATTGATAATAACCACTGCTGTGACTATATATAATAAGAATCGAACTGTAAAGTTAA
AGCAATGGTGTTCGGTCAGCTGTATGCCCTTTTCATCTTCACGTTATCATGTTGTATTTCCA
AACTGTGCAAGCAGATTTCATCCAAGGAAAGCTCTTCCTTTATTTTCGTTTCGACAAAGAGAGT
AACTGGGATACCATCAGCACTATATCTTCAACGGCAGATGTTATATCATCCGTTGACAGTGC
TATCGCTGTTTTTGAATTTGACAATTTCTCATTATTGGACAACCTGATGATTGACGAAGAAT
ACCCATTCTTCAATAGATTCTTTGCCAATGATGTGAGTTTAACTGTTTCATGACGATTTCGCTT
TTGAACATCTCTCAATCATTATCTCCCATTTATGGAACAATTTACTGTGGATGAATTACCTGA
AAGTGCCTCTGACTTACTATATGAATACTCCTTAGATGATAAAGCATCGTTTTGTTCAAGT
TTACCTCGGATGCCTACGATTTGAAAAAATTAGATGAATTTATTGATTCTTGCTTATCGTTT
TTGGAAGATAAATCTGGCGACAATTTGACTGTGGTTATTAACCTCTCTTGGTTGGGCTTTTGA
AGATGAAGATGGTGACGATGAATATGCAACAGAAGAGACTTTGAGCCATCATGATAACAACA
AGGGTAAAGAAGGCGACGATGATATTTAAGCTCCATCTGGACTGAAGGACTACTAATGTGT
TTAATAGTTTCTGCGTTGCTATTGTTCAATTTTGATTGTTGCACTTTCTTGGATATCTAATTT
GGATATCACATATGGTGCCTTGGAATAATCAACAAACCAATAAAAAAACAATTAA

YGR106C, 265 aa (SEQ ID NO 466)

MVFGQLYALFIFTLSCCISKTVQADSSKESSSFISFDKESNWDTISTISSTADVISSVDSAI
AVFEFDNFSLLDNLMIDEYPPFNRFANDVSLTVHDDSPNLISQSLSPIMEQFTVDELPES
ASDLLYEYSLDDKSIVLFKFTSDAYDLKKLDEFIDSCLSFLEDKSGDNLTVVINSLGWAFED

EDGDDEYATEETLSHHDNNKGKEGDDDDILSSIWTEGLLMCLIVSALLLFILIVALSWISNLD
ITYGALEKSTNPIKKN

YGR182C, 854 bp, CDS: 501-854 (SEQ ID NO 467)

CCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAACGACTTAGCGAAGCT
TATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCATTCAGGTTACTAAC
AATGCATAAATTATGAGTAGTCTTTTTCATCACTATATAAAACCTTTTCAAACGAAACGCT
GTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAAACTGTATTTGATACTGCTAT
TACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGTCAAGGCTCGAATAG
CTGCAGGCGATGGAGACGACGATGATGAGTAAACGCTGATTATGTCACACATATACGTGCAA
ACGCTCTCTCTCTCTCAAGCTATATAAGTGGCACTCGTCTTATTTATTTATTTTATTTT
TGGCTGGTTGTTTCATGTTCAACCCAACCTCATAAAGGCACTCAACTTCATATTTTGACACAA
ATCTATGTCTCGCCAAAGCGCATTCAAATTTTCAAGATGGAAATAGACACGAACGAGCCTGTC
TGTCAGATGTTTCAAAAATCCTTATTATAATTTTATATTCTACTAAAGGAAAAAGAGAATTA
GGAAAAAGAATAACTCATTTTATGTATATACATATATTTTGTACATATCTATACCAAGCAAG
TATAGTGCAATACTGTTCTTCGACGTTATTAAACGTAATAGCATTTTCTTGGTATCCTTTGA
ATCTTATATACAAGTACGAGTACATACTGCGCAGTAAATTGATCCTGATGGTGTGTTTAGAT
TTCGCCAGAAGCGGAGGCGTTCTGGATTCTGGAGATGTAAGCCTTTGA

YGR182C, 117 aa (SEQ ID NO 468)

MSRQSAFKFQNGNRHERACLSDVHKILIIILYSTKGKRELGKRITHFMYIHIFCTYLYQASI
VQYCSSTLLNVIAFSWYPLNLIYKEYEILRSKLILMVCLDFARSGGVLDSDVSL

YGR183C, 914 bp, exon1: 501-503, intron1: 504-716, exon2: 717-
914 (SEQ ID NO 469)

AAATACAAATCCAAGAAACCTCGATGAGGATGACTCTGATGATAATGATGACTCTGATGAGC
GAGAGATTTGGTAGATTCAAGCCCTCTACTATGTTTTATAGTTGACATATTTGTATATAAAA
ACTTATACATTATTAACATTTGCGCGTCGATTGACTTTTATTTATTATTAACAAAGAAGTA
ATACCAACCTAATTACAAATACTTCGAAGTGACTATCATAAGTTTCCTTATCTAGCGAAGGC
AACTTTTGAACCTCCCGAGTTGTTAATATGTATCATTATACACGACCCAATCAAACGCGGGGA
AGTCAATGCCGAAAGAATTCTAGGACCTAAAAGCTGCTCAATCCTTGGGCCTTTCCCTAATG
ACATCCCCTCTCAAACCTTAGCTTAGCAGTTGTATTTAATGTCTGTCACGGATAGTCAATA
ATCGTTGAAGGTTGATTTTCATATCCTTCGCAATTCGTAAAGCAACAATAGCAATACGGAC
TAAAATGGTATGTTGGTGTGTGTGTGTGCTGCTTCACATTTTCAAGCTAAAATGTTATCCGT
GGAATCTTCCTTAGCCAAGTATCATGGGCTTTGGAAATTAGTTTCCCACCGATGAGCGCAAC
GACTTAGCGAAGCTTATGAAATTGGTGACAGCAGCTCTATGAATATGTTCCATGCGTTTCCA
TTCAGGTTACTAACAATGCATAAATTATGAGTAGTCTTTTTTCATCACTATATAAAACCTTTT
TCAAACGAAACGCTGTTTTTGTGGTACTATCTTTGCAGGTGCCTTTGTTTTCCAAACTGTA
TTTGATACTGCTATTACTTCATGGTACGAGAATCACAACAAAGGAAAATTATGGAAAGATGT
CAAGGCTCGAATAGCTGCAGGCGATGGAGACGACGATGATGAGTAA

YGR183C, 66 aa (SEQ ID NO 470)

MSFSSLYKTFKRNAVFVGTIFAGAFVFQTVFDTAITSWYENHNKGKLWKDVKARIAAGDGD
DDDE

YKR040C, 1004 bp, CDS: 501-1004 (SEQ ID NO 471)

GGGCTTTTCCAGTGCCGCGGCCTCGAGATCCAGGCACCAGGAAGTAGGCACGCTGTGTATTC
TAACACATTGAAGGGCCTAGGCCCGCTGACGTGGGGTCTAGTTCCACTTTTTCATTACCTTT
TCTCGGTCTTTTCTTGCTCCACAGGCCGTTAATGGCCTGAAACAGTTTGTGACTTTGGAC
TTATGATAACGATGTTTGTCCGGGTGCCACCGGATTCTATCGCGCGGAATCAAGTCTAGTCT
GTTTGCATCCATCAAGGCACTGCTCATTGTGTAAATTTGTTCTACGCTTTTGTTCATCAATCA
TATCTAAACTCACAGCCGCTAGGGTAGGTGTGCCTGGCAGTGGTAAGGTAGCCGGCTCGTCT
TTGGTCATGCGCCAATACTGTGCAACGGCCCGCGGTAGCGTTCTTCGGCTTCAACCTTAGA
GCTGATACCTTTTGCCTGGTCAAAGGCGAAACGTCACCTCGCTTTCACTGCTGCTTTTCGC
TTTCATGACTTCGTTTCAAGCGGTCTTTTCGCTCTCGGTTGTAAACACACTGTAGCCTGCT
ATGCTTTCACCGTACTCGAAAAGCGTAGCCTCATGACTAGTTGTACCAACGCCCTTTCTTTT
CTTTTTTTTCTCTTGACACTTCGGCGTATTCATCGCCACTGGTACAAGCCGTATGGTGGCTT
TTTGCTCATTTTTCGTTTGTGACGTTGCGATGGTTTCGCGGACCAATCGCATGGGTGGTGG
ATGTTGTCTTTGCTAGTTGCAACGTAGTCTTCTTCTCTCCTGCGCTTTCTGACGAAATTGG
CCTTACGTATCTTTTTTTCGGCGTCGTTGTGCTCATCGCTGTTTATATAATCGTCGTCACCTCA

TATCGGCGCTTTTACTGCATGCTGTCTTTTGAAGAGAGTTTCATTGAAAAGTAGTGAAGAAA
AAAAAAAAAAAAAAAAAAAAAAAAAAGGAAAAAAGCTTACATACGGAAAGAGAAAAAAAAAA
AAGAAATTTTAA

YKR040C, 167 aa (SEQ ID NO 472)

MTSFQAVSFALGCNTLVACYAFTVLEKRSLMTSCTNALSFLFFLLTLRRIHRHWYKPYGAFL
LIFVLTLRWFRGPiAWVVVDVVFASCNVFFSPALSDENWPYVSFFGVVVVIAVHIIIVVTHI
GAFTACCLLKRVSLKSSEEKKKKKKKKKEKSLHTEREKKKKKF

YOL127W, 1343 bp, exon1: 501-513, intron1: 514-927, exon2:
928-1343 (SEQ ID NO 473)

TCTTATCTTGTATGCCCCGATATAGCAACCTTGTGGTACCAATCTAACGGTTTCCGTACTTT
GCAATGAAGAGATGAGGAGGCATGGGTCACCTATTTAATATGTACGGGTGTTTACATGGAGT
TGCTTTCTTTTTTTGTCTCAGCAGTCATTGTGCGCCAAAAAAGAGAAAACCGTGAGCCGAA
GTCCACGCTCTGGAGTTAGGCTCTCCCATTACGGAGAGAAGCATTTCTCAGCCTGGGAGCC
CCGTTGGAACAGTCAGGCTAAACTGGGCCTTCCTACCCACTGCTTGCTGTTTCTCACTGGAC
GCACAAGGGGATTTTCTTTCTACCTTCGGCTTGCCTCACTGCGTTGGGGCTTCCCAATGCAA
CTTCGTTTCGTATGCATACAATCTTTTAGATATTATCTTTTAAAATTATTTTAAAACAATTTT
AAATGTATCTCATATGCTTTTCTTCTGCTGTTGAAAAGGCTAAACAAAGAAGATCAATAAGA
TAAAATGGCTCCATCTGGTATGTGAAGTCAATATTAATAGCACGAGAAAATTGAGAGGAAG
ATAGATGGGAAGTAGTAGAGTTGATATTGATGAGATACGAAAACACACGTAAATAAACTAT
CCGACGACAAGAATAGTGCATTAAGGACTTGATTAAGATATGGTGAGCAACGTAATTATCGG
GCTCAACAGTTTATTAGCAATCGTTTGTATAGAAGCGTTGATGCTGTGGAAGTTGTTCTTTT
TACTACCAACAGCCATTAACAAATCCATTAGAGTGTTTCGTTTCGTTTCTGCTCAGATTCAA
GAAAATTATTCCATCCTCATTATACCTTTTCTTCTATTTCGTGCTCCACGTCGAGGTATCA
AGGAACATAGTTTACTAACATTAACGAATTCATCTCCTATGAATTTACTTTTTGTATAGCTA
AGGCTACTGCCGCTAAGAAAGCTGTCGTTAAGGGTACTAATGGTAAGAAGGCTTTGAAGGTC
AGAAGTTCTGCTACCTTCAGACTACCAAAGACCTTGAAGTTGGCTAGAGCTCCAAAATATGC
TTCCAAGGCTGTTCCACATTACAACAGATTGGACTCATACAAGGTCATTGAGCAACCAATCA
CTTCTGAAACCGCTATGAAGAAGGTTGAAGATGGTAACATTTTGGTTTTCGAAGTTTCCATG
AAAGCTAACAAATACCAAATCAAGAAGGCCGTCAAGGAATTATACGAAGTTGACGTATTGAA
GGTTAACTTTGGTTAGACCAAACGGTACCAAGAAGGCTTACGTTAGATTGACTGCTGACT
ACGATGCTTTGGACATTGCTAACAGAATCGGTTACATTTAA

YOL127W, 142 aa (SEQ ID NO 474)

MAPSAKATAAKKAVVKG TNGKKALKV RTSATFRLPKTLKLARAPKYASKAVPHYNRLDSYKV
IEQPITSETAMKKVEDGNILVFQVSMKANKYQIKKAVKELYEVDVLKVNTLVRPNGTKKAYV
RLTADYDALDIANRIGYI

FIG. 2:

YBL051C_homolog_1 1229bp PathoSeq: 1..1229; CDS: <1..>1229 (SEQ ID NO 285)

AGAGAACGTATTGAAGAGGAGAAAAGGGAGAAAAGAGGTCAATTGGAAGAACAACATCGTTCTGCA
TCAAATGCTTCTATGGCTTCTTTATTGTCAGCTGCTTCAACTACAGCAGCAACTAAAAATTTGAGT
GTGGCTGGCACAATCCTTCTCATACCACTGAAAGAATGTTTTTAAATTTACCTTTTAACAATTCC
CTGTTCAATGCCCCACCAGTAGAAATTAATTTTAATGATCTTGAAGTTTGGGAATTGTACACTCAA
TTAGTATTATACCGAGATGATATTACCAAATCTACTTTTGAATTAGCTATATCACCAGCAAATTTG
AATATTTCTCAACGGAAAATCATATCAATTTTATGTAATTATTTGAATTTATTAGAATTGTTTGAT
AATGGGTTGATAATAATTAGAAGAAAACCAGGATACATTGCTCAGTGTATAACTCAACAATCTATT
ATTCTTAATTCTCAACAGGTGTCTGGGCCAACTCACCCGCAACAACATCAACAGAATCAACTTCAA
CAACAGCAACAGCAACAACATCAACATCAACATCCTTCACATTCATCATCGATGATGAACCTTCAT
CAATTGGGTGGTACATTAGCTGTTCCAGCGCACCCCTGAATTATTAAGATCCCAATCGCAATCAGCA
TTACCGTTGCCAAGATTGAGACAGCAAACCTCTACACCAATTCAACAAAATCAACAAGTTCAGCAC
CAAAATCAACCACCACAACAACAACAGCAACAGCATGTTCAACCACAATATAATTATTACAATCAG
CAATCTATTCAAAGCCAACCACATTCTGCGAGACCTTATTCTCAATCATATAATATTTATCAACAA
CAACAGCAACAGCAGCAACAACAAGCTCAACAACAAGCTCAACAACAACAACAACAACAATTACAA
TATCAACAGGGACACCAGTCACAAGTTTCAACACCTACATTGAATTCTTCTAGTGCTGCTGCATTA
CTTAGATCAAGTAGCAGTAGATCATTTGTTGATGTGAGATCCACACCTCCCACAAGTAGTTTGTCT
CAACAGCAACAACAACAACAACAACAGCAACAGCCGCCACTAACTTCATCAATCCATGATTCT
CCAACACCACATCATCATTTACCACTTCAACAGCAGCCACCACAACCAAATCATTACCTATCCAAT
TACCATCAGGGGGTTGGATCTCAACCAAAAACCTCCATTGGC

YBL051C_homolog_1 409aa (SEQ ID NO 286)

RERIEEEKREKRGQLEEQHRSASNASMASLLSAASTTAATKNLSVAGTNPSHTTERMFLNLPFNNS
SFNAPPVEINFNDLEVLQYLYTQLVLYRDDITKSTFELAI SPANLNISQRKIIISILCNYLNLELFD
NGLIIIRRKPGYIAQCITQOSIIPNSQQVSGPHTPQQHQQNQLQQQQQQHQHQHP SHSSSMMNLH
QLGGTLAVPAHPELLRSQSQSALPLPRLRQQTSTPIQQNQVQHQNQPPQQQQQQHVQPQYNYNQ
QSIQSQPHSARPYSSQSYNIYQQQQQQQQQQQAQQQAQQQQQQQLQYQQGHQSQVSTPTLNSSSAAAL
LRSSSSRSFVDVRSTPPTSSFAQQQQQQQQQQQQPPLTSSIHDSPTPHHHLPLQQQPPQPNHYLSN
YHQVGSQPKTPL

YBL051C_homolog_2 2153bp public: 1..2153; CDS: 501..2150 (SEQ ID NO 287)

ATAAACAAAAAGAAGCACGAACGTGTTGGGCAACAACAACAACAACAACAACAAAAAATTT
CTGGAAAATCAAATTTGAACCTCAACCAGCAGCGGCGGCGGCGACAGAAAAATATATTAACAGAAT
ACTTTTTTGTATTCAACTCTCTAACTCTTTCTATTTTTTTTTTTTTTCTATATACTGTAAATC
AATCAACAATAGCAGGATATCCATTCATATACAAATAGATAAACTGTTTAATTAATTAATTAATG
ATTTGATTTGGGAAAAACAAATTTTATATTTGGAGAATTGAATTTCAATCATTTTAACAAATTC
AAGCTTTAATTTCCACCTATCAAATTTCAATTATTATTTTGTTTTCATTATTTTTTTTTTCCCTTTC
TTTCTTTCTTTCTTTCTTTTGTGAACAAAGTAATAGCCGATAAAATAAATAATTCACATAGCCCA
ATTCATATTACATTGACTTTTGACAAGAGGTATATATAATGGATTTTAGAAATTTATCAACTACAC
CGAATCAAATGGGCACTGTAATGCAACGTCGTCCCTCTCTATCATCATTTATCGTCAGCCTCGGGCT
ATTCTTCTTCCAATTATGGTGGAATCCTACACCCAATCCCAACAATTCCAATACCAATAACAATA
GTAGTGGCAATAGTAATAACAACACTCATGGCAATAACACTCCCAATTTATCAACTCAAAGATTGA
CAAATAATAGGAATTTACAATCCTTGTGGATAAACCAACCATCTATTGCTCCTTCTAATGTTGTTT
CTTGGGTGGAACAGCAACAACAACAACCAACCTTGATCTGTTGGAAAATAATACTAAAACAGACTCCA
GTAATGATGCTTCTGCTACTAATAATAATAATGTTAATGTTAATGTTAATGCCAATGCCAATGTTA
ATGCCAATGCCAATATCCATGCCCAACCCATGTCAACACAAATGTTAATGCAAACACAACAGCAA
CTAGTATTAATGCTTCCACGATTTTAAATACTACACCAAGTATTAATGACACTAATGATAATGCCA
AAAAATTAATGTTTCCATGATTAGTAATAACAATAACAATAACAGTAACAATAATAACAACAACA
CTAACAATAGTAGTACAGGAAGTTCTAACATTGCAAACATGCTTCCTTCTGTTTCTAATGCAACGA
CAATGAATAACAGTAATAGTATCAATAGCACCAACAATACTACAATTAACGAAGCTGATGATG
ACGAGTTAATTCCTACTGCGATTGTGATTAAAAATATTCCATTTGCCATTAAAAAGGAACAATTGT
TAGATGTGATGACAAAATTAACTTGCCATTACCATATGCCTTTAATTATCATTTTGATAATGGTG

YBL051C_homolog_2 550aa (SEQ ID NO 288)
MDFRNLSTTPNQMGTVMQRRPSLSSLSSASGYSSSNYGGNPTPNPNNSNTNNNSSGNSNNNTHGNN
TPKLSTQRLTNNRNLQSLWINQPSIAPSNVVPWVEQQQQQTLDSENNTKTDSSNDASATNNNNVN
VNVNANANVNANANIHAQTHVNTNVNANTTATSINASTILNTTTPSINDTNDNAKKINVSMISNNNN
NNSNNNNNNNTNNSSTGSSNIANMLPSVSNATTMNSNSINSTTNNTTINEADDDDELIPTAIVIKNI
PFAIKKEQLLDVMTKLNLPYPYAFNYHFDNGVFRGLAFANFTSTDETSAVVNQLNGREIGGRKLRV
EYKMLPAQERERIEREKREKRGQLEEQHRSASNASLASLLSAASTTAATKNLSVAGTNPSTHTTER
MFLNLPFNNSSFNAPPVEINFNDLEVLLEYLTQLVLRYRDDITKSTFELAISPSIFEYFSTENHINLC
NYLNLELFDNGLLLIRKKPGSIAQCITQKSIIPNSQQVSGPTHPHHHQKNQLHQQQQQHTSTSTS
LTFIIDDEPSSIGWYISCSAP

YBL066C_homolog 3254bp PathoSeq: 1..94/2146..3254, public:
95..2145; CDS: 501..3251 (SEQ ID NO 289)
ATAAAAAAGAAATACAATTAATAAAATTTTCCTTCTGTGAAAAGGCAATTTTCGGGTCTAGTAGTA
AACAAAGCTTAATAATTTCTCCCATTTCAAATTTACAACGGACGATGCAGAAAGTAGTTTTCAAATTT
CAGTTTCTTTTCTTTTATATATTTTTTTCTTACTTTCTCTTCTTCTTCTTCTTCTGACAGTATATTAATA
AATATTCTTTTAACTTATTTTTTCAATCAAGAAGGTACTGAAGATATCAATTAACCTCTCAGTTAAA
TCCATATTACCAGTTGTGGAATAATCAGAAGAAAAAAAAAAAAAGAGAGAAAAATCACGGGAATTAC
GTTCTCAACAGAAAATAACAATAATTTTTTTTTTTTATTCAATTCGAAGGTATAACAAGAACGTTAGGAA
TAATATAAAATTATCACCAAAGCTGCCATCAACGTGTGTCGACAACCAATCGACTCCTCCCTTAAC
TAGAACCATAGAACCTCAACATTTGTTTCTATAGAAAAATGAAGTTTGAAAAAGGTAAAGTGAGAA
TTTTGCCTAAACCATCCCCCTACACCAACCAACCCACAAACCCCATTTGCCATTACTTCCAGCTCAA
CTAAACCTGTAAACTCAAAAAGAAAATCAGCAGCCAGTACACCTGGAAATGAATCAAAGAAATCAA
GAAATCAAATTTCTACAGCTTCAACACCCAACAGTGCTACACCAACATCAGTCGGAACACCTCCAC
AGAAAACCTCCAAACCAACAGGTCATAGGCCAGTGACTTCATGTACTTTTTTGTCTCAACATAAAA
TCAAATGTAATGCTTCAGATAATTATCCAAACCCATGTGAAAGATGTAAAAAATGGGTTTGAAAT
GTGAAATTGACCCCGAATTTAGACCTCGCAAAGGGTCACAAATCCAATCATTGAAACTGGATGTTG
ATGAATTGAAGGCCAAGATTGAAATGTTGACTAAAAATGAATCTTTGCTCACACAAGCTTTGAATC
AACACAATTTGAACCACGCTTCGCAACAGCAACAACCTGTCTGGATCGCAATCTCAACAACAACATC
CTCCAAATCCACAACGTGCATTGTTCATATACGTCTGCAAACTCATCACCACAAGTTGCATTTAGCA
ATGCATCGCCAATTCCCTTCTGTGACAAGTATTCAACAAAATGCACCGTTGACTCACGAAAATTCGG
ACAATTCTCCATACGCTTTAAATACACCAGAAAACATTGAAGAATTACAACCAATCTCAGAATTTA
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TTTTCTGGGCCGTGATTCTTACCGCAAGCTTATCAGAACCAGAACCCAACTTTATATGTCGTTGG
CATCCTTAATTAAACAATTAGCAATTGAAACATGTTGGATTAAAACACCAAGATCAACTCATGTTA
TCCAAGCCTTGATCATACTTTCAATATGGCCGTTACCTAATGAAAAAGTTTTGGATGATTGCTCTT
ATAGATTTGTTGGATTGGCAAAGAAGCTTGTCAATTACAATTAGGTCTACATCGTGGTGGAGAATTCA
TTCAAGAATTTAGTCGGAATCAAGTAAGTCTAGGACCTGATGCAGAAAGGTGGAGGACTCGTTCAT
GGTTAGCAGTTTTTCTTTTGTGAACAGTTTTTGGTCATCATTGTTGGGGTTGCCACCTTCAATAAACA
CTACTGATTATTTATTAGAGAATGCTCGTGTGATAAATCGTTGCCTAAAAATTTCCGTTGTTTGA

TTTCGCTATCTATTTTCCAATGCAAATTAGTTAATATTATGGGTATTAGCGTTACTAGACCAGACG
GTTTATTGGAGCCTCTGAATCGTGCTGGTTCACCTTAGTTTATTGGATAGAGAATTGGAAAGATTAA
GATTTAAACTTCAATTTGAAGAAGGGGGGCCAATTGAAGTATATTATTGTATATTAAATTGATGA
TCTGCTGCTTTGCCCTTTTACCAGGTACACCTATCGAGGATCAAGTCAAGTATGTCAGTTTTCGAT
ATTTATCAGCAACAAGAATCGTGACAATCGTTTCTAAAATGGTGAATGACATTTTCATTGATTGAAT
TGCCAATATATATCAGACAAGCAGTGACATATAGTGTTTTTCATGTTGTTCAAATTACATTTGTCAA
GATATTTGATTGACAAGTATGTGGATAGTGCTAGACAGCTGATTGTTACTGTGCATCGTTTATTTA
GAAACACGTTGAGTTCCTGGAAAGATTTGCAAAACGATATTTCTCGAACAGCCAAAGTTCTAGAAA
ATTTGAACATGGTGTGTATAATTATCCTGAAATATTTTAAATGATCTGGAAAATGAGGATTCAA
GTATTATCACCAGAATGAGGTCACATTTGACAGCATCTTTATTCTATGATTTGGTTTGGTGTGTAC
ATGAGGCAAGAAGACGATCAGTACTTGATAAGGGGAAAAGACAGGCTCAGCCTAACAAAGAAAATCT
TGCCCTTGCCATTTTACAACCAAAATCACTAAGGATGATTTCAAGACAATTACCACGACATCACCTA
ATGGAACACTACTATTACTACATTAGTTCCAACCTGATCAAGCTATGAATCAAGCAAAACTGAAATCTT
TTGATTCCAGCAAACCACTTGAAATAAATGGTATTCCCTTACCTATGCTTGAAGCTACTGGTTCAA
CAAGAGAAGTTTGTAGATTCTTTACCCTCGCAATCTTTACCATCACAAGCACCAACTCTTCAGCAGT
ATCCAATGCAGCAAGATCAACAACAGCAAGAACCATCACAACAACAACAACAAGCACCTGCAGC
AACTGCAGCAATACCAACAACAGCAGCAATCGAATCAACAGCAACCACATCTTCAACATCAAAGAC
AGTTTCAACAATCACCACCACCGCAATTTTCAATGATTTCTTCAACGCCGCCCTTCAGCAACCAC
CTTTTATTTTGGCAAACCTCACCCTTACCACAACTTATTTGCCAAAGATTGATGAAATGAATATGT
CACCAGAAGTAAAACAAGAAAACCTCTGTTGCTCCATTTGCATCTCAAATCACCAACTTTTTTGATC
AACAAACAAGTGGATGGTTTAATAATGATAACCAAGATGACGACTTTTTGGGTGGTTTGATGTTA
ATATGATGCAAGAGAAATAA

YBL066C_homolog 917aa (SEQ ID NO 290)

MKFEKGKVRILPKPSPTPTNPQTPLPLPAQTKPVNSKRKSAASTPGNESKKSRSNSTASTPNSA
TPTSVGTPPQKTSKPTGHRPVTSCFRCRQHKIKCNASDNYPNPCERCKMGLKCEIDPEFRPRKGS
QIQSLKSDVDELKAKIEMLTKNESLLTQALNQHNLNHASQQQQSSGSQSQQQHPPNPQRALSYSYSA
NSSPQVAFSNASPIPSVTSIQONAPLTHENSNDNSPYALNTPENIEELQPISEFILGDVTLPLNRAN
ELHDKFMTTHLPFLPIIISRSATELYHKSQLLFWAVILTASLSEPEPKLYMSLASLIKQLAIETCW
IKTPRSTHVIQALIILSIWPLPNEKVLDDCSYRFVGLAKNLSLQLGLHRGGEFIQEFNRNQVSLGP
DAERWRTRSWLAVFFCEQFWSSLLGLPPSINTTDYLLNARVDKSLPKNFRCLISLSIFQCKLVNI
MGISVTRPDGLLEPSNRAGSLSLLDRELERLRFKLQFEEGGPIEVYLYIKLMICCFALPGLPTPIE
DQVKYVSFAYLSATRIVTIVSKMVNDISLIELPIYIRQAVTYSVFMLFKLHLSTRYLIDKYVDSARQ
SIVTVHRLFRNTLSSWKDLQNDISRTAKVLENLNMVLYNYPEIFLNDSENESSIIITRMRSHLTAS
LFYDLVWCVHEARRRSVLDKGRQAQPNKKILPLPFYNQITKDDFKTITTTSPNGTTITTLVPTDQ
AMNQAKSKSFDSSKPLEINGIPLPMLEATGSTREVLDSLPSQSLPSQAPTLOQYPMQDQDQDQEPS
QQQQQKHSQQSQYQQQQQSNQQQPHLQHQRQFQQSPPPQFSMISSTPPLQQPPFILANSPLPQTY
LPKIDEMNMSPEVKQENSVAPFASQITNFFDQQTSGWFNNDNQDDDFLGWFDVNMMQEK

YBL078C_homolog 908bp public: 1..908; exon 1: 417..449, intron 1:
450..533, exon 2: 534..908 (SEQ ID NO 291)

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CTTTTTTTTTTATTTATTTATTTTGTATTTTGTATATTAATCAAACCTATTATCATTCATCTATATA
TACATCCCCATCGATTCATCTGACATAATAGTATGTATGATCATAACAGAGGGAAAATCACCTTTT
TATTATTACCAAGGTCTCAATGATTAGTGTGGCTAGCGTCTGTACTACTTACCCCGTGTTTGTAG
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ACTTAGAAACATCACTCATAATGAGATCACAATTCAAAGACGAGCATCCTTTTGGTATGTATTACA
TGATTTTTTAGTCCTCTGAATCTTCTTCCGATCATCATATACTAACATTTTCGTGGGTGTTATTCTT
TAATAGAAAAGAGACAAGCCGAGGCAGCCAGAATTGCTCAGAGGTTCAAGGATAGAGTACCAGTCA
TCTGTGAAAAGGTTGAGAATTCCGATATCCCCGAAATTGATAAACGTAAATATTTAGTGCCAGTGG
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TTTTCATCTTTGTCAATGACATATTACCCCCAACCGCTGCATTAATCAGTACAATCTACGAAGAAC
ACAAGGACGAAGATGGTTTCTTATACGTTTTTATACTCTGGAGAGAATACTTTTGGCGAGAACTAG
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YBL078C_homolog 135aa (SEQ ID NO 292)

MRSQFKDEHPFEKRQAEAAARIAQRFKDRVPVICEKVENSDIPEIDKRKYLVPVDLTVGQFVYVIRK
RIKLPSEKAIFIFVNDILPPTAALISTIYEEHKDEDGFLYVLYSGENTFGEKLAIDISSLDFSDIP
DYV

YBR073W_homolog 2891bp PathoSeq: 1..2891; CDS: 501..2888 (SEQ ID NO 293)

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CGTCCCTAAATATGAGTCAAGTCCAACAGAAACCCAAATCGTTTGGTAGATTGTATACCATGTACT
ACTTTCATTTTCCATTTGTTATGCTTACGACAACCTGAAACCATGCTACTTCATACGTTTGTATTGA
TGTTTGCCTTATTGGTTGCCTATGGGATCTACGCTTATTGCTTCAAGTATCATGTTTGCAATCT
CCAGAGCATACTATTATGTTTTTGGCATGGATATTAGTACCATCAACGGTTATGCAAAGTAGCGCT
GTCTACTTAGTTTTATAGTTTTAAAAATTTGTTAATATAAACCCAAAGTTTCTAACAGGCTCTGTTT
GCTCGACTAAAAAAGAATTTTGTCAAACGCGTATCAGAATGTTTACCCTTTTTTTTTTTTACCACAG
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CTACCGATCCCGGCTCAACAAAATACGTGATCCAATGGAGAAAGAAAACCTTCAAAGAAGAACAAAA
CATGGGACGGTGATGGGTATGCCGTGATTAAACAGCTTGAGAATGGGGCATGCGAGATATCTATCA
AGAACTCTGATGGCAAACCTATGGGGAAAAGAGTGTTTACTGCGACACCTAACCTTGACGACGTGA
TTAGTGTGGGACCCCTATGAATTAGAATTAGACGAAAAAGTAGGGTCTAACTCAACTCCCCAGACAG
TGACACGTGTTACCCACCAGTTCAAAAAGGTTGCTCCTCCCACAGCTAGTAGTCGGAAACCGCTTT
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TTAGGAAATGGTTAGGTGCTAATAAGCTAAACGTGTTGACGCTCAACAACCCCAATGTCAAACGAGA
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GTTTGAAGAATAGTGCAAATAAAGTATTGAATAATCTTATCAAGCTCAATATTCCGAAGAAAATTG
TTTTGACGGGTACGCCGATTCAAAACGAGTTGGTAGAGTTTCACACGTTGATCTCGTTTCTCAACC
CGGGTGTGCTTCCCGAGCTAAAATTGTTTCAGCGAAACTTTATAACACCTATATCTAGGGCCCGAG
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AGAAATTTAATCAGTTTGAGGCATTTACCATGATCAATTTGTTTAAAAAGATTTGCAATTCCCCTT
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CCGGTAAAATAAACATTCTTGTGCCGTTGCTATTGGAAATTGCTTCGCTTGGGGAAAAGATTGTCT
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CGTCCAAATCTGATGTGTTTGACAATGATGATTGGAAGAATATTTTTGAGATAGATACATCGACAA
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TTGACGATGGTGAGGCGCTAAAGAGGACGGCTGTTAAATTTGCCTTGAACGATTATCGACACTACA
ATCCAGAGGTGAACCGTAATTTGGATTTTGATTCTGCGCTACACCGAATTGCTAACAATTCAAGCT
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YBR073W_homolog 796aa (SEQ ID NO 294)

MFTLFFFTTDQMNVRPNAPFRPPRIKGGVAVVQKVVKRKLPTTNPKPAILTTDPGSTKYVIQW
RKKTSKKNKTWDGDGYAVIKQLENGACEISIKNSDGKPMGKRVFTATPNLDDVISVGPYELELDEK
VGSNSTPQTVTRVTHQFKKVAPPTASSRKPLYDDCADAIALPPPPKAKDYVKVNIDPHLAKVLRPH

QVEGVKFMYECLMGYRGFGGHGCLLADEMGLGKTLMTITTTIWTLLKQNPMEKGAVVNKVLVVCPU
TLISNWRQEFRKWL GANKLVLT LNNPMSNEKQDILNFGKLVYQVLVVNYEKLVAHFDELSAVKF
DLLVCDEGHRLKNSANKVLNNLIKLNIPKKIVLTGTPIQNELVEFHTLISFLNPGVLPELKLFQRN
FITPISRARDINCFDPEVKKRGEESISQQLIELTQSFILRRTQAILANYLTQKTDILLFVPPTSLQL
KLFDYITNLKKNQFEAFTMINLFKKICNSPSLLADDELFFKKIVEEFNLGMASGKINILVPLLE
IASLGEKIVLISNYTKTLDLLEQVLRKVSLTF SRLDGSTPNNVRSKLVNQFNTNPDINVFLSSKS
GGMGINLVGASRLILFDNDWNPATDLQSMSRIHRDGQLKPCFIYRLFTTGCIDEKIFQRQLVKNKL
SSKFLDNDATSKSDVFDNDDLKNIFEIDTSTISNTHDLLECVCEGDGSMLSQPTIEESEPPPKQAW
VTALELKKKIDDGEALKRTAVKFALNDYRHYNPEVNRNLDFDSALHRIANNSSYENKQLPITFIMS
RVTN

YBR086C_homolog 2643bp PathoSeq: 1..2643; CDS: 501..>2643 (SEQ ID NO 295)

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TTCTTCTAATTTAGTTTACAGAATAGAAAGAATAGTTTGCTTGTTTGCTCATATTTACAATCAATT
GGTTATTGGTGTTTATTATTTTTTTTTTGGTTCCTCTTTTTTACCCCCCTTCCGTCTAATTGAGTTA
TTGTTTGGAATAATTTATTACTTATTCAATATATTTTTTTCTTCTTCCCTTCTTCAACTTCTTC
TTTATACATTTCAATCAACCTTCCAACAATCCTATAATTACTTACTTACCTTCTTCAATTGGATTA
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CTGATTATTATATTTCCGTCAATTATCCTACCACCGATAATGGATCACCAACCCCAAGCTGAAA
AATCATTGAAAACATTAATTGATTTATTATACGATAAAGGGTTTGCCGCCCAAATTAGACCTGGTG
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ATTTAATTAAAAATTATGAATTTGGTGTCACGGGTAAAGATGACGTGTTAGCTTCTAACTTAGAA
TTATTTATCAATACTTAACTTATCCACAATCAGTTGGTGATGTGGTATTACTCCTAATTTCTGGGG
ATTGGAAATTTGTCACCAGTATTGTTCCAATTACTAATGCCCTTAAATGAAACCACTTTAGTTGAAG
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GGGGGGTTTTATTCCTTGCATCATGGCATAGAAGAGAACAACTTTGGTTAATGTATGGGGTGTTTC
AAAATAGTCATTTAATTGAAGAACATAATTCCGAATTGGCTAAAGTCAATGAAAGATATGAAGAAA
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GTGTATTTGTGCCAATTTTGACCATTGTTTATAATGCTGTCACGGATATTATTATTAAATGGGAAA
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ATGATTTTAGAGGATTAGTTTTACAATTTGGATATTTGATAATGTTTGGTCCAGTTTGGCCATTGG
CACCATTGGTTTGTATTATTTTCAATTTAATTTTTTTTCAAGTTGGATAATTTTAAATTATTGAATG
GTAAATATTTCAAACCACCAGTTCCAAGAAGAGTTGATTCTATTATCATCCATGGAATTTAGCCCTTT
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CTCCACCAAATCTATGGGTCAATTTGCCCTTGATAAAGCTAGTGTTTCATGTTTCATCCTCAGTTT
TCTTGTTTTTATTAATGTTTGTTCAGAACATGGATTTTTGATTTTGAGTTATCTTTTATTGAAAT
TCTCTTCTTTGTTCAAGAGTCAAGTTGAATGGGAAAATGATTTTGTTGATAATGATATTAAATTGA
GACATGATTATTATTCTGGGAAAGTAAAACCACTTATAAAGTCCACTCGGATGAGTTGTGGGAGA
AGTTTACCCCAATCAACTTTGAATTTCACTGGTCCTAAACCAACCGCAGAACTGATGATAAAG
TTGAAAAAATTGCTTCTACCGAAGATGCTTATCTGACTTCTGCAGAAAAATCTACTACTACTGCTA
CTT

YBR086C_homolog 714aa (SEQ ID NO 296)

MTLPIQDLEPDYYISVNYPTTDNGSPTPQAEKSLKTLIDLLYDKGFAAQIRPGDLDHLLVFKLSS
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AFNETTLVEDLKINVTQPNLSIATIKKTYGVEVALYFEYIKHYTFWLLLLSIIGLVSHFRKDKRFS
LTFAFINLLWGVFLASWHRREQHLVNVWGVQNSHLIEEHNSELAKVNEREYEEKSTYFHANNTNGF
RFLKQLAFIPIALVFVGVLSYQLSCFCIEIFLTDIYDGP GKSLTLLPTVLISVFPILTIVYNA
VTDIIKWHNDNQYSKNNLSLVKTFVLNFLTGYVPLIITSFIYLPFAHLVQPHLGDIKTITIATYA
GENRFYTKYLLKLKSQEEFKINQGRDAQFFYFIVTNQVIQLVLKYILPLGLRFVFNFIETKIQKK
PQLQTKDDNPDESIWLHNVRSLKLPEYNVDDDFRGLVLQFGYLMFGPVWPLAPLVCIIIFNLIFF
KLDNFKLLNGKYFKPPVPRRVD SIHPWNLALFLLAWIGSII SPVVTAFYRHGTAPPKSMGQFALDK
ASVHVSSSVFLVLLMFVSEHGFLILSYLLFEFSSLFKSQVEWENDFVDNDIKLRHDYYS GKVKPTY
KVHSDDELWEKFTPQSTLNFTGPKPTAETDDKVEKIASTEDAYSTSAEKSTTTAT

YBR093C_homolog_1 1784bp public: 1..607, PathoSeq: 608..1784; CDS:
399.1781 (SEQ ID NO 297)

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CTAACACCTTTTATTTTGTGTTATACAAATTGCACAATCAATTACTATAACTTTTTTTTGAAACGT
GGGCTCTGTTTAGTTTAACTTCTGTAGTTTTATTATTCCGATTGGGTTAGCTCAATAACTGCATT
TCGTACAATAATGTTAATTCAATTCTAAATTCGGATGAACCGAACACACAAAAACATCCAGTTCT
GGAGAGATTTTTCAAAACCTTCTATTATAAATAGAACCCTATAAGTCCATAATAATTCAATTGAAGG
ATTATTTTCTTTTCCCTTTTCTGATTACTTTCACCAATTTTCTTCTCTCAAAAAAACACCTTCT
TCATGGTTTCTGTTTCTAAATTAATCAATAACGGGTGTTATTAACTAGTCAAAGTGTTTCCAAG
ATGTTGCTACTCCGCAACAAGCTTCTGTGCAACAATAACAATACTCAATTTTCTTGGCGGTAGTG
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AAATTCAATTGTATTCAAGACATGGTGAAAGATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAG
CAATTTATGCTAAATTTGAAAACCTACAAAGGTACTTTTAAAGGTGATTTGTCATTCTTAAATGATT
ACACTTATTTTGTCAAAGACCAGAGTAATGCTAAGGAACTAGCCCAAAAAATTCTGAAGGAA
CCTATGCCGGTACAACCAATGCCTTGCGTCATGGTGCTGCGTTTAGAGCCAAATATGGATCCTTAT
ACAAGGAAAACCTCAACTTTACCAATCTTCACATCCAATTCTAACAGAGTACATGAAACTTCAAAGT
ATTTGCTAGAGGGTTTGTAGGTGATGATTATGAAGAAGGTAAAAGTGTCAAGTTTAACATCATCT
CTGAAGATGCTGATCTTGGTGCCAATAGTTTGACTCCTAGAAGTGCATGTTCCAAGAACAAAGAAC
TGAGCAGTAGTACTGCCAAAAATATAACACAACATATTAAATGCTATTGCTGAAAGATTAGTTA
AACCAAACCCAGGTTTGAATTTGACTACAAGTGATGTCAACAATTTATTCAAGTTGGTGCTTATG
AAATCAACGTCAGAGGAAGTTCACCATTTCTGTGATTTATTCAACCAATGAAGAATTCATTAAGAACT
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AAGATTTACCAACATCTTACATCCCATTTCCCTAACCCATACGTCATTCTTCTATTGTTCCACAAG
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ATGCTGTGCTGCCAATTCCAAATGTGCTACTGGTCCAGGGTTCTCTTGTAAGTGTGATGATTTTG
AAAATTTGCTTAAAGAAAGAATTGGAGATGTTGACTTTGTTAAACAATGTGGTGTCAATAGTACCT
ACCCATCTGAGCTTACTTTCTACTGGGATTATAAAAATGTCACCTTACAGTGCTCCTTTAGAATTGT
AA

YBR093C_homolog_1 461aa (SEQ ID NO 298)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHGERYPKSNKGSLEAIYAKFENYKGTGKGLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAFFRAKYGSLYKENSTLPIFTSSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLFIFHSALGLEPAEDLPTSYPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYSAPLEL

YBR093C_homolog_2 1871bp public: 1..1752, PathoSeq: 1753..1871;
CDS: 501..1868 (SEQ ID NO 299)

GAGTTTATGGGATTGGGTTTTTCAATTAAAGACTCTTCGTGATAATGCAATACCAAACCAAAT
TTATTTAACGATGCAATAATTATTTCATGTGAGCTATCCATGAATCAGTGAGAATCTTTATTATG

GAAGAAATTGGTCAAAATTTGACAATGTTTAGTAACTTTATATCTTGGTGTTGGGATGGTGCCACA
AATGGAGATTGTTGAGTGACATGAAAAATACGTAGTTAAATTTTGTTCCTTGTTCCTTATTTATTTA
GCCACTTTTTTATCCGATTCTTCATATTACCTTTGGTAAAGTGATAAGATTAATATCATATTAGTA
AAACACCCCCAATGATGAATGTTTGTATTTATAGCCAGACTATAAAAATTACGGGGATTTAATTTCG
CGACTCACCCACGTTCTCACACAGTATGTGCTTTTTTCATAAGTATGATTTGAACCCTAAAATATC
AACTTTTCATAATAAACATAATTCTTTCCAGACAACATAAATGGTTGGTTTATCACGAGTACTTAATG
CTGGGTTTATTTCTAAGTGGACAATCTGTTTTCCAGGATGTTGCTGCCCCACATCAAGCATCAATTG
AACAAATATAATATTGTCAAGTACCTTGGTGGCAGCGGTCCATATATTCAAAATTCAGGGTATGGGA
TTTCTACTGATATACCAGAAAAATGCACTATTGAACAAGTTCAAATGATTAGTAGACATGGTGAGC
GATTTCCCTAGTAAAGGAGATGGGAAATACTTTAATTCAGTGATGGAAGTTTCAAGAGATATGGTG
AATTTTCATGGAGATTATCTTTTTTAAATGACTATGAGTATTTTCGTTACTAATCCAGATTATTATG
AAAAGGAGACTACTCCTAAAAACTCAAAAGGTCCATATTTTGGAACTACAAATTTATTACGACATG
GAGCTTATTTTAGAAAAAGATATCAATCACTATTTGACCAAAGGAGAAGCTTGTGTGTTTACTA
GTAATTCTGGAAGGTGTTATCAAAGTGGTGTCTATTTTCGCTCGAGGATTTTATAGGAGATGATTACT
CAGAAGATACAGTTGAATTTGTTGTTGTTGATGAAGACAAAAAATGGGTGGTAATTCATTGACAC
CAAGATACGCTTGTAACACTTTGAATCAAGATTTACACAAAGATTTGGTGAATCAGTACGATAAGA
CTTATTTGGACGATATTTTATCTAGATGGCTAGTAGACAATCCTGGATTAGATTTAAGTGCAGATC
AGGTCTCGTCATTATTTCTTTGGTGTGCCTTTGAGATTAACGTTAGGGGGTATTCTCCATTCTGCA
ATCTATTTACAAAAGATGAATTTATCAGAAGTGGGTACCGAAACGATGTTGGTAATTACTATCAAA
CTGGTCCAGGTAATAATATGACAAAGGTAATTTGGCTCACCTATGGTGGAAGCGTCGTTGAAAATGC
TTCAAGAAGATTCAAAAATTTGGTTGACATTTACCCATGATACTGATATTGAGATGTATTTGACAT
CTTTGGGATTGATTGTTCCACCAGGGGATTTGCCCCGTTGATCGAGTACCATTTCCTCAATCCATATA
ATGCAGCAGAATTTTCCCTCAAGGTGCTAGAACTTACACTGAAAAATTGAAATGTGGTGAAAAGC
AATATGTTAGATTTATTGTGAATGATGCAGTTTATCCATATCCGGATTGTAGTGGAGGTCCTGGGT
TTACTTGTGAATTGAATGATTTTATCAAATTAGTTAAAAGTCGTTTACATGATGTTGACTATAAGC
TTCAATGTGAAGTGGACGGACCGGAATTGACATTTTATTGGGATTATAAAGACAGAAAGTATA
ATGCCCGCTTAATAGATCAGTAA

YBR093C_homolog_2 456aa (SEQ ID NO 300)

MVGLSRVLNAGFILSGQSVFQDVAAPHQASIEQYNIVKYLGGSGPYIQNSGYGISTDIPEKCTIEQ
VQMISRHERFSPKSGDGKYFNSVMEVFKRYGEFHGDLNFLNDYEFVTNPDYEEKETTPKNSKGPY
FGTTNLLRHGAYFRKRYQSLFDQKEKLTVFTSNVSGRCYQSGVYFARGFLGDDYSEDVFEVVDDED
KKMGNSLTPRYACKTLNQLHKLVDLVNQYDKTYLDDILSRWLVDNPGDLDSADQVSSLFLWCAFEI
NVRGYSPFCNLFKDEFIRSGYRNDVGNYYQTGPGNNMTKVIGSPMVEASLKMLQEDSKIWLTFTH
DTDIEMYLTSGLIVPPGDLFPVDRVPFPNPYNAAEFFPQGARTYTEKLKCGEKQYVRFIVNDAVYP
YPDCSGGPGFTCELNDFIKLVKSRLHDVDYKLQCEVDGPAELTFYWDYKDRKYNAPLIDQ

YBR093C_homolog_3 1888bp PathoSeq: 1..1656, public: 1657..1888;
CDS: 500..1885 (SEQ ID NO 301)

TGTAGTATAAATAAGGGTATGAAATACCAACATCCCAGAATATCAACGAGATAGAAGAGAGGAGTT
TCAATATATATCTTGTGAATAATAACTTCGTTCTAATTCACTATACACAACCTAGACGTGTACACGC
TCAATCTCAGGTAAAGAAAGTTTATATTCCATCACTATATAACAACAATCAGGCTTTGCAAAAAA
CATTTAAACTAATACTGGTAATATGGAAATATAACGCCTCGTAGTTCTACGCACGTGGCATCCTT
TATCTATTTATTCAATTTACCCCTAATTTATGAATTAGCTTAATAAGAGCAGTCAAATTAACACGG
CTCAATTAATAGTACTTAATAATATGAAGCCGATCAATTAACCGATCCTTTGAATAATTTGAAAAT
AAAATAAAGTAATATAAATAGGTATGCATTTTCCCTACATTTATTTCTCTTTCTATTTTAATTTG
TTTCCTAAACAGCAACAACAACAATTTGAAATTCAAAAATGGTTTCTGTTTCTAAATTATTGAACAA
TGGATTGTTATTAGCTGGTCAAAGTGTCTTCCAAGATGTTGCTACTCCACAGCAAGCTTCTGTGCA
ACAATATAACATCGTCAATTCTCTTGGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGAT
TTCTACTGATATCCCTGCTGGTGTGAAATTTGCTCAAATTCATTTGTATTCAAGACATGGTGAAAG
ATACCCAAGTAAAAGTAATGGTAAAAGTTTAGAAGCAATTTATGCTAAATTTGAAAACCTACAAAGG
TACTTTTAAAGGTGATTGTTGCTTTCTTAAATGATTATACTTATTTTGTACTGATAAAAACAATTA
CGAAAAGGAACTAGCCCCAAAAATTTCTGAAGGAACCTATGCCGGTACAACCAATGCCTTGCGTCA
CGGTGCTGCGTTTAGAGCCAAATATGGATCCTTATACAAGGAAAATTC AACATTACCAGTTTCTC
TTCCAATTCAGGTAGATGTTACCAAACCTCAAGATATTTTGTAGAGGATTTTATAGGTGATGACTT
TAAAGAAGGTAAAACCTGTCAAGTTTAACATCATTTCTGAAGATGCTGATGTTGGTGCCAATAGTTT

GACTCCAAGAAGTGCATGTTCCAAGAACAAAGAACGGAGCAGTAGTACTGCCAAAAAATATAACAC
AACATATTTAAATGCTATCACTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAAG
TGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCTG
TGATTTATTCACCAATGAAGAGTTTATCAAATATTTCTTATGGTAATGACCTTTCCAACCTATTATTC
TAATGGTGTGCTGGTAACAATTACACCAGAATCATTGGTTCAGTGATTTTAAATTCTTCTTTAGAACT
TTTAAAAGACACTAAAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAAT
TTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCCC
TAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAATG
TGGAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCGTGCCAATTCCAAAATGTGCTAC
TGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATGT
TGACTTTGTTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATTA
TAAAAATGTCACCTACAATGCTCCTTTAGGTGATTTTAA

YBR093C_homolog_3 462aa (SEQ ID NO 302)

MVSVSKLLNNGLLLAGQSVFQDVATPQQASVQYQYNIIVNSLGGSAFYIQRNGYGISTDIPAGCEIAQ
IQLYSRHERYPSKSNKSLKAIYAKFENYKGTGKDLAFLNDYTYFVTDKNNYEKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSYKENSTLPVFSSNSGRYQTSRYFARGFLGDDFKEGKTVKFNIIS
EDADVGANSLTPRSACSKNKERSSTAKKYNTTYLNAITERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKYSYGNLDSNYYSNGAGNNYTRIIGSVILNSSLELLKDTKNSNQVWL
SFAHDTDLFIHSAFLGLEPAEDLPTSYIPFPNPVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFVKQCGVNSTYPSELTFYWDYKNVTYNAPLGDF

YBR093C_homolog_4 1886bp PathoSeq: 1..102/1038..1062/1078..1886,
public: 103..1037/1063..1077; CDS: 501..1883 (SEQ ID NO 303)

ACTACTTAAATTGGCATATCCAAACAACTTGAAGTAGGAGTTTCTTATTTTATTTTGTATTTA
TATATTTGATTGCGATTAATGTCATAAATTTTAGTTCCGTAATTATGTCACAAAAACAAACAATCA
ACATATTAAATCGTTATCCCAACTTTGTCAGTTTACTAACACCTTTTATTTTGTGTTATACAAAT
TGCACAATCAATTACTATAACTTTTTTTTGAACGTGGGCTCTGTTTAGTTTAACTTCTGTAGTT
TTATTATTCCGATTGGGTTAGCTCAATAACTGCATTTCTGTACAATAATGTTAATTCAATTCTAAAT
TCCGATGAACCGAACACACAAAAACATCCAGTTCTGGAGAGATTTTTCAAAACCTTCTATTATAAA
TAGAACCTTATAAGTCCATAATAATTCAATTGAAGGATTATTTTCTTTTCCCTTTTCTGATTACTT
TCACCAATTTTCTTCTCTCCAAAAAAACACCTTCTTCATGGTTTCTGTTTCTAAATTAATCAATA
ACGGGTTGTTATTAAGTAGTCAAAGTGTTTCCAAAGATGTTGCTACTCCGCAACAAGCTTCTGTGC
AACAATACAATATACTCAATTTTCTTGGCGGTAGTGCCCTTATATTCAAAGAAACGGATATGGGA
TTTCTACTGATATCCCTGCTGGTGTGAAATTGCTCAAATTCAATTGTACTCAAGACATGGTGAAA
GATTCCCAACAGCAAGTAGTGGGAAAGATTATGAGAAAATTTATGCTAAATTTAAAACTACAATG
GTACATTCAAAGGTGATTTGTCAATTCTTAAATGATTACACTTATTTTGTCAAAGACCAGAGTAACT
ATGCTAAGGAACTAGCCCAAAAAATTTCTGAAGGAACCTATGCCGGTACAACCAATGCCCTTGCCTC
ATGGTGTGCTGCTTTAGAGCCAAATATGGATCCTTATACAAGGAAACTCAACTTTACCAATCTTCA
CATCCAATTCTAACAGAGTACATGAACTTCAAAGTATTTTCGCTAGAGGGTTTTTAGGTGATGATT
ATGAAGAAGGTAAACTGTCAAGTTTAAACATCATCTCTGAAGATGCTGATCTTGGTGCCAATAGTT
TGACTCCTAGAAGTGCATGTTCCAAGAACAAGAACTGAGCAGTAGTACTGCCAAAAAATATAACA
CAACATATTTAAATGCTATTGCTGAAAGATTAGTTAAACCAAACCCAGGTTTGAATTTGACTACAA
GTGATGTCAACAATTTATTCAGTTGGTGTGCTTATGAAATCAACGTCAGAGGAAGTTCACCATTCT
GTGATTTATTACCAATGAAGAATTCATTAAGAACTCTTATGGTAATGATCTTTCCAAATATTATT
CTAATGGTGTGCTGGTAATAATTACACCAGAATCATTGGTTCAGTGATTTTGAATTCATCCTTGGAA
TTTTAAAAGACACCGAGAACTCTAATCAAGTATGGTTATCATTTGCTCATGATACTGATTTAGAAA
TTTTCCATTCTGCTTTAGGATTATTGGAACCAGCTGAAGATTTACCAACATCTTACATCCCATTCC
CTAACCCATACGTCCATTCTTCTATTGTTCCACAAGGTGCCAGAATATACACAGAAAACTTCAAT
GTGGAACGATGCTTATGTTAGATACATTATCAACGATGCTGTCGTGCCAATTCCAAAATGTGCTA
CTGGTCCAGGGTTCTCTTGTAACCTTGATGATTTTGAAAATTTTCGTTAAAGAAAGAATTGGAGATG
TTGACTTTATTAAACAATGTGGTGTCAATAGTACCTACCCATCTGAGCTTACTTTCTACTGGGATT
ATAAAAATGTCACCTACAATGCTCCTTTAGAATTGTAA

YBR093C_homolog_4 461aa (SEQ ID NO 304)

MVSVSKLINNGLLLTSQSVFQDVATPQQASVQQYNILNFLGGSAPYIQRNGYGISTDIPAGCEIAQ
IQLYSRHRGERFPTASSGKDYEKIYAKFKNYNGTFKGDLSFLNDYTYFVKDQSNYAKETSPKNSEGT
YAGTTNALRHGAAFRAKYGSLYKENSTLPIFTSNSNRVHETSKYFARGFLGDDYEEGKTVKFNIIS
EDADLGANSLTPRSACSKNKESSSSTAKKYNTTYLNAIAERLVKPNPGLNLTTSDVNNLFSWCAYE
INVRGSSPFCDLFTNEEFIKNSYGNLDSKYYSNGAGNNYTRIIGSVILNSSLELLKDTENSNOVWL
SFAHDTDL EIFHSALGLLEPAEDLPTSYPFPNPYVHSSIVPQGARIYTEKLQCGNDAYVRYIIND
AVVPIPKCATGPGFSCKLDDFENFVKERIGDVDFIKQCGVNSTYPSELTFYWDYKNVTYNAPLEL

YBR181C_YPL090C_homolog 1635bp public: 1..938, PathoSeq:
939..1635; exon 1: 500..505, intron 1: 506..930, exon 2: 931..1632
(SEQ ID NO 305)

ATATATATATATTTATGTATTTTTTTTATTGTTGTTTCAGGAATTTTAAACATGTTTCATGAATAATGA
TAATCTATGAACAAATTAAAGAACTCTTTGGTTTCATTTGCAACCAATGTGCGTGACTTAGGGCTA
TAGCCCTACTTTTACTTGTACGATACTGCATATTTTGTGTTGTGCGAATAGTTAGCGTAATAATC
TTTTTTTTTGTGTGTGTGCGGTTTACTTACTCTTCTTCTTCTCGCACATATTTTATTAGAGCTTAC
AGTTGTTTGTATAGTGAGAGTTTCACTAACACAAAGCTTCAACAATACTAACAAATTTTCGCACGC
TGTGGAAGGAGAACTTACACTGTACACTACACTACACTGTACACTATACACCACCAACAGAAAAA
AAAAATTATCAAATTTTCAACCTTGAGAGAAAAAAAAGTGGAAAAAAACTTCTTCTTACATTT
AGTTAATTTTCAGACAGGCACAAAGGAATTAATCACCATGAAGGTATGTGATTGAATATAACCTAT
ATCAGTGATTATAATTAGAGTCTTTATTTGGATATTGCAATAATTGGATAATAAGAAAGAGCATA
AGAGTAGGAGTTTTAAACAGGATAATTGGATTCAATAAGAGGAAAAATTTTTATCGTCGTGATTA
TAACAAATACAAAGAAATTAAGCAATGAAGTGATATAAGCAAATGAAGGACTAGTTTATTAGGGGT
GACATTTTTTAGACTACGTAAAAGTACTTTTCGATTCAAGGAAAACCAAATTTTAGTATCTATCAACA
AACTACAAATCAATTTAGTTAACTTCAATAATGACAATAATTTTAATCACTGAAAACAATAAACAT
GCAAACAAGCAAACTAGTCAAGCTTTACGAATCAGTCAATACTAACAAATACTTTTTTTTGTTC
TTTTAGTTAAACATCTCATATCCAGCCAACGGTACTCAAAAATCTATGGATATCGATGATGACACA
AAATTACGTGTTTCTACGGAAAAAAGAATGGGTCAAGAAGTTGAAGGTGACTCAGTTGGAGATGAA
TTCAAAGGTTACATCTTCAAAATCACTGGTGGTAACGATAACAAGGTGTCCCAATGAAACAAGGT
GTTATGCACCCAACCAGAGTTAGATTATTATTATCTAAAGGTCCTCTTGTACAGACCAAGAAGA
ACTGGTGAAAGAAAAAGAAATCCGTTAGAGGTTGTATTGTTGCTCAAGATTTGTCAGTTTGGCT
TTGTCTATTGTTAAACAAGGTGACAATGAAATTGAAGGATTAAGTACACCACTGTTCCAAAAAGA
TTAGGTCCAAAGAGAGCTAACACATTAGAAAAATCTTTGGTTTAACTAAAGAAGATGATGTTAGA
GATTTCTGTTGTTAGAAGAGAAGTTACTAAAGGTGACAAAACCTTACACCAAAGCTCCAAAGATTCAA
AGATTAGTTACTCCACAACTTTACAAAGAAAGAGAGCTTTGAAAGCTAAAAAAGTCAAGAATGCT
CAACAACAAAGAGATGCTGCTGCTGAATACGCTCAATTGTTGGCTAAGAGATTGCATGAAAGAAAA
GAAGAAAGAGCTGAAATTAAGAAAGAGAGCTGAATCTTTAAAGAACTAA

YBR181C_YPL090C_homolog 236aa (SEQ ID NO 306)
MKLNISYPANGTQKSMDIDDDTKLRVSTEKRMGQVEGDSVGDEFKGYIFKITGGNDKQGVPMKQG
VMHPTRVRLLLSKGHSCYRPRRTGERKRKSVRGCIQAQDLVLSIVKQGDNEIEGLTDTTVPKR
LGPKRANHIRKFFGLTKEDDVRDFVVRREVTKGDKTYTKAPKIQRLVTPQTLQKRALKAKKVKNA
QQQRDAAEYAQLLAKRLHERKEERAIEIKKKRAESLKN

YCL016C_homolog 1520bp public: 1..1079/1081..1520, PathoSeq: 1080;
CDS 501..1517 (SEQ ID NO 307)

GTGACGAGAACTTCTGTCATCTCGAGTCTGCCAACTGCCTCTAACAGCAACAACAATAAGAACAAT
GATAACGGAGGAGGATTATCCCATACAAACAGAATAGTTGTTGGTGTAGTTGTTGGGGTTGGTGGT
TCTATATTAATTGGTTTGTGTTGGCCGTTTTATTTTACTTGAGAAAGAGAAACAACCGTGATTATGAA
GGTGGATGGACTTTCTGGAGAAAGAATGAGAAATTGGGAAGTGATGAGTTCTTCAATGGTGAATTG
GGTGTGAGAGACAGAAATATTAATCAAGGATCAAATTTTAAACAAGGCTTATTTTGGATGAGGGT
GGTTTTTTTTATAAGTATTTTGTAGTTGAATTTAAAATTTTGTACCTTAAAGTCTTTTAAATTTAAT
TTTAATAAAAAGTGGTGATTGTTGGCAAACTTCAAGAGTATATTTGGTGAAAAAATAAATTTG
GAACTGAACGCGTCTAACATCTTATACCTCTAAGCAAATGTCAGAGTACTCTGTGTATCAACAGT
TGAATGAAGATACAAACGCAACTAAATATACTTATAAATTACTACAGCTACCATCAAAGATACTAA
ATCAACTTGAATCCAAGTCAACTAACTTGTATATAAATCTGATATCAATTCCTAGCATTATGCA
CTGATTCAGAACTTTCAAGTTACGACAAATGAACCATCCAATACAGTCTTGCTATTGAACAAAG

AACCTGACAACAAGTTAATTGGGTTTCAGAAAACCAGTTATGAATATGAGTTGACAGAAATCAAAG
GTTTCGATCGATACGTCCGATATCCCTATTTTCAACGGACAAACAGCACAGCAACCTATTGATTTGA
TAGCATTGGAAGATAATTCGATTTGTTACATCAAGAGTTTATCGAATTGGTATGAGTTGGGAG
GTTGTGAAATTGATAATGGAGCATATATAATGAGTGCAGATATTATTACTGAACTATTATATCTAT
TAATCACCAAATTGATGAGTTTACAAGTGCACGAGTTTCTCCGGAAGATGTTTCATCCATCATCA
CGCCCCCTTATAATGACTCAATGGTAACATCAATCATAACACAAATTTTGCCTATAGAAAGTGAGA
AATATCAATTGAATGATTTAAAAATTACACAGTGGTTTGGCATTGTTGAGATGTCAAAAATCAATC
ATAAAATGACCGATATTTTCAGAGTTCTTATTGAATTGGAAAACCTAGTTTGCCGTCATTCTATAACC
CTCCATTGGACATCAGTCAATTGGCAGGCTATTACTGCTCCCAATCGAAAACAAATATTGTATG
TCGACCCAGAATCTTTATCAGAAAATTTGAGTCAACGATTCAAAGAATTGTTTGAATTGGATAAAA
GTTGGAACATATGATGAGTTTATTCCATTCATTAATAAAGTTTGTTCCTGCCGGTAAAAAGGTCGACT
CAATTATTTTAAAGTATGGCAAGAAGAAGAAAGTTGGTAGAGATAGATTTATAGTCTGTCCTAGAT
AA

YCL016C_homolog 339aa (SEQ ID NO 308)

MSEYSVYQQLNEDTNATKYTYKLLQLPSKILNQLSKSTNLYIKSDINSLALCTDSETFKLRQMNH
SNTVLLLNKEPDNKLIGFQKTSYEYELTEIKGSIDTSDIPIFNGQTAQQPIDLIALEDNSICSHQE
FLSNWYELGGCEIDNGAYIMSADIITELLYLLITKLMSLQVHEFSPEDVSSIITPPYNDMSMVTSH
HKFCTIESEKYQLNDLKITQWFGIVEMSKINHKTMDISEFLLNWKTSLPFYNPPLDISQLAGYYC
SPIENKILYVDPESLSENLSQRFKELFELDKSWNYDEFIPFIKKFVPAGKKVDSIILKYGKKKKVG
RDRFIVCPR

YCR073WA_homolog 710bp PathoSeq: 1..710; CDS: 315..707 (SEQ ID NO 309)

GGTGGGGTCCCATTTTAAATTTAAAAAATTTTTTACCATCCAAAGGATTTTATTTACCCAAAGAC
CAAAAAATTATTATTGAAATGGGGATTAAATGGGGATAATTTTATTTGCCTGATGAAAAGATT
AGTACCCGTTTGAAGTCCTGATTCAAATTATGGTCAAGCTAAAAGAGAAATATTTGATTTAATTA
CTGGTGATAAAAAACCAAGAATTTTCCATGTTGATGAATCATTAATTGATGATTCTCAAGAAGCTG
CTGATGAATATGAAAAACAATTGATTAATAATTTTGCTAAAAAAGATTCGGTGAAATTACCTTTAT
TTGATTTATTTTATTAGGTTGTGCACCGGATGGTCATATTGCTTCATTATTTCTAATCATGGTG
AACAATTGAGAGAAAAATTAGCTTGGGTTTACCAGTATCAAATGCTCCTCTGGGACCAGAAAAATA
GAATAACTTTATCTATCCCAGTTATATGTCATTCCGCAAGAGTGACATTTGTTGTTGAAGGGTTAA
CTAAGGCACCAATTATTAAAACCATTTATGGAAAGACCAGAAAAAGGTTTACCAAGTTCAATTGTTA
ATGAAGGTGCTGCTGGTAGAGTGAGTTGGTTTGTGATGATGATGCATTGAATGATTTGTTTGATA
TAACTAAAAAGAAATACAAATATTTATCTATACCTGAACCAAGTCATTAA

YCR073WA_homolog 131aa (SEQ ID NO 310)

VKLPLFDLFLGCPDGHIALSLFPNHGEQLREKLAWVLPVSNAPSGPENRITLSIPVICH SARVTF
VVEGLTKAPIIKTIMERPEKGLPSSIVNEGAAGRVSWFVDDDALNDLFDITKKKYKYL SIPEPSH

YDL010W_homolog 1190bp PathoSeq: 1..1190; CDS: 501..1187 (SEQ ID NO 311)

TGTTACAAAACATTCCTGTTGGAGAGATAATTGAATTCAAATTAACGTGTTGAATCCAACATTGAA
CAATGAATACACGTCCAAGAAAAATTTGACATGATTAGAATCGCGGTCAATTACATCCCGGAACG
TCTTGGACTIONTTGGATACAACAATGGAAAATGAGGAAAATGAGGAAAATGAGGAAAACGAGGAAA
ACGAGGAAAATATTTACCGAAGAGTAATTATATTACAAGCATTGAAAGAGGAGAAGTGAACGCCCC
AAACAGAAACAATACCGAACATCACAAAAAAGACAACAGCTAAAATTTTTTGGTCAGAA
CACAACTTTGGAAGAAAGAAAAAACCAGAAAAAGAAATTCATCTAAAACACATACACAATATAT
ATATATATATATAAATATATCCATATACATATGCTTTAATTTAACCTTCCCGCCTTTCTTTTCTTC
TTTTTGAATTATATCGATTTTAAAAACTACACTTCATCATGGCTGGAGTTAGACAATTAAGAATAA
TAGCATTAAACGGCCTTTGTCTTGGTTTAAATTTTACTTTACATAAAGTTGGATCCAACGCTGCAT
CCTTGGTTCATGCACAAGCATCAGACCAACAACCAACAAACATAACACCAAAAGTACTACATATA
CCGCCACTAATGACGAATCAGTTGCCAATCTCATTGATTCTAAAAATGATCCTCAAACCTGATGACA
AAATAAATCAAAAAATATCACAAGATCAAGATGAAGCCATCAATGGTAATAAAGACACTAATAAAG
ACACCACCAAGTCAAACCAGATAATGGTGAATATGATCCAATATCTGATTTGATAAAAAATTAGAT
CATTATACCAATGACAATTTTCAGTAAATCATATTGTCCATATTCAAAAAGATTAAACAATTGT

TATTAGAAAAATATGATATAACACCAGCACCAAATGTTGTTGAATTAGATCGATATGAATATGGAG
CTGAATTACAAAGTTATTTGACAGAGAAGAGTGGGAGAAGAACTGTGCCAAACGTATTGGTTGGTA
AATCATTGTGAAAGTAGGGGTGGTTGTGATGAATTTGAAAACTTCATAAAGATAATGATTTGATTA
AATTGTTAGTTGAATGGGGTCTGGTCGTTTACAAGTTGCAAAGAAGAATACCCCATCAAATGCCT
AA

YDL010W_homolog 229aa (SEQ ID NO 312)

MAGVRQLRIIALTAFVLGLIFTLHKVGSNAASLVHAQASDQQPKNHNTKSTTYTATNDESVANLID
SKNDPQTDDKINQKISQDQDEAINGNKNKDTTKVKPDNGEYDPIISDLIKIRSLSPMTIFSKSYC
PYSKKIKQLLLEKYDITPAPNVVELDRYEYGAELQSYLTEKSGRRTVPNVLVGKSFESRGGCDEFE
KLHKDNDLIKLLVEWGSGRLLQVAKKNTPSNA

YDL083C_YMR143W_homolog 1256bp PathoSeq: 1..1256; exon 1:

501..521, intron 1: 522..848, exon 2: 849..1253 (SEQ ID NO 313)

AGTGGTTGTTCAATAATGGTAAGTTCTTGGAATAGCCATTGTTGCTTTCTGGTGGTTAGACTTGT
AGGAAGTAGAACTGTTTTCCAATGAAAAGTAGTTTTAATTAGAAAAATTTTCAAAGTGCGTGAAGC
CCAGTCTGAATGTGCGAGGAAGCCAGTCAGTTAGTAGTGTCTTCCCTCCACTGTCTGTAATACA
AAATTTCCCTTAGTGAAAATGCGAAATATATCTGTACTGGGAACCCCCCGGAAAAAATAACCTA
TGCTCAAACTATATGTACTGTACACAATCTAGGGCTATAGCCCTAATATTGTACAGGAAGAACTT
TAACTATGGTGCGAAGAGCGTTTCCAATTTTTTTTTTTTTCAGGTGTAGTCTGTTCTATGGCAATAC
TGTTGTTAGTAGAGAGTGTCTCGCACTAACAGAACATTTTTTTTTCAGAACAGGAAAATTTTTGAAAT
CTAACATCTTTTACTGAAAGCCAAGCATCAACACAATAATGTCAACCCAATCTGTTCAAGTATGTA
AACGAATTGAAATAAAGAGATAGAGAGATGTTTTATTATCAAAATACGAAAGGAAAGGCAATTAAA
AAAGGAAATCAAAAAGTCCCAACCTTGCAGTAGAAGAATTGAGGTATATGAATTTGATAGATAGCC
AGAACGGTGTTACATAAATGGGATATAGAACAAACTATACGAGGAGTTTGTTTCAACGATCATTC
AATAACCAGAAAACGATAATATTTTAGCGACCATTAAATGACACTTGAAGGCTCACTGGGCCAATA
GAATATCTCCATATACACTTTTGAACATTTTACTAACAATTTACTTTTGTCTTAGACTTTTGGTA
AAAAGAAGACTGCCACTGCCGTTGCTCATGTTAAAGCCGGTAAAGGTTTAATTAAAATTAACGGTT
CCCCAATCACCTTGGTCCAACCAGAAATCTTAAGATTCAAAGTTTACGAACCATTGACTTTGGTTG
GTTTAGATAAATTCCAAGGTATCGACATCAGAGTTAAAGTCACTGGTGGTGGTCACGTTTCTCAAG
TCTACGCCATCAGACAAGCTATTGCTAAAGGTTTGGTTGCTTACCACCAAAAATACGTTGACGAAG
CTTCTAAGAACGAATTAAAGAAAATTTTCGCTTCTTACGATAAGACCTTGTTAGTTGCCGACTCAA
GAAGAATGGAACCAAAGAAATTCGGTGGTCTGTTGGTCCAGAGCAAGATTCCAAAATCTTACCGTT
AA

YDL083C_YMR143W_homolog 142aa (SEQ ID NO 314)

MSTQSVQTFGKKKTATAVAHVKAGKGLIKINGSPITLVQPEILRFKVEPLTLVGLDKFQGIDIRV
KVTGGGHVSQVYAIRQAIKGLVAYHQKYVDEASKNELKKIFASYDKTLLVADSRMEPKKFGGRG
ARARFQKSYR

YDL125C_homolog 959bp public: 1..959; CDS: 501..956 (SEQ ID NO 315)

GTGGTAAGATATAGAAAGCTTACCACTTTGACAAGTTTGAAATAGGATGGGTGAAAATTTGGACAT
CTTGAATACTTAAAATTCTGAACTTGATCACCAGATCCTTTTCTTTTACATAATTAGATATGATGG
ATAGGTTAGAATCGTCTTTTAAAGAGAAGGTATAATATCTAACTGATTTGGCGAGGTGTTGGAAAAG
TCACTCCACTGTATATATTCTCGGAGTTTAACTGACTACAGTTCAGTGGGGTGAATACCTAAATAG
GGGGGTAGAATACGAACTCCTACAAATTTTAAAGGAGACTATGACCCGAAAAGAGAAGAAAATTTA
TTACTCTAAGAACTTTATATACCTCCACAACCTCACTTTTTCTTTAGTTTCATTCTGCTTTTTTTTT
CTTACACATCTTAAGGTCAAACAATTTAACTTATTAGCTTGTGAAAATCTCACTTCAATTCAAGTT
CTCTTTCAATTGACATTATAGTATTTCCCAATTCAATTATGGCTTCTCATGCTTCTGTATATTCT
GTAAAATTATCAAAGGTGAAATTCCTTCTTTCAAGTTAATTGAACTGCAAAGACTTATTCCTTCT
TGGACATTCAACCAATTGCTGAAGCCCACGTTTTTAATTATCCCTAAACACCATGGGGCAAAGTTGC
ACAACATTCCAGACGACTACCTTAGTGACATTTTACCAGTTGTCAAAAAATTGACAAAAGTCTTGA
AATTGGACGAAAATAATACTCCAGAAGGTGAAGGTTATAACGTTTTTACAGAACAACGGAAGAATTG
CTCATCAAGTTGTTGATCACGTTCACTTCCATTTGATTCTTAAAGGATGAGGCTACAGGTTTAG

GTGTTGGTTGGCCTGCTGAAGCCACTGATTTTGTATAAATTAGGAAAATTGCATGAGAAATTAAAGG
AAGAATTGGCTAAGGTAGATAATGAAAAATTATAA

YDL125C_homolog 152aa (SEQ ID NO 316)

MASHASCIFCKIIKGEIPSFKLIETAKTYSFLDIQPIAEAHVLIIPKHHGAKLHNIPDDYLSDILP
VVKKLTKVLKLDENNTPEGEGYNVLQNNGRIAHQVVDHVHFHLIPKKDEATGLGVGWPAEATDFDK
LGKLHEKLKEELAKVDNEKL

YDL133CA_YDL184C_homolog 297bp PathoSeq: 1..297; CDS: 220..294
(SEQ ID NO 317)

CATAATTATTACATATAAACTCGCACTATAATTTTTTTTTTCTATTCTGTGTGTGTGTGTGTGT
GAGAGCCAGAGAAACCAAACCTGACTGAGTGATCGTCTCTCAACAATTTATTTCTCCTCGTCTTATT
TTTTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTCTTTA
CCAAAACACTAGTATTTCAACATGAGAGATAAGTGGAGAAAAAAGAGAGTTAGAAGATTAAAGAGA
AAGAGACGGAAGGTTAGAGCTAGATCCAAGTAA

YDL133CA_YDL184C_homolog 25aa (SEQ ID NO 318)

MRDKWRKKRVRRLKRKRRKVRARSK

YDL136W_YDL191W_homolog 1303bp PathoSeq: 1..1303; exon 1:

501..503, intron 1: 504..943, exon 2: 944..1300 (SEQ ID NO 319)

TATTGTCTGATGCTATACGGAATGGGCGTTACAAATATACAACTTATATTTGAAAGTAAATTCTA
TTATTTTCTTCTATCGTATGCATACCGATTATTATCACAAGGACAATTGCCTATTGTTGTGTGGAA
TAAATTTAAAATCCTTCTTATTGGTGTCTAGACTTTGCTTTTTGTGGTGATTAGGGCTTTAGCCCT
ATCACGTGAAATACTGTATATAAAAAATTCTTTATAGCGCGATAAAACATATTTTTTTTCCGTATT
AACAAATATGTGTGAAGTTTGTCTGTTTCTCACTGTTTTTCTTTTCTTTTCTTTTCTTTTCTTTT
CAATTAACGCTTAGATCCAATACAGTTTGGTAACTTGTACACGAACAAAATCTCAAATTTGTTAC
TGTGTGAACCAACAAGGAAGAGAAAAAAAACCCATACAAAAATTTTTCAGTATCAAGGAATTAGA
AGAGACGTTTAAATCAACAAAGTTCAAATCTATCAACAATGGTATGTTTAATATCGATATTATCCA
TAGATGTACATGTATCCTAATGGGTTTCATTATTTGGAAAGTTATGTTTATGGGAGTTCTATTTAT
TAAGATATGGGATAAGAATTAAAGTATTGGATGAGTAGTACAAGACCAACAAAGAGAAATAGCCCC
CTTTCCCTCCACTATTCAATATACTCAACAACATTATCAAGTTAAAAGTTCAGAAGATACACGTAA
ATGAAAAGTTAATACCAAGAAGAATACAAATTACCAGTCCATACCGTGTTTGGGTTTAGATTACTA
TATTTTACAAGAAACATATTATATGAAATGATACCCAATCCACAGCGACTTTTCAGATAGCCAAAT
AACTAAGCAACTCAAGATAACATAGGATCATGCATCAATCACAATGAAACATTAATACTAACTAA
CTTTTTTTTTTATTTATTAGGCCGGTGTTAAACTTTTGAATTAAGAACTAAATCTAAGGAACAATT
AGAATCTCAATTGGTTGAATTGAAACAAGAATTGGCCACTTTAAAAGTTCAAAAATTACAAAGACC
AAGTTTACCAAGAATTCACACTGTTCGTAAAAACATTGCTAGAGTATTGACTGTTATTAAGTTGAA
TCAAAGAGAAAATGTTCTGTCCTTTTACGCTGGTAAAAAATACATTCCAAAAGATTTAAGAGCTAA
AAAGACTAGAGCTTTAAGAAGAAAATTGACTAAATTTGAAGCTTCTCAAGAACTGAAAAAGCTAG
AAAACAAAGAATTGCTTTTCCACAAAGAAAATTTGCTATTAAAGCTTAA

YDL136W_YDL191W_homolog 120aa (SEQ ID NO 320)

MAGVKTFELRTKSKEQLESQLELVELKQELATLKVQKLQRPSLPRIHTVRKNIARVLTVINLNQRENV
RAFYAGKKYIPKDLRAKKTRALRRKLTKFEASQETEKARKQRIAFPRKFAIKA

YDL167C_homolog 2690bp PathoSeq: 1..1640, public: 1641..2690; CDS:
501..2687 (SEQ ID NO 321)

CTCTGTGTAAATTGATGAAATCCACACAATAAAAATTTTCTTTCTTTCTTTTAAAGAACCTAAAAACA
GAATCAACATTATTTGCCCCATACATATCCAAGAATTAAATACTTATTAGTTCTAAGTGGAATAGA
AGAGAATCAAACCTTAACATTACTGTTACGCAACGTCAAGAGGGCATTTTTTTTAGTTTTAATTTGT
TTCATTTCAATTGAATCTTTAAGAATCACCGAGTATACATACTTTCTTTTGTATTTTATCAGGGAA
GCCACATCCAACCACCAGTTACATCCCACAAAATCCCTTAATCTTGTTCTTAGTTGTATTATTAAT
CTATTGAATTTAAGTTTGATATGCGAGAGAATATTGTGGATTGTATAAGTTTGAAGTTGACTTGA
ATACTTTGAGGGGCTTAATCATATATTGCATTTTATACCCTACTCGCGGTGTTGCTTACCACACTG
ACTAGTATGATCTTTCTGAGATTTCTAGCCAATAAATTATGAGTGATATTTATATTATTATTCATA

TTTCTACTACCTGTGATGACTCGCCGACATTTGTCACCTAAGGATTCTTCCGAGTTAATTGAATTTG
CTTGGGAAACAGTCGATAGTGTCACTTTGGAACTTTATACAAAGGATCAAACCTTGGTTCGTCCAA
CCAACACACCTATCACACCTTACTGCTCGAAGATTCATAGAATAACATGGGACAATGTCAAAAATG
CTGGGTCGTTCAAAGACGCCATCACAACTTTGATCAATACGTACAAGAACACATAATTTCCAAGA
AAAAGGAGTTTTCAATTGTGATGTTTGACATTTCCAAATTGAGAGTTCAGTTGGTTCGTGAAGCTA
GAGACAAATCCGTGGTTTTACCCTCGTATCTACAACATCCAAGGATTTTTGATTTACCAAGAGAAT
ATTTAAATTGGCAATCTAGCCACCCTGAAACATTATCATACCCCCCACTTCTTTAACTAATATTA
TTACTGCATTAGAAGTTGAGGTTGAGAATATATCTGAATATGTGCGACTTGCCAACTTTTCTTCCA
CACCATCACCATCAAAGCTTCAGCAACAACGACGACGACAACCTGCAAATGTCACAGCCATTGACG
TCCTTTCCAGTGAAACAGAACCAAATGGTAAAGTCATTGCAAATTTGCACGCCAAAATTGCCAAAC
AATTGATCAAAAAATCCATCCCTGTTGAGAATCACCTAATGTATTTACAAGACCTTTTGATTCCG
CTCAAGATATCACTGCTTTTACATCAGAAAGATCAAAAGTACTCTATCTTTCCAACCTTGCCAAACG
ACACCACACAATCAGAGTTGGAATCATGGTTCCTCAGTATGGTGGGAAGACCAGGTGGGTTTTGGA
CTTTTAAGTCTGCAGATGATAACAATAATAACAACAACAATAGCAATGGCGGGAAAGGATATC
AGAATGCGAGAAAATATGGTATTTTCAAGGTTTTGTGGCCTTTAATACTCATGAGGAAGCAGTTGATT
GTTTAGCTTTGAATGGGAGAGTGTGAATGATCGTCCTATTGAAGTTCAAGCGTCTTCTAGTAAAG
TGTTTGATATGGCCATGGATAAATTGTTGTTGACTCTGTTCCCACTCTCAAAGAACAGACCTAGAC
CCGGGGATTGGACTTGTTTATCTTGTGGGTTTTCCAATTTCCAGAGAAGAACACACTGTTTCAGGT
GCTCTTTTGGCGCAGTGGCGTTTTCAAGGATGTTTTTAACAGTAATACAGGCAATGCCAACGGTAATG
GCAATGTTAGCGGCAACCACAACCACAACCACAATAGTGGAGCTCGCCGTGGCATGAATTTACAGC
CTGCTCAAGCTAATGAGAAAATTGGAACAGGCAATATTAGTATTCCTTCTTACAACGATCCAATCA
AGGGTCCAACAGGTAATGTCACCTAATCACCTCAACAATTCTGAGACCAATTTACTGAACAACACTA
ATCTTAACAACAACAATCATCATAGTAATAATTATCACAATAACTACCATCACCACAACAACAATA
ATAACAATCATGGGAATAGCAATGGTAACACCATAACATGGTTCGTTCCCATTTATAACAATAGTGTTT
CATTTAGAGCAGGTGACTGGAAATGTGAAAATTGCATGTATCACAATTTTCGCCAAAATTTGTGTT
GTTTAAAATGTGGTGTGCGCCAAACCTGCTATTAACAATCAACAAAATAATAACAATTCATTCGGTGA
ATTCAACGGCCGCTGCCATAGCTGCAGCAACAGCCAGTGGTCAACCTTTAACTTGAATAATAATG
CATTTTTGAACCTTCAGCAACAACAGTCTCAGTCACAACCCCAAGGTCAGCACCATTACAACCAAC
ATTCTCGTAACAACAATGCTTCTGGGGCATCAAAGTTCAACAATGGCTACAACCCAAAGAATCAGT
ATTACAATAATAATAGCAAGAATCTTAGCAACAATTTTGGTCTTAATGGTATGCATCAGCAAAACC
AAAATCAAATTTTGATGTATTCACAACAATTGCAACAACAACAGCAACAACAACAGCAACAACAGC
AACAAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACAGCAACAACATGATTTAA
ATGGAAGTAGCTCTTCCCATCAACTGAACTTCAATTGAATAATACTTGA

YDL167C_homolog 729aa (SEQ ID NO 322)

MSDIYIIHISTTCDDSPFTVKDSSELIEFAWETVDSVTLETLYKGSNLVRPTNTPITPYCSKIH
RITWDNVKNAGSFKDAITNFDQYVQEHIIISKKEFSIVMFDISKLRVQLVREARDKSVVLPSYLQH
PRIFDLPREYLNWQSSHPETLSYPPTSITNIITALEVEVENISEYVDLPNFSSTPSPSKASATTTT
TTANVTAIDVLSSETEPNKGVIANLHAKIAKQLIKKSIPVENHPNVFTRPFDSAQDITAFTSERSK
VLYLSNLPNDTTQSELESWFTQYGGRPGGFWTFKSADDNNNNNNNNNSNGGKGYQNARKYGISGFVA
FNTHAEAVDCLALNGRVLNDRPIEVQASSSKVFDMAKLLLTSPPLSKNRPRPGDWTCLSCGFSN
FQRRTHCFRCSFAAVAFQDVFNSTGNANGNGNVSGNHNHNSGARRGMNLQPAQANEKIGTGNI
SIPSYNDPIKGPTGNVTNHLNNSSETNLSNNTNLNNNNHHSNNYHNNYHHNNNNNNHGNNSGNTIH
GRSHYNNVFPFRAGDWKCENCMYHNFKNLCLCKGVAKPAINNQQNNTIHSVNSTAAAIAAATAS
GQPLNLNNNAFLNLQQQQSQSQPQGHYNQHSRNNNASGASKFNNGYNPKNQYYNNNSKNLSNNT
GLNGMHQQNQNLQILMYSQQLQQQQQQQQQQQQQQQQQQQQQQQQQQQQQHDNLNGSSSSSHQSKLQL
NNT

YDR238C_homolog 3359bp public: 1..1467/1469..3040/3042..3359,

PathoSeq: 1468/3041; CDS: 501..3356 (SEQ ID NO 323)

AATAGCATTGAACAAGAAGAAGAGGACAACGATAGACCAAGGTTGGTTTTAGCCAATCCTGATTAT
GATAGTGATGACAGTTCATAGACAATTTACAGCCTTAAATGGATATATATGTATATTTAATAATAA
AGGACTTGTTTTTTTAGTAAGTGTGATCTCTTTTCTGGGTGTACATTTTCGGATAGCCAACCA
GGTTATATTTTAGCAGTTTATAGACAGTGTATCGATGGGTAATATAAATAAAAGCTCATTGAATA
CTATCTAGTGAAAAGTCGTGTGTAAATCGATTTGAAAATATAAAACCATACACGTAAATGAAATG
TGTGTGAAAGTACAACCAACAACGAAAAAGAACAAAAAATGTTGTCCGCCAAAAAAG

AGAACAACAAATCAAAGTTTCAAGACTATCTCAAATCTTGTTGTCACCATAACTATCAATTGTTCA
CCTCTTGAACCAACATCAAATTGAATAAACATAGGATCATGAGTGACAGTGTTTATACATTAATCT
ATGAGCCTAATACGGCTACGAAAGTATCTGTCAATGAATTTAAAAATTTGTTGGAAAAGGGTAAAG
ATGATGTGAAAGTAGATACCATGAAGAAGATTTTGATTACCATATTAAATGGAGACCCCTTACCTG
ACTTGTGATGCATATAATCAGATTTGTCATGCCTTCCAGAAATAAAGAATTGAAAAAGTTGTTGT
ATCATTATTGGGAGGTTTGTCCAAAAATGGATGAATCAGGTAAAATGAGACATGAAATGATTCTTG
TGTGTAATGCCATCCAACGTGATTTACAGCATCCAAATGAATATATTTCGAGGCAATACTTTGAGAT
ATTTGACGAAATTGAAAGAGCCAGAATTATTGGAACTTTAGTTCCTAATGTCCGTCAATGTTTAG
AACACCGTCATGCCTATGTCAGAAAAAATGCTGTTTTTCGCATTATGGTCTATTCATAAAGTCAGTG
ATCATTTAGCTCCTGATGCTGACGAGTTAATTTACAGATTTTTGTATGAGGAAAACGATTCTGTTT
GTAAAAGAAATGCTTTTGTGTTGCTTGGAGACTTGAATAGAGAAGCTGCTTTGCAATATATTCAGG
ATAATATTTTCACTTATTGAGACTTTGGATCCATTGATACAATTGGCTTTTATTGAGTTTATCAAAA
AGGACTCTATTCAAAATCCAGCTTTAAAGCAACAATATGCCCAATTAATGACAGAAATTATTGAAA
GCTCTTCAAATGTTGTTATGTATGAAGCTGCTAACACGTTGACTGTTTTGACTTCAAACCCACAAT
CAATTTTGTGTTGGCAGGAAACAAGTTTGTGTAATTGGCTACTAGAGAGTCTGATAATAACGTTAAAA
TTATCACTTTAGAGAGAATAAATCAATTACACAAGCAACATCCTGGTGTGTTACAAGACTTGTCTAT
TAGAAATTTTACGAGGTTTATCTTCCCAAGATTTGGATGTTAAAAAGAAAGCTCTTGATGTTACTT
TACAATTTATCACCACCAGAAATGTTGAAGATGTTGTTAAGTTATTGAAGAAAGAATTGCAGTCTA
CAGCTTTATCCAATGATGACAAGAATGCAGATTATAGACAGTTGTTAATTAATGCCATCCATCAAT
TGGCTATTAAATTTGTGGAGGTTGCTGCCAATGTCATTGATTATTGTTGGATTCTATAGCCGATT
TGAATACCACTGCCGCCTACGAGGTTATCACATTTGTTAAAGAAGTTGTTGAGAAATTCCCAGATT
TAAGGGACGCTATTTTGAGAAGATTGATTTTGGCTTTGCCACATGTGAAAAGTTGGTAAAGTTTCC
GTGGTGCATTATGGGTTATTGGTGAGTATGCCTTAGAGGAATCATTAAATACAAGAATCTTGGAAT
ATATTAGAGGAAGTATTGGTGAAGTACCAATTATTGCTAGTGAATTGAAACTGAAAAAGCGTGATG
ATACTGAGGAATCACAAGAGGAAGAAACCGAGTATGATGGTAAACCTCGCAGAAAGGGTCCAGTTG
TATTGCCAGATGGTACCTACGCTACTGAGTCAGCATTGACAAGCGAAACAACCTGACTCTTTGGAAA
GTGACAGCAAGACTCCTATCAGAAAGCAAATTTCTTGCTGGTGATTTCTACTTAGGTGCTGTATTAG
CATCAACTTTGGTGAAATTGATTCTCCGATTGCAAAGTTTGAACAAACTCAAGAAAAAATTTTGA
ACGGATTAAAAGCAGAAGCATTGTTGATTATGGTTTCGATTTTAAAGAGTTGGGGAATCTAGCTTGG
TTTCTAAGAAAATTGATGAGGATTCTGCTGACAGAATTTTGTCTTACATCAAGATTTTGAACGATG
AAGAAGACCTTCAGGAAATCAAGACAAGCTTCCTTGAAGATACTAAAGATGCATTTAAAGCACAAA
TTAATAATGCTGAATTGAAGAAAGCAGAAGCATTGGCTAAGGATTTGCATGATAACGCTGAACAAA
TTGACGATGCAATTGTTTTTAGACAGTTGGATAAAGATAACAAAAAGAGTAAAGCTTCTGTGGATG
ATGTTGCTGCTGCGTCAGGAAGCAATGAATTAAAGAAAGAAAATTTGTCGTCGAGATTGAACAAAA
TTATACAATTGACTGGGTTTTCCGATCCTATTTACGCAGAGGCATTTGTCAAAGTTCATCAATACG
ATGTTGTGTTAGATGTCCTTGCTAGTGAATCAAACCACAACCTACTTTAAGAACTTATCAGTTGAAT
TTGCTACATTGGGTGATTTGAAAGTGGTTGATAAACCAACTACCGCAAATATTGGACCTCATGGTT
TCTACAAAGTTCAAACAACCTATTAAAGTTACTTCGGCTGATACTGGTGTCTATCTTTGGTAACATAG
TGTATGACGGTCAACACTCGGACGATTACGTATAGTTATTTTGAATGACGTTACGTTGACATTA
TGGATTACATTAAGCCAGCCACTTGTTCAGAAAGTCAATTCCTGTAATAATGTGGAACGAATTTGAAT
GGGAGAATAAGATAACCATTAAATCACCTATTGAAACATTGAAAGAGTACTTGGATGAATTAATGA
AGGGTACAAATATGCAATGCTTGACACCGGGTGCGGTAATTGGAGAAGAATGTCAATTTTTATCAG
CAAACCTTGACTCAAGGTCAAGCTTTGGTGAAGATGCATTGGCTAATTTATGTATAGAGAAACAGA
GTGATGGACCAATAATTGGTCATGTCAGAATAAGATCAAAAGGTCAAGGTTTGGCTTTGTCATTGG
GTGATAGAGTAGCTTCCATTTCAAGAAAAGGTAAGAAGGCAACTATTGCTCGTGTTTAA

YDR238C_homolog 952aa (SEQ ID NO 324)

MSDSGYTLIYEPNTATKVSVNEFKNLLEKGDVVDVTKKILITILNGDPLPDLLMHIIIRFVMP
RNKELKKLLYHYWEVCPKMDSESGMRHEMILVCNAIQRDLOHPNEYIRGNTLRYLTKLKEPELLE
LVPNVRQCLEHRHAYVRKNAVFALWSIHKVSDDLAPDADELIYRFLYEENDSVCKRNAFVCLGDLN
REAAALQYIQDNISVIETLDPLIQLAFLIEFIKKDSIQNPALKQQAQLMTEIISSSNVVMYEAANT
LTVLTSNPQSILLAGNKFVELATRESNNVKIITLERINQLHKQHPGVLDLSLEILRGLSSQDL
VKKKALDVTLQFITTRNVEDVVKLLKKELOSTALSNDKNADYRQLLINAIHQLAIKFVEVAANVI
DLLLDSIADLNTTAAAYEVITFVKEVVEKFPDLRDAILRRLILALPHVKSGKVFRGALWVIGEYALE
ESLIQESWKYIRGSIGEVPIIASSELKSKKRDDTEESQEEETEYDGKPRRKGPVVLPGTYATESAL
TSETTDSLESDSKTPIRKQILAGDFYLGAVLASTLVKLILRLQSLKQTQEKILNGLKAEALLIMVS

ILRVGESSLVSKKIDEDSADRILSYIKILNDEEDLQEIKTSFLEDTKDAFKAQINNAELKKAELA
KDLHDNAEQIDDAIVFRQLDKDNKSKASVDDVAAASGSNELKKENLSSRLNKIIQLTGFS DPIYA
EAFVKVHQYDVVLDVLLVNQTTTTLRNLSEFATLGDLKVVDKPTTANIGPHGFYKVQTTIKVTS
DTGVIFGNIVYDGQHSDDSRIVILNDVHVDIMDYIKPATCSESQFRKMWNEFEWENKITIKSPIET
LKEYLDELMKGTNMQCLTPGAVIGEECQFLSANLYSRSSFGEALANLCIEKQSDGPIIGHVRIRS
KGQGLALSLGDRVASISRKGGKATIARV

YDR294C_homolog 2270bp public: 1..278/280..2270, PathoSeq: 279;
CDS: 501..2267 (SEQ ID NO 325)

GTTTGTATCACATGTGTTGTGAACACTCGGGTAATACAAAATAGTGAGAGAGAAGAAGGGGAAAAAA
AAAAGCAGAACACAAAACATGGAATTTGAAAACAATTTTGTAATTCAATCGATCCGAGACTTCCAT
AGCAAAGTTAACAAGCACAATTGTCAATTTAACTTAATTGGTGGATTAATCGGGATCAATCTGAAT
TGTTTCCCGTATTGTTTAAAACCAAAGAAAAAGGATAATCAAACTAAATCTTTCATATTAACACT
ACCATTTTGTAGTGGTCAGTTTATATAATTATCCACTGTTCTCTTCACAATTAAAAAAAAAAAAAA
AAAGAAAAAAGAAAGCTCTCTCTCCCCCAAAGAAAAAGCAAAGGTAATTCCTTCATACACACCTT
TGATATCTTTCCTCTTAGACTTTTCTTTTAATACTTGCATCAATTGGAATATTACTTGTTTACTACT
GGAGTTTTCATTGAACTAAATATTATTAATAATATTATTATGCTTGAATTGAATTCAATTACGATTC
CTCGGAATTTCACTGAATTCCAACCTCACAGCATTAAAGATCTACTATCAACTTAAGATTTTATTTT
TTGCCACATACTGTGCTCAAGGATCATTTGGCTTGAACGGTTCAGTCTGTTTAGCAAGAGATATTT
TTGTTGGCTATGTTGTATACACTCAATTATTAAAGCTTTATCGAGTATTAAGAGGGTACGGTATTG
TAGATTCTATTCGAAGGTTATACCTATATGTTAGTTCTACGGTGTCACTCAAATCTTTTCACTAC
CATTTATTAAATCCAAAATTGACAAGGAATTGCAAGCGACTATTGGCAAAGTAGAAGAAGAGATTA
TGAAAAACGATCCACAGTTATTACAGTTTCCCGAATTGCCAGAACAGGGTATTGACGCTGACAATG
TTTCTTGGAGTTGGATAAATTACAAAACCTTGAAACATTCTGACTGGATCAATGGAAGAGTCAGTG
GAGCAGTTTATCATGGAGGTGAGAATCTATTGTCATTACAAGTTGAAGCTTACAAGAAATACTCGG
TGGCCAATCAATTGCATCCCGATGTTTTCAGGTGTGCGTAAGATGGAGGCCGAAGTAGTTCATA
TGGTTTTGGATATCTTTAATGCTCCGAGTGACGGGTGTGGATCGACAACCTTCGGGAGGTACTGAGT
CGTTATTGTTAGCCGGGTGTCAGCTAGAGAATATGGGAAGAAATATCGTGGAATAACTGAGCCTG
AAGTCATTGCCCCCGTGACAATACATGCGGGAATTGAAAAAGCCTGTTTATTATTGGAATGAAAT
TACATAAAGTTGACTTAGATCCGGTTACCTTTCAAGTTGACGTTAAGAAAGTAGAAAGATTGATCA
ATAGTAATACAGTTTAAATCTGTGGATCAGCCCCAAATTATCCTCATGGAATAATTGATGATATAG
AGTCCTTATCCAAGTTGGCAGTCAAGTATAATATCCCGTTGCACGTTGATGCATGTTTGGGGTCAT
TTATTGTTTCGTTTTTAGAAAAATCAAAGTACATGGCGATAGGAAATTGCCCATATTTGATTTTC
GATTACCAGGTGTCACGTCAATCTCATGTGATACTCACAAATATGGGTTTGCTCCCAAGGGGTCAT
CAATAATTATGTACCGTTCCGCCAAATTACGTGAGTGTCAATACTATATTGCAAGTGATTGGACGG
GTGGAATGTATGGTTCTCCAACCTTTGGCTGGTTCTAGGCCAGGTGCTCTTGAGTTGGATGCTGGG
CTACATTAATCAATATTGGGAACAAGGATACACCAAGTTTGTACGATATTGTGCTGGCGTCAA
TGAAAGTTAAACGAGCAATTGAACTGACCCGATACTATCCAACATTTACAAATTATTGGTGATC
CAATTGGGTTCGTAATTTTCGTTTCAACTTGCACCTCAGCAATCGGGAAATTTAAGTATTTACGAGA
TTAGTGATTTGTTGACCAAAAAAGGTTGGCATTTTGCAACTTTACAAAACCCATCAGCATTACATT
TTGCATTTACAAGATTGACTGTCCCGGTGGTCGATGAATTGATTGCAGATTTGGTTGAAGCTACAA
AAGAAGCGGTGGCAATTGCCGAGGAACACAAAAAGAATGGAGTGACCAAGCTCCAGGTGATACTG
CTGCGTTATATGGTATAGCTGGCAGTGATACATACAGCAGGGTTGGCTGATAGATTAATTGTTGCAT
TTTTAGATACCTTATACAAAATTTGA

YDR294C_homolog 589aa (SEQ ID NO 326)

MLELNSITIPRNFTEFQLTALKIYYQLKILFLATYCAQGSFGLNGSVCLARDIFVGYVVYTQLLKL
YRVLRGYGIVDSIRRLYLYVSSTVSSQIFSLPFIKSKIDKELQATIGKVEEEIMKNDPQLLQFPEL
PEQGIDADNVSLDKLQNLKHSWINGRVSGAVYHGGENLLSLQVEAYKKYSVANQLHPDVPFPGV
RKMEAENVHMLDIFNAPSDGCGSTTSGGTESLLLAGLSAREYGGKRGITEPEVIAPVTIHAGIE
KACFYFGMKLHKVDLDPVTFQVDVKKVERLINSNTVLICGSAPNYPHGIIDDIESLSKLAVKYNIP
LHVDACLGSFIVSFLEKSKVHGDRKLPIFDFRLPGVTSISCDTHKYGFAPKGSSIIMYRSPKLREC
QYYIASDWTGGMYSPTLAGSRPGALVVGWATLINIGKQGYTKFCYDIVSASMVKRAIETDPIL
SKHLQIIGDPIGSVISFQLAPOQSGNLSIYEISDLLTKKGWHFATLQNPALHFAFTRLTVPVUDE
LIADLVEATKEAVAI AEHKKNGVTKAPGD TAALYGIAGSVHTAGLADRLIVAFLD TLYKI

YDR430C_homolog 3605bp PathoSeq: 1..330/1927, public:
331..1926/1928..3605; CDS: 501..3602 (SEQ ID NO 327)
TTCAATTTTTTTTAAAAAATAGCAAAAAGGTATTTCTTAGAAATTGAAAAAATAATCACAAAAA
AATTTATAAAACCGGATAGGGCCGTTATCGCAGGACGTGTCCCATGATCAATCTACAATGAAATGA
TTCACATGAAATATGTTACAATTCCACACTTGCTGCTAAAAAGCAACAGTTTGTCAATAGAGAAAA
GCATGATATACTATCGATAATATCTTTTCGATAAGAACTTAAATGTAGCAACGTTGAATTTTAAAT
AAAACCTTCCTTTTCCTGGTGATAAATTTTGACTTTGAAGCATAAAGAAGACAGAGCTAAAAA
CTACTCTCTAGACAAAATCAAACCTCGAATATATTTTTTGGTGTCTTTTCTTTTTTTTTTTTGCCT
CTCGTTGAAATCATCTCCATTCTTCTTTTCCACGTCTTTGTTGAAAACCTTGCAACCTAAAAAAT
AAGAATCACTCCAACAAGTTTAACTACATTATCAATTATGTTGAAAACCTAGATTAAAAACAAAGCA
GGGCCATAAGTCGGGTTGTAAGAAGATATGCATGCTCACACCCCATTTCTCCCAATCTTGATAAGT
ACCCAGTTGGTCTAAAATTGCATGGTTACGAAGTTACCCAAACATCACCTATCCCAGAATTTTCCC
TCACTGCTGTATCATTTAAACACACAGAGAGTGGTGCAACTCACTTACATTTGGATTCCCCTAATG
ACAGTAATAATGTATTTCTGATTGCCTTCAAACAAATCCTCCAGATAATACTGGGGTTCCCCATA
TTTTAGAACATACAACTTTGTGTGGTAGTAAAAAGTTTCCGGTCCGTGATCCATTTTTTAAATGA
CCAACAGGTCGTTGAGTAACTTTATGAATGCAATGACAGGCCATGATTACACATTTTATCCATTTG
CTACCACCAATTCAAAGGATTTTGAAAACCTAATGGATGTGTATTTATCGTCAGTGTGTAACCGC
AATTAAACCATAACCGATTTCTTGCAAGAAGGATGGAGAATAGAAAATCAAATGTTTCATGACATAT
CGTCCAAGCTTGAATTCAAGGGAGTTGTATATAATGAAATGAAGGGCCAGTATTCGAACTCTGCAT
ACTACTTTTATATCAAGTTCCTTGAGAGTATATATCCATCCTTGAATAATTCAGGGGGTGATCCCA
AGAAAATTGTTGATTTGCTGTACGAGGGTTTACTAGAGTTTACCTGAAAAATTATCATCCATCAA
ATGCAAAAACATTTACTTTATGGAATAATTACCATTTGGAAGACAGTTTAAAGTAAAATAAGCAAATACT
ATGAATCATTCGAAAAAAGGTGTCTTCAGTTGACGTCAAACAACCTATATTTTCTACAGATAAAT
CAGAAATCTTTGATGTCACCATCCCGGGTCCAGTTGATACAATGAATGGTAAAGAGACTTCAGAAC
AGTACTGCACATCTATCACCTGGAACCTGGGTAATCCATTGGATCCAAACATGCAGTATGATATTT
TTAAATGGAAAATATTGAGCTCATTATTGTTTGATGGACACAACCTCTCCTTTCTATCAAGAGTTAA
TTGAAAGTGGATACGGTGACGATTTTCTGCAATACTGGGTTGGACTCAACCACCGCGTTGCTTT
CGTTTACTGTTGGTCTCAACTACTTAACCAAGCAAAAAGTTGATAATTTAATGAAAAAGTTATGG
AAATCATTAATAATAAAATCATTTCCCGAATTAAGTAACGAAGAGTCCCTCTTCATATCATGGTAGAA
TTGATGCTATATTGCATCAAATAGAAATAGGATTCAAAGACACAAGCCCGATTTTGGATTGAGAT
TATTGAGCTCTATTGTTCCGTGATGGGTGAATGGAGTTGATCCAATTGACACCTTGCAAGTGGA
AGATATTGTCGCATTTTAAAGAAGATTATAAACAAAATGGTTTAAAGGATCTTTAAAGAATTATTAG
AAAAGACATTGTGTAACCCCTCATTCGCAAAAATTTAAATTCACCATGGAGCCAAGAGAAGATTTTA
CCAAACAATTGGTAAAAGATGAGAATTTGATGATCGAGAAAAGAGTAAGTGAACCTCACAGAAGATA
ACAAGAAGGCAATCTATGAGCAAACTTGAATTAAGCTAAATTACAATTGGAGGATCAAAATACAG
AAGTTTACCCACATTGACTATTGATGACATTCCAAAGAGAGGTGATTTTTATGCCATTGATTTGG
GCCAAGTAAATAAGAAAGTTGTACATGAAAGGGTAGTTGATACCAATGGCTTGGTTTATGCCAACG
CTTTAAAGATATTTCTTATTTACCCACCAAACCTTTACAAGTACCTTCCATTGTTTAAACAACCTGTT
TGACGAACCTTGCTGGAACAGAAAACACACCCATTACGGAGTTGGAAACTAAAATACAAATGTTAA
CTGGCGGGATAACATTTAGTTCTAAAATATCGACTGACCCCTATAATATTGAGCAACTAAAATTAC
AGTATGTGTTAAGTGAATGGCTTTGAAAGAAAAGTCATCCTCAGTTTATGATTTATGGTTGGAGA
TTTTAACTACTACCAAATTCGACACCAGTGATGAGGTATTAGAAAAGTTGTCAGTTTGTGATTAAAA
ACATGGGACAAAACCAAATCAATAATATTGCTGATCGCGGTCATTCTTATGCGGCTGCTGTGAGCT
CACTGAAATTGACACCGCTGAAATACATCAGTGACATCGTTTCAGGTTTGAGTCAAGTTCAATTTG
TAATGGAGTTGAACTCCAAATTAGAATCAGAAGGGAAAGAGTACTTGGCCAAAGAGATTATTCCGA
TATTGCAAGAAATACAAAAGTATGTATTGCAAGGTGAATTCAGGTATAGACTAGTTGGAAATCAAG
AGATTATTGTTGAAAACGAAAAGCTTATTGAGAAATTTGATAAGGATATTTCTTCGAACAGACCAA
CTTTATCGTTAACAGTAACAGATGGTTTACTGGCATTGTTGAACTCATTCAATTACAATCATACAA
GTGAAAATGTCTTAGTTAACTTACCATTTCAAGTGGGATACTCTTCATTAGGTAAGATTGGCTCTT
CGTATTCATCAAAGGATGGTGCTTCTTTACAAATATTATCTCAGTTATATTCCTTTAAAAATCTAC
ATTCCAAAATAAGAGAAAGCAATGGTGCATATGGAGGTGGTTTGACATATGATGGGTGTAACGGGA
CATTAACTTTTATTTCGTATCGTGATCCTAATCCTGTTAAGTCGATTCAAACCTTTTAGAGATTCTT
TACTGTATGGACTTGATGCTAATTGGAACGATAAGGATTTACAAGAGGCTAAGTTGCGGGTTTCC
AAAGCGTCGATGCTCCAATTAATATCTCTCTCAGGGTGCTAGTGCTTCTTTGAAAATATAGATG
ATTACTTGAGACAGGAAAGAAGAGAAAACCTTTTTGGGTACCACTTTAAAGGATCTCAGAGATGTGA

CTGAAAAGTATCTTGTTGATAACCAAAACAACCTTGTCACCTGTTATTGGTGACAATGAAATTTTAA
ATGTCGATAATAAATGGCAAATTAGAAATTTTCAAGTATAG

YDR430C_homolog 1034aa (SEQ ID NO 328)

MLKTRLKQSRRAISRVVRRYACSHPISPNLDKYPVGLKLHGVEVTQTSPPIPEFSLTAVSLKHTESGA
THLHLDSPNDSNNVFSIAFKTNPPDNTGVPHILEHTTLCGSKKFPVRDPFFKMTNRSLSNFMNAMT
GHDYTFYPFATTNSKDFENLMDVYLSSVFEPQLNHTDFLQEGWRIENQNVHDISSKLEFKGVVYNE
MKGQYSNSAYFYIKFLESIYPSLNNSGGDPKKIVDLSYEGLLFHSKNYHPSNAKTFTYGKLPLE
DSLISKISKYYESFEKKVSSVDVKQPIFSTDKSEIFDVTIPGPVDTMNGKETSEYCTSTWNLGNP
LDPNMQYDIFKWKILSSLLFDGHNSPFYQELIESGYGDDFSANTGLDSTTALLSFTVGLNYLTKQK
VDNFNEKVMETINNKIPELSNEESSYHGRIDAILHQIEIGFKRHKPDFGFGLLSSIIVPSWVNGV
DPIDTLQVEKILSHFKEDYKQNGLRIFKELLEKTLNPHSQKFKFTMEPREDFTKQLVKDENLMIE
KRVSELTEDNKKAIYEQNLELAKLQLEDQNTTEVLPTLTIDDIKRGDFYAIIDLQVNNKKVHERVV
DTNGLVYANALKDISYLP TKLYKYLPLFNNCLTNLAGTENTPITELETKIQMLTGGITFSSKISTD
PYNIEQLKLQYVLSGMALKEKSSSVYDLWLEILTTTKFDTSDDEVLEKLSVLIKNMGQNQINNIADR
GHSYAAAVSSSKLTPSKYISDIVSGLSQVQFVMELENSKLESEGEKEYLAKEIIPILQEIQKYVLQGE
FRYRLVGNQEIIVENEKLEKFDKDISSNRPTLSLTVDGLSALLNSFNYNHTSENVLVNLPFQVG
YSSLGKIGSSYSSKDGASLQILSQLYSFKNLHSKIRESNGAYGGGLTYDGLNGTLNFYSYRDPNPV
KSIQTFRDSLSYGLDANWNDKDLQEAELRVFQSVDAFINISSQGASAFFENIDYLRQERRENFLG
TTLKDLRDVTEKYLVDNQNNLVTVIGDNEILNVDNKNWQIRNFQV

YDR450W_YML026C_homolog 1366bp public: 1..1366; exon 1: 501..548,
intron 1: 549..976, exon 2: 977..1363 (SEQ ID NO 329)

TTAAGAACTAGCAGATGTAAAATGTTTTATGTCATTATATAATTTGTTAATACATGTATATAGATT
TTTTAATGAATGTATTCCTAAATAGAACAGAATTATGATGCTGTTACAGCAAAACTGGTTTGAG
TATTGGAGAATGTTATAAACTGAAATTTGATTTACAACCAAAACCCGTGTCACGTGTAAGTAATTA
GGGCTTTTAGGGCTTTCTATATACAGGCACCAGAATTTTTTTTTTATGGGCGATAGAAATAATGTAT
GCGCGCGATTCTTCCTGCTAGAGGTTTTTCTTTTTTGTATGCTGTAAACAGTGGGACTCACATAGTT
AAGTAATTTTAAAGCCAGAGATTGTGTACAGTCGCACGCCCCCTAATCACATAGTTAATTCTCAA
CTTTCTCTCTTTCTCTCTTTGCTTTTCTCCTAAGGAAAAAAAATTTATTTTCAATTTGTTGAAAAT
TTTTGTATAGTTTCAAGTAAACACACCAGTAATCAAACATGCCATTAGTTGTCCAAGAACAAGGTT
CATTCCAACACATTTTACGGTATGTGAGTGTATTATAAGATTATTTGAATGAGATAGAAAAGGGTT
AAGGAAGGAAAGAAATTATCCAACACTACTGTTTTGGGAAAGATTAAATCAGAAATTTGAATGCAATGA
AAAAACTTTTTCAAGAGATGGATATGGAACAAGATTCGATTGTTATCAACAAATATAAAGAAAAGC
AATGATTTACTACTGTTTGGGAAAGATTTTGGATATGTGTATCAACAATACTACTATTTACTTTGG
AGTAATATGTTTTCAATATTATCAGAGACTTATCAAAATTTATGAGTTTATTATTATTGAAGTTCA
ATACCATCAAGCCTTTTTTTTAACCATCACTCTATTCAACAATCATTTAAATATTAAAGTCTTTTT
TTTCCCTGTTTAAAGTATTCGATTACTAACATTATGAATTATTATTATAGTTTGTAAACACCAA
CATTGATGGTAGAATCAAGATCATGTACGCCTTGACCAAGATCAGAGGTGTCGGTAGAAGATATGC
CAACTTGGTTTGTAAAAAAGCCGATGTTGAATTAACCAAAAGAGCTGGTGAATTGACCCAAGAAGA
ATTGGAAGAATTGTCACCATATGCAAAACCAACCACTATAAAATCCCAGCTTGGTTCTTGAA
CAGACAAAAGATCAAGTTGATGGTAAAGATTACCATGTTTTAGCTAACAACCTTGAATCTAAATT
GAGAGATGATTTGGAAAGATTGAAGAAAATCAGATCTCACAGAGGTATTAGACACTTCTGGGGATT
GAAAGTTAGAGGTCAACATACTAAACTACTTCTCGTGGTCGTAA

YDR450W_YML026C_homolog 145aa (SEQ ID NO 330)

MPLVVQEQGSFQHILRLNLTNIDGRIKIMYALTKIRGVGRRYANLVCKKADVELTKRAGELTQEEL
ERIVTIMQNPTNYKIPAWFLNRQKDQVDGKDYHVLANNLESKLRRDDLRLKKIRSHRGIRHFWGLK
VRGQHTKTTSRGR

YDR471W_YHR010W_homolog 1327bp PathoSeq: 1..1327; exon 1:

501..530, intron 1: 531..946, exon 2: 947..1324 (SEQ ID NO 331)
ATAGTTATTACAATATAATAAAGCAAATAAATAAAGAAATGATAAAGAACCATATTAACAAAGTT
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GTAATACCTAATTCTATTTGGTGTGGTGCATCACGTGCTAGGGCTATAGCCCTAATAGTATATGCA
GTCGCATACATTAATTGGTCATCTCATAAGTAAATTATATAATGTATAGTGTGCGCGCACTGTAAT

TTTTCACACTAAGTTAAGGAGAGTGCGAAAAATTTAGTACTAACAAAATTTGTATTGTGTTGTGTGT
GGCTATTGGGCAGAGCGAAAAATTTACCCCTACTGAGAGGAACTGTGAGGGAGAGAGATACACAC
AAACTCTGTGCGCAAGAAGAAAGACAAAAAATTTTTTTGAAAAAAAAAAAAAGAGACAACCAACCTT
TTATTGTATTAAACATTTTAAGATATCAAGAACTAAAAATGGCTAAGTTCATCAAATCTGGTAAAG
TTGGTATGTAAAAATGAGTACCTATATGGGTAGACAATGATAGATTTATTGGCCAACCTATGAATGG
GATAGATATATATGATATGGGAGAGAATTTTGAAGGATTGAAATATTTTATATAAAAAGAGAGAAGC
AAAGAGAAATAATGAACAATTGAAAAGAAGATACAAATACTGTTAATTAACTAGAATATGCCATT
GAAGATTTAAATGATTACCATCGTAATAAATTTATTGGAATTTGGGAGATTCTTTTGGAGTTAAGA
AAAAAGCAAGTGATTGATCAATCACTATGGAGCCGTCACAAGACATCAACGAATCCCACAACATTT
TTATTTATTTCATATCCATCATATGGCAGTAACAATCATGAATCTACAAATTACATTTAAAAAAGC
ATTATACTAACTAAATTTTTTAGCTATTGTTGTAAGAGGTCGTTACGCTGGTAAAAAAGTAGTCAT
TGTGAAACCACATGATGAAGGTACCAAATCTCACCATTCCCACATGCCATTGTTGCTGGTATTGA
AAGAGCTCCATTGAAGGTTACCAAGAAGATGGATGCTAAAAAAGTTACCAAAAGAACTAAAGTCAA
GCCATTTGTAAATTAGTAACTACAACCATTTAATGCCAACTAGATACTCATTAGATGTTGAATC
ATTCAAATCTGCTGTCACCTCTGAAGCTTTAGAAGAACCATCTCAAAGAGAAGAAGCTAAAAAAGT
TGTCAGAAGGCTTTTGAAGAAAAACATCAAGCTGGTAAGAACAAATGGTTCTTCCAAAAATTACA
CTTTTAA

YDR471W_YHR010W_homolog 136aa (SEQ ID NO 332)

MAKFIKSGKVAIVVRGRYAGKKVIVKPHDEGTSKSHFPFHAIVAGIERAPLKVTKKMDAKKVTKRT
KVKPFVKLVNYNHLMPTRYSLDVESFKSAVTSEALEEPSQREEAKKVVKAFEEKHQAGKNKWWFFQ
KLHF

YDR486C_homolog 1157bp PathoSeq: 1..1157; CDS: 501..1154 (SEQ ID NO 333)

TTCCAGTCATTCCGAAATGCATAAGCAAGACGTTAGTTGTATTGTGGTTGTTTAGTCTAATCCAAA
AATACTTGCCATGACGACCCACTGAAGTAACAACCTGCATTTGTAAAGGCTTTTCTCATCTTATTCA
ATTCTTTTTTCAGCATCATTCGTATCTTTAAGCACAGGGAATAGCAATGGATCATGTAACAAATTCA
CTTTCGTGATTTCGAAAGCCCAAAATGTTTCGTTTTAACAACGCACACACATGTGAAACCTAAACCG
AGTTAGTCGTCAAGAAAATAATTCAGTGTAAAGTCTGTACCTTAAGCGTCAAACGTACTTCTGCA
ACCTCTGGCATTGAGTGTAATTTAAATATTCATGATAATCTGGAACCTACAAGCTACGAAAAA
GAAAAAGAAAAATAGTACGAGTCTTGGTGAGATAAATAATGGAGAACACTTTTTTTTTTCTCTTT
GGAGGTTTTAGAAGGCCAAAACCAAATCTAGACAAGGAGATGAACAGATTATTTCGGAACGAAAAGCA
CTGCGCCCAAACCATCTTTGAATGATGCAATCAAGGGAATCGATGAAAGAGTGGGGTCTTTGGATG
TTAAATTAAGCAAGATCAACTCGGAATTATCCACATACCAACAAAAGATAAGCAGAATGAGAGACG
GACCCGGAAGTCGGCACTAAAACAAAAGCAATCAAGTTACTAAGACAGAGGAAGCAGATAGAAG
CTCAAAAGGATCAGTTAGAGAATCAATCTTGAATATGACACAAGCTTCCATGACAACAGATAACT
TACAAAATACCATGGTCACAATAAATGCAATGAAAACAGCCAATAAACTGTTGAAACAACTTATG
GAAAAATTAATATCGATGAATTGGAAGATCTTCAAGATGAAATGTTGGATTTGATTGATAAATCAA
ATGAACCTACAGGAGGCACTTCTGACGAGCTATGATGTACCCGATGACATCAGTGAGCTGGAGTTGG
ATGCTGAATTAGAAGCTCTTGGCGAAGAAATTGATTTTGAATGAAATGGCAGAGAGTGGGATAG
GTGCACCTAGTTACTTAAATGATACAGAACCTACAGCAGCAGATAAATTGCCTACATTTATTGACG
AACAACCAGAAGAAGCTCAAAAAATCGCAAACCTAG

YDR486C_homolog 218aa (SEQ ID NO 334)

MNRLFGTKSTAPKPSLNDIAIKGIDERVGSLDVKLSKINSELSTYQQKISRMRDGP GKSALKQKA
LLRQRKQIEAQKDQLENQSWNMTQASMTTDLNLTMTINAMKTANKSLKQTYGKINIDELEDLQD
EMLDLIDKSNEALSTSYDVPDDISESELDAELEALGEEIDFENEMAESGIGAPSYLNDTEPTA
ADKLPTFIDEQPEEAQKIAN

YDR507C_homolog 4550bp PathoSeq: 1..1424, public: 1524..4550; CDS: 501..4547 (SEQ ID NO 335)

GAATGAGATTTTTTTTTTTTACTAAGGGTGCACTACTACTAGTTATTTGTTTTGTTGTTGACGATCA
TTAAAGAAAAAATTTACAGTATACACAAAACACTTTACTTCTGCTGTTTTTTTTTTTATTTTAGTTT
TTGGTTTCATAAATTATTAAGAAAGCAAATAATTATTGAAATAAATTTTATATTTTGGTTTTT
TTTTCTTTGGTTTCTTTGAATTTTGCAAACCAATCCAAATTTTTTTTGAAATTTTTCCTTCTTCT

TCATTTGTTGACTTTTGAAGTTTATTCATCCATATTCTTCAAGTTAAAATAGTGTTCAATATCT
GTCCAACCAAGAAGAAAACCAATAAACACATCAATTCCAACCTTGTTTACATCAAACAGAAACAA
AAAACAGATAATTTATAGACACCTTCATTCATTCGTTATTTTTTTTCCAAGTACTACACGTCTTTAT
TTTTAATACATTTATCATAAACAAAATTTATATCAATAATGCCACATTCAGACAACCTTCGATAT
CGTCATCGATTATGTCCCAATCAAATCATAATCATCCACAGAAGATCGGACCTTGGAATTAGGTA
AACTTTAGGAAGAGGTGCCACCGGTAGAGTCTTATTAGCTACTCATCAAACCTACTGGTCAAAAAG
CTGCCGTTAAAGTAGTTTCCAAATCCGAATTACAAGACGAAGAAACCGAGAAAAATGGAGATGGAT
TACCATATGGTATAGAAAGAGAAATTATTATAATGAAATTATTAACCTCATCCTAATGTTTTGAGAT
TATATGATGTATGGGAAACATCTAAGGCTCTTTATCTTGTCTAGAAATACGTTGAAGGTGGAGAAT
TATTTGATTTATTGGTGGAAACGTGGTCCATTACCTGAAGTCGAGGCTATCAAGTATTTCCGTCAA
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GCAAATTATTAGAGACTTCTTGTGGTTCACCTCATTATGCTGCTCCAGAAATCGTTAGTGGATTGA
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GATTACCTTTGATGATGAAAATATTAGAAATTTACTTCTTAAAGTCCAGGCTGGTAACTTTGAAA
TGCCCGTTGATGAAGTTAGCAGAGAAGCTAGAGATTTAATTGCTAGAATGTTAGAGGTTGATCCTA
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AAGATTTAATCAGTGAAAAATCATTACCACATCCACATACTGGTTACAAATCTTTAGGGTCAGTTA
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ACAAGCATAATCAAGACGATAACACTAATAACAATTCACCAAAGAAATCAACGAGTTTCAATAATA
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AGTCACCATAACAGATCACCTTATAGATCACCATATAAATCGCCTTCTAAGAGATATTCATATAATC
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TAAAGGCAAAGCCAAGAAATATTTACAATGAGATTGTTGATGCACAAAGCAACTTTTCTCTACCTC
CATCGCTTCCACCTTCCCTTACCTTCAAAGATTCTCGTTATATGATCGATGAACCCAATCAACCCC
AGTTGCAACAACCTGCTTTAAGTCAAGTCCCTGAAAATCCTATTGTTGATGAATCCCCTGATTTAA
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CAACTGTGGAAGATTCCAACCTTGACTGATGACTACATGACAGAAATCAGAAAATCAAGACTTTTGA
ACAGTCAGTTAAATGTTAGGGATCCACTTAATGAAAAAAGAAAATCTGAACCCAAGACTCTTATTA
GCAATGTTCAAATACCGAGTGTTACTAGAAAATCAAGAAATTTCACTACTTCCAACAAAAGGTTGT
CGGTATTGTCTATGTATTCAACAAAGGAATCATACCGTGATTTGAATTCTATAATTAACCTACCAG
ATGAAAACCCCGAACAGCATCAAAACATGAACAAGCCAGCGTTACGAACCAGTATTGCTGATCGTT
TGGATAAAGCTGGATTGGCTGAACCAGAATATGAACTGAGACTGATGGTGAAGATAAAGTGTCTG
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CATCTAGAGCTTCAACAACTAAACGTTACAATGTTTCATTCCAGTTCAGAAAAAGACCAAAATCCA
AAGTTCCTGATTTGCCAAAGAATGATTATGATGACACATTTGTTCAGTAATAGTGATGAAGTTCATA
AGCGTCAGTATAAATCGATGGTTTCTGATGAGTCTAGTGCATCTGATGATGATTTTGATAAGATTA
AATTACCAGATGGTAAATCAACTAAATCTTCCATTGATGAATTGGCTAACGGCACGTCTACAAGTG
GTCATAGAAAACCAAGATAAGACATTCTCAACCGGGCCAGAAATGTTGATTCTCATTTGAATG
GAGGTATTGAGTCGTCTCAACCAATGTCTAAAGTTTCGTGGTAACAATTCAAGTGGTCATGATGATA

GTGTTCCACCACCACCGCCAGCTCACAAGGTGAATAAAAAACCATTTGGATGATAAGACGAATTTCC
CTCCACCAGAAGTGGATCCAAAAAGAAAAGGTTTATTTTTTAGAAAACCTTTCTTGGGGATCCAAAA
AAACCATTTGAAAATAATACAAACGCCGCCACTAATACCACGACTCAACAACAATTACCAAGTCCTG
CTGAATCAAAAGAGGAGAAACCAAAAAGTTTATTTTTTTCAGATGGTTTTTCGTCATCTAATACTCCAT
CTGCTGCTGAAATTAGAAAATTCAACACCATTTTACCTAAACATGAAATGTCTACTGCTTTATTG
CTTTATTGAATTCTTGGTCTAATTTTGGTTTGAAAGATTTACGGAATGATCAAGTTGGATATTATA
TTACTGGTGCTATTTCTAAACATAATTTCTTTTAAATTTAAAGAGTTGTAAATTTAGAATTAAGATTA
ATCAAAGAGATTTTAAATCAAAAATCAGAAATTGTTTGTGTTAGAGTGAAAGGATCTAAAGTTACAA
CTGATACTTTATTTTGTGAAATTGAAAAGGTCTTACTCAAAGAAGGTGGTTTAGATAAATAA

YDR507C_homolog 1349aa (SEQ ID NO 336)

MPHSRQPSISSSIMSQSNHNHPQKIGPWKLGLKTLGRGATGRVLLATHQTTGQKAAVKVVSKESELQD
EETEKNGDGLPYGIEREIIIMKLLTHPNVLRLYDVWETSKALYLVLEYVEGGELFDLLVERGPLPE
VEAIKYFRQIILGTAYCHALGICHRDLKPENLLDSQLNVKLADFGMAALESNGKLLTSCGSPHY
AAPEIVSGLKYHGAASDVWSCGVILFALLTGRLPFDDENIRNLLKLVQAGNFEMPVDEVSRARDL
IARMLEVDPMRRISTEKILRHPLLTYPMSNEDLISEKSLPHPHGTGYKSLGSVRNIDKQILSNLTI
LWNRPEEEIVDCLLDGNSPEKTFYALLMRYKHNDQDNTNNNSPKKSTSFNNKVVRSGSKYSLNG
TPRRKRASHISVSRPTSFQYKSNPGAGATANRNSVARHSVASSANNSPRKSPYKSPYRSPYRSPYK
SPSKRYSYNQSPTKSPYGRSNSQRQFENEPLKAKPRNIYNEIVDAQSNFSLPPLPSLPSKDSR
YMIDEPNQPOLQOPALSQVPENPIVDESPDLMSAKISSGKRNSIIGKNNNSNSNKRMSKRKSIR
ASMTTGLKRNSITMKLLSTYAKLSGDDWEYMDKQTKRTSATFAALCDKIFNQEDYDEEDEQLVDP
EEKEAKEYERLMELERKKHEAELKARRELEKKRRQKRRSILSSKLSIIVKNDADPNNSEQELVD
EGIKQPKRQSKNLTALRALSEGNHASEELTLEDVENLKRRSASQVPKRRQTPVLTRRPVSRLDPL
WQAHENEQLDRAKDALEQEWDRDSQKRSSTVSRKKVNRESMISVMDDIVEEDQGRVNRSTRNTYYE
RERDYELPEPTVEDSNLTDDYMTETIRKSRLNSQLNVRDPLNEKRSKSEPCTLISNVQIPSVTRKSR
NFTTSNKRSLSVLSMYSTKESYRDLNSIINSPDENPEQHQNMMNKPALRTSIADRLDKAGLAPEYET
ETDGEDKVSVIDLDDHLADRRTSYDGSGRASRASTTKRYNVHSSSEKRPKSKVPDLPKNDYDDT
FVSNSDEVHKRQYKSMVSESSASDDVFDKIKLPDGKSTKSSIDELANGTSTSGHRKPKIRHSQPG
PEMLIPHLNGGIESSQPMKSVRGNNSSGHDDSVPPPPPAHKVNKKPLDDKTNPFPPEVDPKRKGSF
FRKLSWGSKKTIEENNTNAATNTTTTQQQLPSPAESKEEKPKSSFFRWFSSNTPSAAEIRKFNTILP
KHEMSTALFALLNSWSNFGLKDLRNDQVGYIITGAISKHNSFNLKSKCFRIKINQRDFNQKSEIVC
VRVKGSKVTTDTLFCIEKVLLEGGGLDK

YER102W_YBL072W_homolog 1121bp public: 1..1121; CDS: 501..1118
(SEQ ID NO 337)

ACAATACTAGGCACTGTTGAGTGAGTGAGCATTTTTTCTGTTTCTCACTCAGTTAACAAAATAAAA
AAAATTTTTCATAATTTAGAAAGTTTCATTTACAGTCTTTTTTCAATTAACAGTGATACAAGAGTGTA
TGTAAGACAAACATGTACTAGCAACTATAATATGATTTACCAATGATTGGGATCACAATAAATGTG
TTAATATGAATGAGAGAAGGATAGTGAATAAGAGATTACGAAAGATAGATTCAACAAGTTCAGAA
TGGTATACAACATAAATGGAATTATTTTCAATATGCAACTATCATTATGACTACTACGACAACAA
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TGGAACAAAGTTTACTAACAACATTGTTATAGGTAAAAATGGGTATTTCTAGAGATTCACGTCACA
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AATTCAGAGCTTTGAGAGTTGAAACCGGTAACCTCTCTTGGGGTCCGAAGGTGTTTCCAGAAAAA
CCAGAATTGCTGGTGTCGTTTACCATCCATCTAATAACGAATTGGTTAGAACCAACACCTTGACCA
AATCTGCTGTTGTTCAAATTGATGCTACTCCATTCAGACAATGGTACGAAAACCACTACGGTGCTA
CTTTAGGTAAAAAGAAGGGTGGTGCTCATGCTGCTCAGCTGCTGAAGTTGCCGATGCCAAGAGAT
CAAGAAAAGTCGAAAGAAAATTGGCTGCTAGATCTGGTGCTGCTGCCATTGAATCCGCTGTTGACT
CTCAATTCGGTTCTGGTAGATTATACGCTGTCATTTCTTCAAGACCAGGTCAATCTGGTAGATGTG
ATGGTTACATCTTGAAGGTGAAGAATTAGCCTTCTACTTGAGAAGATTAAGTCTAAGAAATAA

YER102W_YBL072W_homolog 206aa (SEQ ID NO 338)

MGISRDSRHKRSATGAKRAQFRKKRKFELEGRQPANTKIGPKRIHSVRTRGGNQKFRALRVETGNFS
WGSEGVSRKTRIAGVVYHPSNNELVRTNTLTKSAVVQIDATPFRQWYENHYGATLGKKKGGAHAH

AAEVADAKRSRKVERKLAARSGAAAIESAVDSQFGSGRLYAVISSRPGQSGRCDGYILEGEELAFY
LRRLTAKK

YFL014W_homolog_1 819bp PathoSeq: 1..819; CDS: 419..816 (SEQ ID NO 339)

TTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
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AATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTGCTATCGATAACGAAGG
TGAAGGCAGTTTAGCTTGGAGACATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAAAT
CGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCACAGCAATATAGCAA
TCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCCTTGAATCTTGTTTTTT
TCGACATACACCATAAATCCCATAGAAAACCTGCAAAATGTCTGACGCCGGAAGAAAAACATTTCT
ACTAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAACAA
GTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTCAA
ACTGTTGCAGACAGCGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCGAA
CAAGCAGAGGGCGAACAAAGACCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAACCTG
AAATTGAAAGGCTGCTGAATACGTGA

YFL014W_homolog_1 106aa (SEQ ID NO 340)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADSVQQGSDN
AKADLKKQSEQAEQEQRPLSKQLKNMSRLPKSKLERSSENT

YFL014W_homolog_2 884bp public: 1..884; CDS: 501..881 (SEQ ID NO 341)

CCTTCTCCTGTGAAAAGTTTCGAGATGTAACGTTTCGCAGTAATAGAGAGCCAGAATCCATTTTGTG
TGTACTACAGACAAATTCAGAAGTTTCAACTGCTGCATATCGCCTTAAATGACTGTAGCATTTCGTC
CAAATTGAGACCCTCAATTACATTTTGTCAAAAAAATTGGTCCCTAGTGTGCTATCGATAACGAA
GGTGAAGGCAGTTTAGCTTGGAGGCATTTAGAGAACTTAGTTACATCTCATCTTCCGTTTCGAGAA
ATCGTTGATTTACCGTGCAGCGCTTATATTGATTGCTACTTGTTCACGACCACAGCAATATAGC
AATCATAAATAAATTGCCCCGCGGTTGACAGTGTATATCTTCGAGGAATGGCAACCTTTGCCCCCTC
TCTCGAAAAACAATATAAATAGAGTCAATTTCTCTAGTAGAGGTAAATTCCTTGAATCTTGTTTTT
TTTCGACAAACACCATAAATCCCATAGAAAACCTGCAAAATGTCTGACGCCGGAAGAAAAACATTT
CTACTAAATCAACGAAGCTATAACCCCCGAATCCGAAAAGTCTACCTTGGAAAAGGGCAAGGAAC
AAGTCACCAGTACCCTTGACAAAGCTGTTGGCTCAAATGTTCCAGATAACCAAAAATCTTTCACTC
AAACTGTTGCAGACAACGTGCAACAAGGTTCCGATAATGCTAAAGCTGATTTGAAGAAACAATCCG
AACAAAGCAGAGGGCGAAGCAAAGACCCTTGCTGAAACAGCTCAAGAATATGTCGAGGTTGCCAAAA
CTGAAATTGAAAGGCTGCTGAATACGTGAGTGGAGTTGTCACCGGTGCTACCGAAGGTGCCAAAA
CCGGCGCTGATAGTACTAAAAAATAG

YFL014W_homolog_2 127aa (SEQ ID NO 342)

MSDAGRKNISTKINEAITPESEKSTLEKGKEQVTSTLDKAVGSNVPDNQKSFTQTVADNVQQGSDN
AKADLKKQSEQAEGEAKTLAETAQEYVEVAKTEIGKAAEYVSGVVTGATEGAKTGADSTKK

YGL011C_homolog 1244bp PathoSeq: 1..1244; CDS: 501..1241 (SEQ ID NO 343)

GAAGGGCACCATAATGAAATCGACTCACTTCAGGATTATAATGGTATGAAACATTGTACTTGTAT
TAGTGCCAGGATGATTAGGATCATATATTGGGGTGTCTTCTCGAGTCTTGGTATCGGTGTAAACG
TATCTGTTTCACTTATCAGTATCGTCATTTATATTAATACTACTTTTCTCCTATGGTTATATATTGGT
AAACAAAGAAACAAAACAACAAAAAGAAGTAGTAGTTTTGAAAATTGTCAATAAAAGAAACAAAG
AATGAAAGAATGATTGAATGAAAGAAAAAAAATATGAAAGTGAGTGCGACATAATGTAGAAAAA
TGTCGAATGTCTTGAACCTTACCCATTGAGTAGTTGTTGTAGTGTAGGAGGAAGAAAAACAACAGAA
AGAAAGAGAGAAAGAAAAATTTCCGCACTACAAATATTCAACAAGTTTCATATAGTAATATAATCC
CAATTGATCATTACTTTATTCCACACAATTCATAAACAATGTCCAATTCAGCAGGTTTGTATAGAC
ATATCACTATTTTTTCTCCTGAAGGTAGATTATACCAAGTAGAATATGCTTTTAAAGCTATCAATT
CAGCAAATATCACCAGTTTAGGAATCACAGGTCAAGATTCTGCCGTTATTATATCACAAAAGAAGA

TCCCAGATAAGTTATTAGATCCTAAAACCGTGTCATATATTTTTTAAAATCACTCCTAGTATAGGAA
TGGTTGCCACTGGATCAATTGCTGATGCTAGAGCTCAAGCCATGAGAGCAAGATCTGAAGCTACAG
AATTTAGATATAAATATGGTTACGAAATGCCGGTGGAAAGTTTATCAAGAAGAATGGCGAATATAT
CTCAATTGTATACTCAAAGAGCTTATATGAGACCATTGGGTGTTGCTTTAACTTTTATTCAAGTTG
ATTTTGCTGATGAAGGTAGAGGTCCACAAATTTTTAAATGTGATCCTGCTGGATATTTCACTGGGG
TGAAAGCCGTGGCCACTGGTCCAAAACAACAAGAAGCAACGACTTATTTAGAGAAAAAATTCAAAA
AAACCGATGCTGTTAAAGGAGATTGGCAAAAAACTGTTGAATTTGCAATAATTGCCTTGAGTTCTG
TGATTGGAAGTGAATTCAGAAAAAATGATATTGAAATTGGTGTGGCCACTGAAGGAGAATTTAGAA
TTTTGACACCAGAAGAAATAGACGAAAGATTGATTTCAATAGCTGAACAAGATTAG

YGL011C_homolog 247aa (SEQ ID NO 344)

MSNSAGFDRHITIFSPEGRLYQVEYAFKAINSANITSLGITGQDSAVIISQKKIPDKLLDPKTVSY
IFKITPSIGMVATGSIADARAQAMRARSEATEFRYKYGYEMPVESLSRRMANISQLYTQRAYMRPL
GVALTFIQVDFADEGRGPQIFKCDPAGYFTGVKAVATGPKQOEATTYLEKKFKKTDVKGDWQKTV
EFAIIALSSVIGTEFRKNDIEIGVATEGEFRILTPEEIDERLISIAEQD

YGL031C_YGR148C_homolog 968bp PathoSeq: 1..968; CDS: 501..965 (SEQ ID NO 345)

CATTGTAGGTACACCTGTTTTTGCTCAATGTACACACACACGCACCAGCAGTAGGAAAAAAACAA
AATTAAATGAAAAATCATTTTCGTTCAATATTAAGCTTCTTAAGATAACCAACCAATTAATATGTA
TGTGACATACCATATAAATAAAGCTACAAATGGGGATAACTATGTATTTAATGATAAATGAATGGA
AGACCAGAAATGTATAATGTTATAAGATAGTGATTTATATTGAAAACACCCTTAAAAAAATCAACCA
CCCATCTAACCGTCGAATTGGAAATGTCAATTTAGTTAGCATCGAAAATCAACAAAGACATGGGGA
ATCATTTACATATAAAATAATGAGAGAGAATTACAAACTGCTACGTTATGTTTTGTTTCATTATGTC
TTGTTTCATTATGTCTTGTTTCATTATGTCAAAAAATCTATAGTTACCTACCTCTACATCAATTTATG
GTCTGAAATACTAACATTTTTTTTTTATTTATAGTGAAAAATGAAGATTGAAGTTGACTCCTTTTCAG
GTTCTAAAATCTACCCAGGTAGAGGTACTTTATTTGTCAGAGGTGACTCTAAAATTTTTAGATTCC
AATCCTCAAAATCTGCTTCTTTATTCCAACAAAGAAAGAACCCAAGAAGAATTTCTTGGAAGTGT
TGTACAGAAGACACCACAAAAAAGGTATTTCTGAAGAAGCTGCTAAAAAGAGAACCAGAAAGACCG
TCAAGCACCAAGAGCTATTGTCGGTGCTTCTTTGGAATTGATCAAAGAAAGAAGAAGTCAAAAAC
CATCTGACAGAAAAGCTGCTAGAGACTCTAAATTAGCTAAAGACAAAGAAGCTAAAAAAGCTGCTA
AAGCTGCCAGAAAAGCTGAAAAGGCTAAGGCTGTTGCTTCTGGTGTCTTCTGTTGTTTCTAAACAAC
AAGCTAAAGGTTCTTTCCA AAAAGTTAAAGCTACCTCCCGTTAA

YGL031C_YGR148C_homolog 155aa (SEQ ID NO 346)

MKIEVDSFSGSKIYPGRGTLFVRGDSKIFRFQSSKSASLFQQRKNPRRISWTVLYRRHHKKGISEE
AAKKRTRKTVKHQRAIVGASLELIKERRSQKPSDRKAARDSKLAKDKEAKKAARKAEKAKAVA
SGASVVSQQAQKGSFQKVKATSR

YGL043W_homolog 1418bp public: 1..436, PathoSeq: 437..1418; CDS: 501..1415 (SEQ ID NO 347)

AATCTACCATTAGGCAATGTCATATAATTTAGATTACGAACAGCTGATGACGCAGTTTCATTATCT
CCATAATTTATAATGGCATAACCTTTGGATTACCTGTTAATTCATCAAATAATAACTTCACATCT
AATACTGGTCCAACCTGATCTTGCAATATCCCGCACCTGTTCTTCAGTGTAATCAAATGGAAATTTA
CCTATTGAAACACAAGTGCTTTTACTATCCATATTTAGTTTGAGCTGCCTAGTTTTCCTGATTCTT
GGTAACAAAAAACTATAATTATTTAACAAATTATCGATAGAATCTCTTCCAAAGTACAACCAATTT
CGATACATTTTTTTCTATGAGATGTTTTTTTCCCCTTTGTCTTTAACTAATGTATTTGGGTACACT
ACCTGAACCTACCAGTTCAGTTCAGTCTAAAAAATTTTTTATTTATTGTGTTTGTATTACTACCC
TTTGCATATATTACTAATATTTATCTTACCCTTTCATCATGGATACAAAGGAAATAAGATCTACCG
TATCTAATCTTGAAAAAGCAGTAGATGACACCACCATTTTAAAGTTGTTGAATATCTTGAATGATG
GGGTAAACCATCCGAAAAACTCTTGAGAGAAACCAAGTAGGTGTAGCTGTCAACAAATTCAGAA
GTCACGACAGTGCCGAAATCAACGGTTTAGTTAAAAAATGATCAGAAATTGGAGAGATGCCGTGC
AAGCCGAAAAGAACAAAAAGAAGTTAGCAATAGCAGCTGGAACAGGAACAGGAACACCTTCAA
GCTCAGCAATTTGCGCCATCATCATCGGGTCTGGAAGTACAACACCAAAACCATCAGAGTCAACCA
CACCATCGGCTGCCCGTAAAGGTCCAAGAAATCCAAAAACTGACGGTGTAAATACTCAATTATACG
AAATGATACCAGAAATGCATCGGTTAGTGCTTTATACACGTCGTTAGCAGTTGATCGTGACGATT

CACCAAAACACATTTTGAGAATAGCTATTGAAATCGAGGCTGAAGTATACAAGAGCGAATACCTGA
AAGTAAGTGACAGTTATAGAAATAGGTAAAGAAGCTTTACCATGAATCTTCGAAATAAGAAAAACC
CAGAATTAAGAGAAAGAATCTTATCGAAACAAATTTTACCTGCTGCGTTCATTAAAATGACCCCTA
ATGAAATGGCTCCTGAGGCATTGAAAAAGGAAATTGAAAAATTGCACAAACAAACTTGTTTGATG
CTCAAGGTGCTACTGAAAAGAGAGCAGTGACCGATAGATTCACTTGTGGCAAGTGTAAAGCACAAGA
AGGTCAGTTATTATCAAATGCAAACCAGATCAGCGGATGAGCCTTTAACTACATTTTGTACTTGTG
AAAATTGTGGCAATAGATGGAAGTTTTCATAA

YGL043W_homolog 305aa (SEQ ID NO 348)

MDTKEIRSTVSNLEKAVDDTTILKLLNLDGVKPKSEKLLRETKVGVAVNKFRRSHDSAEINGLVKK
MIRNWRDAVQAEKNNKKLAIAAGTGTGTPSSSAISPSSSGSGSTTPKPSESTTPSAARKGPRNPK
TDGVNTQLYENDTRNASVSALYTS LAVDRDDSPKHILRIAIEIEAEVYKSEYSKVSDSYRNRLRSF
TMNLRNKNPELRERILSKQILPAAFIKMTPNEMAPEALKKEIEKLHKQNLFDAQGATEKRAVTDR
FTCGKCKHKKVSYQQMQRSADEPLTTFCTCENCGRWKFS

YGL103W_homolog 1301bp public: 1..688, PathoSeq: 689..1301; exon
1: 501..548, intron 1: 549..899, exon 2: 900..1298 (SEQ ID NO 349)
ACATTTATTGTTGGCTATACTTTCCAGTTTTAAAGGAATGGTTAGGCGGGTCAGTCTACTTTATT
TTTACTGTAATGTGTTGTGCCAGTGTATGGTTTATCAAGACTAAAGTTCCTGAGACAAAGGGTAAG
CATTCGTACCAGGAAGTCTGGAATTAAACGGTAGTTACTTCCAGTATATATGGTGTTCATTGTGTT
TTGTGTCTAAAGTTGCGTTAGGGCTAAAGCCCTAATCAATAGTAGTGTACTTTGTTTGAAAAAAT
AATACATGCAAAATACTGCATATTAGAATTATAAGGGAATGAAAATGAAAAAAAAGAATAATTT
TGTAAGATCGCATAGTGTGAGCGCGCACACACACAACTTTGTAGTGCTACAGTTTCTCTCTTTC
CCATACACTCTCGCAGTCGCACGCTTGACAAAAGTTAATTAGAAATAGAAAAATTTCTCATTCCTT
TTGAGTTTTCCACCATAATCAACTAGTAATAACCAACAATGCCTACTAGATTAATAAAACCAGAA
AACACAGAGGTAATGTTTCTGGTATGTACAATTTCACTAAAGTTTTAACGGATGAAAGAGTATTGA
ATGTTCAAGGACATATGGAGATTTAGAGAAAACATGGAAAATAATCGAAAATGAATAATGAATGG
AAAATTTTTTAACTGAATATCAGAATAGACACAACACACAGATCCAGAGTCATTATCACATTGA
TCATACAACCAAGCAATGAATATGAGTAGTTTGGGAAACCACAACATACGAGTTATTTTTCAGAA
CAATCAAGTTTATCATTTACAGAAGACAGTTCCATCAATATGTCCAAAATACTCTTTGAAGTCAAT
TAAAGTCAAATGAACGAATTACTAATTATTTTTTTCTTTAGCCGGTAAGGGTAGAATTGGTAAAC
ACAGAAAGCACCCGGGTGGTAGAGGTAAAGCTGGTGGTCAACATCATCACAGAACCAACTTGGATA
AATACCATCCAGGTACTTCCGTTAAAGTTGGTATGAGATACTTCCACAAACAACAAAACCACTTCT
GGAGACCAGAAATCAACTTGGACAAATTGTGGACTTTGGTTGATTCTGAAAAGAAAGACGAATACT
TGAGCAAATCATCTGCTTCTGCTGCTCCAGTCATCGACACCTTGGCTCACGGTTACGGTAAAGTTT
TGGGTAAAGGTAGATTACCAGAAGTTCCAGTCATTGTCAAAGCCAGATTTGTTTCTAAATTAGCTG
AAGAAAAAATCAGAGCTGTTGGTGGTGTGTCGAATTAGTTGCTTAA

YGL103W_homolog 149aa (SEQ ID NO 350)

MPTRLTKTRKHGRNVSAAGKGRIGKHKHPGGRGKAGGQHHHRTNLDKYHPGYFGKVGMRYPFHKQQN
HFWRPEINLDKLWTLVDSEKKDEYLSKSSASAAPVIDTLAHGYGKVLGKGRLPEVPVIVKARFVSK
LAEEKIRAVGGVVELVA

YGL147C_homolog 423bp PathoSeq: 1..423; CDS: <1..420 (SEQ ID NO
351)

GCTATCAAAATCACTGTTTACAATGGTGACAGAAAACACGTTGCTGCTTTAAGAACTGTCAAATCT
TTGATTGCTAACTTGATCACTGGTGTCACTAAAGGTTACAAATACAAGATGAGATTTGTTTATGCC
CATTTCCCAATTAACGTTAATATTATTAAGGATGGTCAAGATTACGTTGAAATTAGAAATTTCT
TTGGGTGAAAAAAGAGTTAGAGAAGTTAAATCCATGAAGGTGTCACCATGGAAATTTCTTCTACT
CAAAAGGATGAATTGATTGTTTCTGGTAACTCCTTGGAGCTGTTTCTCAAATGCTGCTGATATT
CAACAAATCTGTCGTGTCAGAAACAAGGATATCCGTAAATCTTGGATGGTATTTATGTTTCTGAA
AGAGGTACCATTTGTTGAAGAAATCTAA

YGL147C_homolog 140aa (SEQ ID NO 352)

AIKITVHNGDRKHVAALRTVKS LIANLITGVTKGYKYKMRFVYAHFPINVNIIKKDGQDYVEIRNF
LGEKRVREVKIHEGVTMEISSSTQKDELIVSGNSLEAVSQNAADIQQICRVNRNKDIRKFLDGIYVSE
RGTIVEEI

YGL213C_homolog 1655bp PathoSeq: 1..1655; CDS: 501..1652 (SEQ ID
NO 353)

GATGATCGCTAACAAGGTACCCGATTTATTCATCAACAAAGAAGCTACTTCATAGAATTGATTCTC
AACCTTAAATAGCTTGTAGTTTTTATGATTGGGACTAATTGTGCAGCATCGAACAATATTGCCAGT
TGCATAGAATAAATCGGTATTATTACGGCATAACCAATCGATTGTAGGGGGTTGAAGCTGGTGCTAA
TTCTGGGGTTGTTGCATTTCCAGTCCATAAACGTTGAAACACAAATTGCTGTGTAATTTGGTGAAT
GAATTGATCAGATGATCCTATGGGTGGCATTGTTAAGGTTGTTTCGCTACGATGTATTTCTAGGATA
ATGAAGGTAAGTACGAACCTTATGAGTTTTGATTTCCCTTCCTGATGTTTTTTTTTCCCTGTTTTCTT
TTGTCGTTGTAGCAAGAAGAAAAAAGTGTCTTCACAAGTCTTGGACTCAATTTTCACCCCT
CCACAACTCAATTTCAATTAATCAATAATCCAATATGGGTAAACAGTATATATCTACCGTCA
GTGCATCTCAGGCTCATAAGCTGGATATTCCTTGGTGTAGCTATTACCAATAAGTTCAGTGTATCCG
TGTCTAGTGATGGATATGCGAAATTTTGGGACAACAAGCAAGACGAAGTTCATCTGCCTAAAGAAT
TTGTCCAACCTGGTATTTATAGATAAAAGCGGAATCCATGCGGTGGCTGCTTACGAAAATGTTTTGC
CAAGCTCTACATTGAAAGTGACATTATTAGCATTTGCATGTTTCAATGGATCTATCATCTTCAGAT
ATTATATCAATGATGACTTTTCAACTATCGAAAGTCTAACTGATGATATAAAATCATTTGAAAGCA
ATTGTTGGACCCCTGGCTTTTATCGCGATCCAGAATCCAAACAAGACTATTTTATTACAACCAAGA
CCAATGGCACTACAGAGGTTCAATTTATTGAATATTGTTGATGAAAATGAGAAGGCTGTAATCACAT
TTGAAAAGTTTGGGCAATTAAAAGGAACTCTTCTTCTTCCCAAATCTTTGGCTATATGTCCAA
CAGAGAATAAAAAATGTGCTGTGGGTACATCAATGGTGATGTCTTGTTATATGACTTTGTTAGCT
TGAAATTGATATACACATTTTCGTTTCGAGTGATTTGGTGACCAGTAGAAATTCCTCAATCGACGTCTA
TACCTAGGGTGTGTCATTTTCCCCTGGTGGAACCTTGTGTTGGCTGTGGCAAGAGACAATCAAGCTG
CTGGGTCAATTACATTATACGACGTTGAGCATGGTGAGAATGTGGGGTCTTTGGCCACACCCCTCAC
ACTCGGCCAAATCTGTTGTTGGTGGGTTTGCACATCAAGGCTGGATTTTGGGGTTGAGTTTGTATG
AGGAAGGTAAGCACTTGGCTAGTTGTGGATTGACAAATGCATAAGAGTCTGGAATTTAGAAACAA
GCGAAAGGGAAGCAACAATTAGTATATCTATATCAGACTTAGATGATACTACACATAATGATCAAG
ACGAGAGTGTCTGCTTCTGGTGTGCTTTTATTAAAAAGGGGGTTAGAGGTGGCTCTGGTGGTGACA
GCAATGAAGGATTATGTGTCGTGAGTTTCGATAGAGGAATAAGATGGTACCGAGAGGCAGGAGGAA
TATAG

YGL213C_homolog 384aa (SEQ ID NO 354)

MGKQYISTVSASQAHKSDILGVAITNKFTVSVSSDGYAKFWDNKQDEVHSPKEFVQSVFIDKSGIH
AVAAYENVLPSSTLKVTL LAFACFNGSIIIFRYIINDDFSTIESLTDDIKSFESNCWTPGFIYRDPES
KQDYFITTKTNGTTEVHLLNIVDENEKAVITFEKFGQLKGNSSSFNLSLAICPTENKKCAVGYING
DVLLYDFVSLKLIYTFRSSDLVTSRNSQSTSIPRVLAFSPGGTLLAVARDNQAAGSITLYDVEHGE
NVGSLATPSHSAKS VVGGAHQGWILGLSFDEEGKHLASCGFDKCIRVWNLET SEREATISISISD
LDDTTHNDQDESVASGVAFIKKGVRRGSGGDSNEGLCVVSFDRGIRWYREAGGI

YGR085C_YPR102C_homolog 1418bp public: 1..1418; exon 1: 501..503,
intron 1: 504..896, exon 2: 897..1415 (SEQ ID NO 355)

ATAGAGATGCTTATTCTGGTGGTTCAGTTAATTTATATCATGTCACTGAACAAGGTTGGACTTATC
ATGGTAATTTCAATGTTGGTGATCTCTTTTGGGAAGTTAAAGAAAAGGAACAATCATTTGTAAATG
TAGATGGATAAAGTAAGTTGATTGTATAAAAAAGAATGGATTCATTAATATAAATTTACAAATCT
GATAATAAACTACAGTAACTATTATGCAACAATTGAAAGTATCCTGTGTCACGTGATTAGGGCTCA
AAAGCCCTAACAGGTTGCACGTGATGTTGATTTATTTATCCCTGCACACATTGAGTTTTTTTTCTA
TGGTGAAAATTATTAGTGAGACGATGTTGTTTCGCATTTTACCACACACTCTCACACTGAGTGTAGT
CATACTAACAATCTTCTCACACTATACACAAAAAAATCTTTTCGTTTGAAAAGTTTGAAGGTTTC
GTTTTCTCAATAGTATATCCATACAATAACTGCCAAAGATGGTATGTTCAAGTGTTTAAAGAGATC
GAAATGTTTTGTTTTAATTGGAAGTGATATCATAATGAGAAAATATGGGAAATAGAGATAGGACCG
AATTAATTGAAAGAGTTTTCTTTTGGGGAAATGGGTTCAATAAGATTTTTCAAGATTGGAATCAAA
TTATGTCAGATGTGAAGAAGAGTAAATATAACAAGAAGTTCAAATCATTAATAAATTTTATGTAAAT
ACAACGATTATCAATTACAGTCAACGAATAGAATAAAACAAAAGCCAGCATATAACAGATACCAGT
GATTCATCCCAGTGATATAAATAATGATATTCAATTAAAAACAATATTAAGACATTTTTTTATTTAT

GTATCAACAAAATACTAACTTATCTTTCTTTTAATTAGTCTGACAAATCCCAAAATGTTATGCGTG
AATTACGTATTGAAAAATTAGTTTTAAACATTTGTGTTGGTGAATCCGGTGATAGATTAACCAGAG
CCGCCAAAGTTTTAGAACAAATTATCTGGTCAAACCCAGTTCAATCTAAAGCTAGATACACTGTCA
GAACTTTCGGTATTAGAAGAAATGAAAAAATTGCCGTCCACGTTACTGTCAGAGGTCCAAAAGCTG
AAGAAATCTTGGAAGAGGTTTGAAAGTTAAAGAATATCAATTAAGATCTAAAAACTTCTCTGCTA
CCGGTAACCTTGGTTTCGGTATTGATGAACATATTGATTTAGGTATCAAATATGATCCATCTATTG
GTATTTACGGTATGGATTTCTACGTTGTTATGGGTAGAGCCGGTGCTAGAGTCACCAGAAGAAAGA
GAGCTAGATCCACTATTGGTAACCTCTCACAAAACCAACAAAGAAGATACCATCCAATGGTTCAAGA
CCAGATACGATGCTGAAGTTTTGGATAAATAA

YGR085C_YPR102C_homolog 174aa (SEQ ID NO 356)
MSDKSQNVRELRIEKLVLNICVGESGDRRLTRAQVLEQLSGQTPVQSKARYTVRTFGIRRNEKIA
VHVTVRGPKAEELERGLKVKEYQLRSKNFSATGNFGFGIDEHIDLGIKYDPSIGIYGMDFYVVMG
RAGARVTRRKRRARSTIGNSHKTNKEDTIQWFKTRYDAEVLDK

YGR118W_YPR132W_homolog 919bp PathoSeq: 1..919; CDS: 482..916 (SEQ ID NO 357)

TATTGCGTAATCGTTATCAATGTTTGGATTGTTGCAACGCTGGGTGTTGTGTGTATATGCGAGAAATG
AGTAATTGTTTAAAAATAATCGATGCAGCAGTCTGCCACTAAATAAAATGTCATATTGACAT
GATAAGGATTTATCAATACTGTTAGGTCTATAGCCCTAACTTTAATCATTACACGTGATACAAAA
AAGTTGTTTGATCCCGCACGACTATGAGTACGCACTCACTAATTATAGCCTGAAAAAAAATTTTC
CACATAGTAAGGGGATTTTGTATGGTGGTGCGCTCGCCTAAGACGTCTGCATACATTTTCTAAAGT
CACACTGATATAGGGATGTTGTGGTAGTGATTGTGTGTTCCCAACAAATAACTTTGCGGACACTCT
CATATACTCAATTTTTTTCTTACAAAAATTTTTTTTCTTCTACTTTTTTCAAGAATTCTTCTTTTA
CAATTCACAACATCAATCATGGGTAAAGGTAAACCAAGAGGGCTTAACTCTGCTAGAAAATTAAG
AGTTCACAGAAGAAACAACAGATGGGCTGATCAAGCTTATAAAGCTAGATTATTAGGTACCGCTTT
CAAATCTTCTCCATTTGGTGGTTCATCTCACGCCAAAGGTATCGTTTTTGAAAAAATTGGTATTGA
ATCTAAACAACCAAACTCTGCTATCAGAAAATGTGTCAGAGTCCAATTAATCAAAAACGGTAAGAA
AGTCACTGCTTTCGTTCCAAACGATGGTTGTTTGAAGTTGTTGACGAAAATGACGAAGTCTTGT
GGCTGGTTTCGGTAGAAGAGGTAAAGCTAAGGGGGATATTCCAGGGGTTAGATTCAAGGTTGTTAA
AGTTTCCGGTGTCTCTTTATTAGCTTTATGGAAAGAAAAGAAAGAAAAGCCAAGATCATAG

YGR118W_YPR132W_homolog 145aa (SEQ ID NO 358)
MGKKGKPRGLNSARKLRVHRRNNRWADQAYKARLLGTAFKSSPFGGSSHAKGIVLEKIGIESKQPNS
AIRKCVRVQLIKNGKKVTAFFVPNDGCLNFVDENDEVLLAGFGRRGKAKGDIPGVRFKVKVSGVSL
LALWKEKKEKPRS

YGR277C_homolog 1164bp PathoSeq: 1..724, public: 724..1164; CDS: 196..1161 (SEQ ID NO 359)

AATTCATTTGATCTCTAAGAAGATGAACAGGCCTTGAATGGGAGGGGTTGGTTCGACTTCCACGAA
ATGTGGTTGGAAAACTTGAGTCCTCAAAAAGGTTCTCTCGTAAAAGGCCAGAGAAAGAAAAACC
ACCAACCCCCACCACCAACCTAACCCTTTCTTCCATCCATTCCTCTTTCTTACTTTGCAAATG
TTGAATCCAGTTATATTCAATTAAAGATCCTATAAAATACGATTATTCACAATTTATTATATCTTTA
CTCCCGAAATTCATTAATTGTAATCGTATTGATTTAGTTATACTTTGTCAAATCACCGAATCAAAT
CAATTGAATGAAATTTTATGTTTTTATTATCAATTAATTCGTAATCATAAGAATAATGGAGATACT
GATGGAGATACCGACAGTTTGCCTATGTTTGATTATCGATTTGAAATTAATATATTATTTAATTTA
TCAACAAAAAATTGAATCAATTATGTTTAAATAATTGGAATCATGGATATATTGCGGAAGGTGAT
AATGATAACAGTACTAACTTGTCTATCTTTGCCATTGTCAATAACACAAATATCAAACATTGAAATT
CCAACAATCCAATCAAGAGCAAATAGTAGTAGTGCTTATAATGATGAGGATGATAAAATTACTACT
AGTCGGCAATATCAACAATTTAAACTACTGCTGTAGGTGGAACATTTGATCATTTACATGATGGT
CATAAAATTTTATTATCAATGGCAATTTTTTTTAACTTCAAATAAATTAATTATTGGTATAACTGGT
TCTAATTTATTAATTAATAAAAAATTTAAATCTCAATTACAACTTTTAAATCAAAGACAAAATTTA
GTTATTCAATTCATAAATTTATTATTATTGAGTGAAACCAGTGTTATTTTTTTTGAATTTTATGAA
ATTAATGATGTTTGTGGTCCAACCTGGTTATATTAATGATATTGATAATTTAATAATATCTCAAGAA
ACTAAATCTGGTGGTGAATTTGTTAACAAATTTTCGTAAAGATCATGGATTTAAATTTATTAGATATT
ACAATAATTAAAGTGATTGGTGGGAATATTGAAGAAAATTCATGGAAAGGTAAATTAAGTTCAA

CTGATATTAGAGAACAAGAATATAATCGATTATTAAATCAATAA

YGR277C_homolog 322aa (SEQ ID NO 360)

MLNPVIFIKDPIKYDYSQFIISLLPKFINCNRIDLVILCQITESNQLNEILCFYYQLIRNHKNNGD
TDGDTDSLPMFDYRFEINILFNLSTKKLNQLCLNNWNHGYIAEGDNDNSTNLSSLPLSITQISNIE
IPTIQSRANSSSAYNDEDDKITTSRQYQQFKTTAVGGTFDHLHDGHKILLSMAIFLTSNKLIIGIT
GSNLLINKKFKSQLQTFNQRONLVIQFINLLLLSETSVIFFEIEINDVCGPTGYINDIDNLIISQ
ETKSGGEFVNKFRKDHGFKLLDITIIVIGGNIEENSWKGLSSTDIREQEYNRLLNQ

YGR284C_homolog 1427bp public: 1..1427; CDS: 501..1424 (SEQ ID NO 361)

CAAGAGTAAAATCTAAATCGTTCCAATGATTTTGGACAGCTCATAGGTTAAGAGGTCTACATGTGT
TGGTGGCAGTAGTATTGGTATTAAGTGGGTGGGTGCTGGTATTAGAGAGTGGGTGTTATAAAAGAA
GGTTGTGATTTTTTTTTTCCACTGGTGGTGGTGGTGTGCTGATTGTACTGCTGTTCACTTTATTGTTT
CGTTTCGTTTTTCCCTTTGTTTTGTTGACGTTGACATTTTTTTTTGCTGTTGTTGTTGTATGGGAATT
TTTGTATTAGTTGTTCTTTTTTGTTTTTTTTTTACTTGTTCAAAGTTTCATATAATAATAATATTCT
TGTTTTTCATATTTTTTTTTTTCAGAACAAGAACAATAACAACCTTATATAATTTGATCTTACTCTTAT
CCCCAGGTTTTTCTATTTGTTTTTGGGTTTGCCATTCATATATATATATCTATTATTCAAATCAAT
TTGAGGAGTATCATTAATTTAAATTATATCAGTTAAACAATGTCGTATCGTGGTCCTAATCAATTTG
GTAATCAACCTCCACATCATGGAATACCTTCTCAACCTCAACCACATATTGGTCCAATATCTTCCA
GCAAAAGTCCTTTAGAACAATTTGAAGATGTTGCTAAAAAAGTTGAAGATTGGATCGATGATTATT
TTAAAGTCTTGAAACCATACGTCCCAGCAATTGGTAGAGCATTTTTTGGTGGCCACTTTCTATGAGG
ATACTTTAAGAATCTTCACTCAATGGAATGAACAAGTTTATTACTTGCACAACTATAGACACTATT
GGCGTTGGTTGACCGTTTTATTCTTGATCAATAATATGGTGGTTATGACAGTTGCATCCACTTTAG
TAATTGCCAGAAAAAAGAATAACATTGCTACTATTGCATTGATCGTTGTTGTTATTATACAAGGTA
TTGGGTATGGTTTATTGTTTGATGCTCAATTTGTTTTGAGAACTTGTCCTGTTGTTGGAGGGTTAG
TATTAGCATTTTCCGATAGTATTGTTAGAGATAAAAGATCCTTAAACATGCCAGGTTTACCGATGT
TGAACAATCAAGACAACAAAAAGTATTTCTTTTAGCTGGTAGAATTTTGTTAGTATTATTATTTT
TGGGATTCGTCTTTTCTTCTGATTGGTCAATTGGGTAGAGTTTTTCATTATTATAATCGGGTTAACTT
CTTGCTGCTTCAATTGTTGTTGGTTACAAGACAAAGTTTTTCAGCTGCTATCATGCTTATTGTTTTAT
TCTTATACAATGTGTTCACTAACCAATTCTGGGCTTATGCATCTCAAGATGCTAGACGTGACTTTT
TGAGATATGAATTCTTCCAAGTTTTGTCAATTGTGGGAGGATTATTGTTAGTGGTTAATGCAGGTG
CTGGTGAATTCTCCATCGATGAAAAGAAAAAGATTTATTAA

YGR284C_homolog 308aa (SEQ ID NO 362)

MSYRGPNQFGNQPPHHGIPSPQPHIGPISSSKSPLEQFEDVAKKVEDWIDDYFKVLKPYVPAIGR
AFLVATFYEDTLRIFTQWNEQVYVYLNHYRHYWRWLTVLFLINNMVMTVASTLVIARKKNNIATIA
LIVVVIQIGIGYGLLFDAQFVLRNLSVVGGLVLAFSDSIVRDKRSLNMPGLPMLNNQDNKKYFLLA
GRILLVLLFLGFVFSDSLGRVFIIIIIGLTSCASIVVGKTKFSAAIMLIVLFLYNVFTNQFWAY
ASQDARRDFLRYEFFQVLSIVGGLLLLVNAGAGEFSIDEKKKIY

YGR285C_homolog 1876bp PathoSeq: 1..1215, public: 1216..1876; CDS: 501..1781 (SEQ ID NO 363)

AATTATTAGTTGAAAAACAAATCATACCTATTGCCAGAGCTCAAATGAAAGTGAGAATTACGTTAT
CTAAAAAAGCATACTTAAAGACTTTTCAAGATGAAATAAAACCTGTTATTGATCAAATTGTGGAGG
AAGATAACAATGGGAAACAATATGAGATTGTTGGGATTATAGATCCTATAAATTATAGAGTCTTGG
TCACATTAATTGAAAATACAGATGGAAGCAACAAAGTCGCTAAAGGAGAAGGGTCTATAGAAGTAT
TAGATATGTCTGCCATAAAAGAATAAACTAACTAGACAAGTGTATAGAATCTTTTTTATTAAATA
GATGCTTATCTTAGTTATGTTCCAGAACAATTCATGTTAGGAGAGAGAGAAACGCAATCACTCAAT
TTTTGCACAAACAAAAACGAGAAGATGAAGAAGCAAAAAAGAAAATTTTTTTTTCTCAACCATCT
TAAATCCTCCTACAATTAATTTCAATACCAATAAAGAACATGCTATTGTATTACCATCAGGAACCTA
CTGACGGATTAAAGCCGTCTCCAATACTCTGCCCCAGTGCCTCGTCCAATTGAACCAGTTGGTC
GTTACTTCTTAGCCACGCCTCAAGAATTTGCGTGGACACACTTGGTCTGAATTTGAAAAATTGG
AAGCTGAAAAGAATGTTAAACAAATCGAAGTCAACGAAGATGAGGATTTGGGAGATGAAGAACA
GTGAAGAGTTATTAGAACACGATCCAAGAGAATGGAAGACTGCCAATTTATATGCTGTTTTAGGTT
TATCTCATTTGAGAAGTAAAGCCACTGAAGATCAAATCAGAAGAGCCACAGAAAACAAGTTTGA

AACATCATCCAGATAAAAAATCCGCTAGTGGTGGATTAGAAAACGATGGATTTTTTCAAATTATTC
AAAAAGCCTTTGAAGTTATGTTGGACCCAGTCAAGAGAAGACAATACGATTCTATTGATGTTGAAA
ATGATCCAAAACCACCAGCTCCAAAATCCAAATACGATTTCTTTGAAGCTTGGGGTCCAGTATTTG
AAAGTGAAGCAAGATTTTCTACTAAACAACCAGTTCCATTGTTGGGAAATTTAGAAAGCACCAAAG
AAGAAGTTGATGCTTTCTACAGTTTCTGGGGAAGATTTGACTCTTGAAGACTTTTGAATTCAAAG
ATGAAGATGTTCCAGATGACACTGCCAACAGAGATCACAAACGTTATATTGAACGTAAGAATATTG
CCCAACAGAAAGAAATTGAAGCAAGAAGATCACAAGAGATTATCGAATTGGTCGAAAGAGCTCATG
CTGAAGATCCAAGAATTAAATTGTTCAAAGAAAAAGCCAAGAAAGAAAAGGCTGCTAAGAAATGGG
AAAAAGAATCTGGATCAAGAAAAGCTGCTGAAGAGGCTGCTGCCAAAAGGCTGCTGAAGAGGCCG
CTGCTAAGAAAGCCGCCGAAGAAGCCGCCGCTTTGAAAGCCAACTCTAAAAAGCTAAAGAAGCTG
CTAAAGCTGCTAAAAAGAAAAACAAGAGAAACATCAGAGCTGCTGTTAAAGACAATAATTACTTTG
GTGACTCAGCTAAATCTGCCGACATTGATGCTGATGTCGATTTGTTAATCGAAAAATTCGACGATG
TCAAATTAGGTGAAGTTGCTGATAAAGTTAAAGATGCTGATGCTGCTTCAGTGAAATCTACTTTTG
TTGAAGTTGCAAAGGAATTGGTTGGAGCTGGTTCTTTAGATGCTTCTTATTTGAAATATTTTAACT
AGATTTTTTTTTTTGTAGGAAAATAATATATATAGAATGTAACTATCAAAAACAATTATACAGAAG
CTGAACCTCAAACAAGACTAAACAGCAAG

YGR285C_homolog 427aa (SEQ ID NO 364)

MSIVLPSGTTDGFKAIVSKYSAPVRRPIEPVGRYFLAHASRTLRGHTWSEFEKLEAEKNVKQIEVNE
DEDLGDEEQSEELLEHDPREWKTANLYAVLGLSHLRSKATEDQIRRAHRKQVLKHHDPKKSASGGL
ENDGFFKIIQKA FEVMLDPVKRRQYDSIDVENDPKPPAPKSKYDFFEAWGPVFESEARFSTKQVPV
LLGNLESTKEEVDAFYSFWRFD SWKTFEFKDEDVPDDTANRDHKRYIERKNIAQQKEIEARRSQE
I IELVERAHAEDPRIKLFKEKAKKEKA AKKWEKESGSRKAAEEAAKKAEEAAAKKAEEAAALK
ANSKKAKEA AKA AKKKNKR NIRA AVKDN NYFGDS AKSADIDADVDLLIEKFDDVKLG EVADKVKDA
DAASVKSTFVEVAKELVGAGSLDASYLK YFN

YHR021C_homolog 1178bp public: 1..537/917..1178, PathoSeq:
538..916; exon 1: 501..503, intron 1: 504..932, exon 2: 933..1175
(SEQ ID NO 365)

TTTCATTTGTAGGCATTGTGTAGAATGTGGACTGTAGGAAGGTGCAAAATATATATCCAATAAGTC
ACATCTCAAATTGGTAGTAGAAGAATTCAACCTTGGGACAGTATTCTCTGCTTAAAATGAGTTTAC
TGATCAAATAAAATATTGGCTCAACCATTGAAAAGCTATTCTTGACACTTTTTTGCAGTTT TAGTTT
TGGTTGTTT CACAATTGAAAAA A AATGTTGAGCCCTAATAGCCCTAATTGTTTGCACGTGATGT
ATTGCTTTGAGTGAAAAGTG TACATTTGTACACACACACAAAAA A AACTA ACTTCTTCCCCCA
ATATGCTGCGTATAGTGAGAAATCTTCTTCTCTCTTGCCATACTATCGCATTTTTTTTTTTTGGTAA
CTCACGAAACCTAATTGGAAGAAGAAAAGAGAAAAA A A AATTTTCAGTTTTC AATAGATTTT
AGTTTTTTGAATTATACATATTAGAGAAACAAGTTAACAATGGTATGTTTATTAGATTTACCATGAG
TTATGGAGGGATATTCCTGGATGATCAGAATATCATAATATAGGAGTATACTATTTTACTGGAATC
AAGATATAATTGAATTGAAATAAAAATTGAATAAGAGGAAGCATAGAATACGGAATGATGATTAAC
AAATCAGAAAACATTGTACTACCGAATAATGAATTAGGATCAACATATTAATATCAACTACTACTT
TAAAAGAACAGGAAAATGAGAAGAGAATCAGCATGAAAGTTACCACCTCAGAAAACGTCAAAGAAA
TATACTTTTGGTGTGGATCCATGTGTTATTACTGAAATCATCGAAACGAATATAACCCTCCTTTTC
CCACATTGACATAACTCAGACACAATCTTTCAAATAAAACATGTAATACTA ACTATTATTTTTTTT
TCGTATAGGTTTTAGTTCAAGATTTATTACATCCATCTCCAGCCACTGAAGCTAAACAACACAAAT
TGAAAACTTTAGTTCAACAACCAAGATCTTTCTTTATGGACGTTAAATGTCAAGGATGTCTTAATA
TCACCACTGTTTTTCAGTCACGCTCAAACCTGCTGTCACCTTGTGACTCTTGTCTACTGTTTTGTGTA
CCCCAACTGGTGGTAAAGCTAAATTGACTGAAGGTTGTTTATT CAGAAGAAAGTAA

YHR021C_homolog 82aa (SEQ ID NO 366)

MVLVQDLLHPSPA TEAKQHKLKTLVQQPRSFFMDVKCQGCLNITTVF SHAQTAVTCDSCSTVLCTP
TGGKAKLTEGCSFRRK

YHR141C_YNL162W_homolog 1179bp PathoSeq: 1..1179; exon 1:
501..503, intron 1: 504..861, exon 2: 862..1176 (SEQ ID NO 367)
TTTATATTGTTTTTTGTTTCTATGTATAGTAATTATTTAATTTGATGTTCCATTATTCATGTAATT
GTGATGTATTTTTTTTGTGTTGGTCTTCTTTGTGTTTTGATATTTTGCAGCTGGTCGGATCATACAA
ATTTGGAAGGAGCTACCAAAGCAGAAATGATAGCAAAAAAACAGGAGACTTTTGGAAATTTCTTG
GTTTAGGGCTCTAGCCCTAATGCCTGTATATAATTGATTGATGCTTTAAAATTTGTGCGGTGAAAA
ACAGAAGCGAAAAAAAAGAGCTGGAAAGTGTGATTAACAACAACGAGGGAAGAAAAAACTTAA
TTAGGTGAACAAAAATTAATGTGTGAGCGTGTACATGCACAATTTTCAATTGGTTATTTCTCACGCA
CTAACAACTCAACCTCCATTGTGAGAAAAGAGATTTTCTTTGAAAAAAATTTACATACATATC
TTAGTTCACTAGTAATTTTCAAGACAACATAGACAAGATGGGTATGTTCCAGTATAGCAATATTC
AACAATGAGATACAAGATATTCCTCCAATACAAAGAGATTAATGGTGTTTTTGATAGAGTGTAAG
CCATGTGTTTAATAAGAATGATTTGTCAAGGGATAAGATGAAAAGTGGAAATTTGTCCAAACAACAT
TGAAACGAATTTTCTGGGATAGCGTTCAAACAATCAAACCTATCCAGGTTTCTTATGACAATTAAG
AAAACAAGTCAATATTATCAAAGATGGAGTTTATAAGGAGAGATATTGAAACATCAAATTTGTTGA
AAGAAATAGCCAACTATTTGGCACCATTTCTGTGATCATAGAAATACTAACAATCCTCTTGTGTT
ATAGTTAACGTTCCAAAACTAGAAAGACCTACTGTAAAGGTAAAGAATGCCGTAAACATACCCAA
CACAAAGTTACCCAATACAAAGCTGGTAAAGCTTCTTTGTTTCGCTCAAGGTAAAAGAAGATATGAC
AGAAAACAATCCGGTTATGGTGGTCAAACCAACAAATTTTCCACAAGAAAGCCAAGACTACCAAA
AAAGTTGTTTTGAGATTGGAATGTGTTGTCTGTAAAACCAAGGCTCAATTACCATTGAAAAGATGT
AAACATTTCAATTGGGTGGTGACAAAAAACAAAAGGTCAAGCTTTACAATTTTAA

YHR141C_YNL162W_homolog 106aa (SEQ ID NO 368)
MVNVPKTRKTYCKGKECRKHTQHKVTQYKAGKASLFAQGKRRYDRKQSGYGGQTKQIFHKKAKTTK
KVVLRLECVVCKTKAQLPLKRCXHFELGGDKKQKGQALQF

YIL112W_homolog 3583bp PathoSeq: 1..3583; CDS: 365..3580 (SEQ ID
NO 369)
GTGCGAATAATACAAGCGATCGTTTGAATAATCCAATGATTAGCTCTGATCAACGAATTCAAATTT
TTCCCTCAAGGACGTAGTACAACAAGAGATGAGAAGGGGTTTGAAGTGTTCAGAGGAGA
TGACGGTGCAAAAAGATCTACCACCAAGAAGCACATAATTTTTTTGAATGATTCACGAAAGAGTTC
CATTAGTGATATCTCAAGCCAAAAATTTTCAAGGGAAAGTTCCCGTAATGTTTCACGGGAAAGCAG
CAGGCGAAGTTCAATAATAAAAATTTGATCATCTACTAATGTGGACGTGTCAACGAAACCGGAAAA
TATAAATAGCAGAGATAACAAAACCTGAGAAGAATATGACTTTGAGTTCAGAGTCAACCAACCGAG
TGTCGAAGAAGTTAGTAAATCTTTGAAACCAACAATTACCAAGAAAACCTTCATTCATGATTACTT
AAAATCTGCCAAAACCTAAGGCTAAAGAAGAAAAGGTAAACAATCGAAAAAGTGACAAAACGATTAA
TTCAGAAGAACGAAAAACGGAACCAATTCAACAAAGCGAGCAACTTTTAACGGACAAAAGGATAA
TAACTGGAACCAATAGTGAAGTAAATTTGAAAGACAATAATGACGACCTGAAAGCTACAGCTGG
CTGTGCCCTAGGACCTGATAAGAATACTGGAAAAACGATTTCAGATAAATCAGAAACGACTCAACC
AAAACCTTGCCCGCTCAGAATCATTGCGGATACATCATTATTGTCTCCAGTTAATGAAAGTGATAC
TGATTTCAATTTCAATGAGTTAGCAGAGATACCGGAAGCAAAGGATGGTTTCAGTTGTGGCAGCAA
TGTGCTGGAGAACATTGATGAGAATGAAAATATTTTCAAGCTGAAACTGTTATAGCAGATGACCT
TCCACGTCTCGATGAAGGAAAGAACTTTTACGTGAACAAACAGCAGATGTAAAGAGACATAAAT
GAAGAAAACAAAATTTGAATACTATTTTTTAGTTCCGATGAAGAGGAGGAGGAGATTCAAGAACCAGA
TTTCAAACCTCAAGAACCAGAAAACTACCAGAAGATGACCAACATCCTGATTTTCAAATTTCAA
AGCAACAACAGAAATCAGTAACGATAAAACAGAAGTAAATAAGCCAGAAGTGAAAGAGGTTGGCGA
GAAAGAGAGAAATCACCAACTAGAAGATAGATTACCAATTAAGAAAGAGAAATGCGGTGCGGAGAA
TGCAAAGACATCTGAAAACGGTGTGAGTTCAAATCAGAATCTAAGATTTCAAAGTCAAGAAACT
ACCTTACAAAGTTAAACGTGATTCAAGTGGTCGATCATTATTACAACGAGCTTGCAAGAAGGGTAA
TTTTGCAGATGTCCAAGATTACATAGAGAGGGGTGCTAGTGCCAATGAAAAGGATTTCTGTGGATT
CACATGCTTGATGAGGCAGCATTGGAAGGTCATACACAAATTTGTGAAATATCTCATCGAAAATGG
TGCTAATGTAAATGCGAAAGCTGATGAAGCTGGTGAATTCGAGACACCATTTGATCGATGCAGCTGA
AAACAAACATCTTGATTGTGTTAAAGTGTACTAGAAAATGATGCTGATCCTACTATTTTCAATAT
TGATGGATTACCGCTTTAACTAAGATTTATAATGAACATGAAGGAGAAGAAGGATATGATGAAAT
TATTCAAGTTCTAGAAGAAGCAACTGCAAACTATAACAGTCGTTTACCAAGAGAAGTTTCAGTTTGT

ATCAGATGCTCCTATTGGTAGTGGACCAATCATGGAGGATCCAAATGACAACTATTTTGCAGAGCT
AATTAAAGGTAAGGGAATATATAAATACGCTGCAGAGAATTCAAAAGAGAAAACAGCAGAATATTT
TGTTGCTGGTCATAATTTAGAAGGAAAACAGATATTTTAATTTTAGCTGCTAGAAACGGCCACAC
AGAACTTGTTGATATTATACTAGGGCTAAACCCTACACCTTTTAATATTGATACCGAGTCAAGTTG
TGGTGTTACTGCATTATTGGCCAGTATTGGACGCGGTCATTTTGAAGTTGTCGATTCTTTGTTGTC
CAAAGGTGCTGATCCATTCAAGACAAGAAAAAAGATGGGTTGAATGCTTTAGAAATTGCACAACA
CTCGCCACATTTTGATTACAGGGAAGTTAGTGTAAATAATGAAATTCATGGAGAAGAAGAGTGGAAC
CAAAATTTTGTCTGGTATTCCGTCAAGGGTAGTATCTCGTGCAACATCTCGTGACCTTCTGTTCC
CGTATCATCAGACGAAGATGACGTAGTGAAGAAAAAGAAATTACAGCACACACAGAAAATAAAAG
TGCTGAAAAGAAGCTGGAGGATAAAATCACGAAAACAGTTAATGAGCATGTCAGCAATCGGAAACC
CCACGAGTCTACAGGTCGAAAACCTGAAAAGACTCATAGCAATGAGGAAAGAAAGCGGAAACGTGA
ATGGTCAGACGATGAACCTAAAGAACCACATCTTTTGAAGAAGTCAAAGTCTGATTTGAAATTGAA
ATCACTACATAGAGAATTCATTCTGATGATCACCACACCAGTGAAAGCCATTGAGATTCTTTTGC
AGAAAAAAGAAAACATTTATCGGCAACGCCACCTGCTCCTCCGCCACCACCACCACCACCTTC
TCAAGCAGTTATCAAGGCACAAGAAGACAAAAAATCAAAGATGCTGAAGAAGCTAGATTGTGGCA
AGAAAAGGTGCAAGCTAAAAAGAGGGCTCGAAGAGAAATGTTTAAAGTCCGAGAAAGAGAAAGA
GCAGAAACGGAAAGAAGAAGAATTCGAGACACAAGAAGAAAAACGAATTGCCAAAGCAAAACA
GGAAGAACAGGAGAGACTTGCTAGAGAAGCAGAAGAGAAATCGAAAGAACTAGAAGAAAAGAAAGT
GGGGTTGCGACAACAGTTGACATTAGATCATTATCCGGTTGGATTGCGTTATTGCAAGTTTGATGG
AAACCCAAATATCTCGGCTGTTGATAAATTTTGCCTTTCTATGTATTGTAAATCGACGATAAAAA
GTATGCTGTTGATTTGCAAGTCTCCTTGATCACGTCAACGGTTGTCAGCAAGGTTATCAATACTGT
ACAACCTCATCAGAAGAGAGAAATAAATGCAACTGAAAAAGCAAATTGTGGAAGCTCTTTTCAA
GTTTATTGGTATTGATCCTAGGAATCCAAATTGTGATCAAAGAAGCTCAATAACAAATGGTCAAAA
ACAGTTTCAAATTTGTTGCTTCATTTTGTGGAGGTAGATTTAGCTGAAGAATTTTAAAGGAATT
TCCAGAAGTACACTCAAAGCAAAAGATAACCAATTGATGTTAGTTTAGAGTCTTTGAGTGGGTT
TTCTGATTGCGTCAAGGATGATATAATAGTTGATGGAAATCTTGAAATTGATATTGATTCCAAGAA
AATCGAAAAGTTTATTCCTCCTCATTGTAATACTAGGAAAGACATTATTAGGACTGTCAGTACTTT
AGCACACCCACTATGGTGA

YIL112W_homolog 1072aa (SEQ ID NO 370)

MTLSSESTKPSVEEVSKSLKPTITKKTSTFDYLKSAKTKAKEEKVTIEKSDKTINSEERKTEPIQQ
SEQLLTDKKDNKSEPNSEVNLKDNNDSDKATAGCALGPDKNKGKNDSDKSETTQPKLARSESFADT
SLLSPVNESDITDFNFNELAEIPEAKDGSVVAANVSENIDENENISEAETVIADDLRLDEGKLLR
EQTADVVRHKLKTKLNTIFSSDEEEEEIEPDKLQEPKLPEDDQHPDFQNSKATTEISNDKTE
VNKPEVKEVGEKERNHQLEDRLPIKKEKMRSENAKTSSENGVSSKSESKISKSKKLPYKVKRDSSGR
SLLQRACKKGNFADVQDYIERGASANEDFCGFTCLHEAALEGHTQIVKYLIENGANVNAKADEAG
DSETPLIDAAENKHLDCVKVLENDADPTIFNIDGFTALTKEYNEHEGEEGYDEIIQVLEEATANY
NSRLPREVQFVSDAPIGSGPIMEDPNDNYFAELIKGKGIYKYAAENSKEKTAEYFVAGHNLEGKPD
ILILAARNGHTELVDIILGLNPTPFNIDTESSCGVTALLASIGRGHFEVDSLLSKGADPFKTRKK
DGLNALEIAQHSFPHDSREVSVMKFMKKSGTKILSGIPSRVVSRASTRAPSVPVSSDEDDVVEE
KEITAHTENKSAEKKSEDKITKTVNEHVSNRKPHESTGRKLEKTHSNEERKRKREWSDDPEKPHL
LKKSksDLKLKSLHREFTSDDHHTSESHSDSFAEKRKHLSATPPAPPPPPPPPPPSQAVIKAQEEQK
IKDAEEARLWQEKVEAKKRARREMFLLKSEKEKEQKRKEEEELRAQEEKRIAKAKQEEQERLAREAE
EKSKELEEKVGLRQQLTLDHYPVGLRYCKFDGNPNISAVDKFLPFYVVIDDKKYAVDLQVSLIT
STVVSQVINTVQPHQKREINATEKSKLWKLFFKFIGIDPRNPNCQDRSSITNGQKQFQNLHLHFE
VDLAEEFLKEFPEVHSAKDNQIDVSLESLSGSFSDCVKDDIIVDGNLEIDIDSKKIEKFIPPHLNT
RKDIIRTVSTLAHPLW

YIL148W_YKR094C_homolog 659bp PathoSeq: 1..659; CDS: 501..656 (SEQ ID NO 371)

TAGTTTCTTTTGGCGGTATATCCTCACTCATGATTGATGTATTTGCCCACTAAAAAGAAAACCAAT
GAAACAATAAGATTGATTGATAGATTTGGTTGTAATTAATCTGATGCTTTCAACATTTGTTTTTGT
TCGTGTCTCGGTCATTGAGGTTGGGTAAATTGTTTTTCTTTTGAGAATTGTGAGCATGCAATGTCTG
CATGCAAATATGATGTCGCTCAATTGCGACATACTACTAGGGCTATAGACCTATTGCACGTGCGT

TAGTTTTAAACCTAAAAACAATTTTGTGCAGTCGTGCACCATTCTGTTCTATTTTCTACTGTGA
TTGACGTACAAACCTTCACAGTTCACGCACACTTTTGTTCGATTCTCAAACCTCTCTCACAGGCTTG
GTAGGAATGAAAAAATTTTGGTAAAGGCGAAAAAATAAACTTGAATATTTTGGAAATC
CCCTTTTGTATTACTACAATAGATTAAAGTAACTAAAGATGATTGAACCATCCTTGAAAGCTTTAG
CTTCAAATACAACCTGTGAAAAATCCATTTGTTCGTAAATGTTACGCTAGATTGCCACCAAGAGCCA
CCAACCTGTCGTAAGAGAAAGTGTGGTCACACCAATCAATTGAGACCAAGAAGAAATTGAAGTAG

YIL148W_YKR094C_homolog 52aa (SEQ ID NO 372)
MIEPSLKALASKYNCEKSICRKCYARLP PRATNCRKRKCGHTNQLRPKKKLK

YIL150C_homolog 2297bp PathoSeq: 1..1162, public: 1163..2297; CDS:
501..2294 (SEQ ID NO 373)

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CTAACTCCATATTGTTGTTCTTACCTCTTTCGATAGAGACTTTGATCGTGACATTTTGTAAGTGG
TAGAGGTATGGGTAAGATTATTTTCACCACCGTTTTCCTTTAGCAAATAGTCTAAAGCATTTTCTG
AATTGTTGAGTTTCGGTACATCATTAGCTATCTTTTGTACAATTGATTGCTTCTACCTCTAGTCA
TGGAATAACAAGTTAACAGCGTGTGTTGTTGGTTTGTGGAACAAATAAATTTGTGGTGTGTAAT
GTGTGTGTTTGTGTTTTTTTTTTTACCAGCATTTTGTCTTGTCTAAAAATGAAACAGCGCAATGAT
TCTTTTCATAGTTTTTTTTTTTCCATACATAACTTCTGACGCGTGCCTATATCTGCTAACATACTC
GGCAACAACAAGAAAGAGAATTTGAACTAATCCGAAGATGAACGACCCAGAGATGAACAAATTG
ACTCCGATGATGTATTAACAGAAGATTCATCTGATGAATTGAAGGACTTGGTGCAGGAGTTTGAAT
TGAAATATGCAGAATTAAAGAAGAACAAAGCCTTGAAAAACGTCGTTTACAGTCACCACTGGAAG
ACATGCTGAATAAACAGAAACCCCATCAACCGGAGGTCCCCAGAACCCAGAAAAAGCTAAAGTCC
ATTTGGATAAGGTAGTAGAAGAACCAGAAAGAAATTTTACCAAGAAGGAGCCTCGGGATTCCA
AGATAAAAGAATCAAACCTTCTTAAACAACCTCTACGAGACAAGTAATAAGCATGATAAAGAAGATG
CCCATAAATAGATTTTCAGTAAAAGAAGGTTTGTGTTTCAATTGGATAAGTATACTTTTACGCCAA
AAGACGTTGTTGATGATTTAGAACCGATATCCAAGCTTTACTTGCAGCAGAAGATACCTTGCCCAAC
TGCAAATTGCCGACATTATTGCCGAACTGATAGCAACATGAAATTCCTTAAATTTGACAAGTTTT
TAGCGAAAACCCATAAATCAAACAACCTATGCTGAACCCAGTATTGTAATTGGTGTCTTGTGCTT
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GAAATTTTATGAATTCTGTAGACTTGATGCTTTTGTGATAAGGCTTTTCAGAAAAACGGGAAAATCC
AACCGGGTGATTTATTATTTCATTTTGAATCCATTGATCAACAAGTATGAAATACAAGTTGGCAAGG
GCCAGTTTCAGTCTGGGTTCAATTTGAAAGTAGAAAACACCAATGTGTCAAGTATTTTAGAGATAG
GATCGTTAAGAGATTTTGGGTTTTCGAAAGTTACTAGAAAGCTAGATAATAGCAGATGCAAAAGGG
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GAATGGAATTAAATGGAAGTGTTCGATTAGATCCCCGCAAAAAACAAGAAAAAGATGTACATGA
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GTTCTCCTCTTGATCCAAAAAGGTACCAAGACCCGAAAGTACTCCAGAACCAATCAAGCGGCGCA
AACTAATAGACGACAAGGCAAAGGAGATGCTTGAACAAAAGCTATCGAAACTAGGTTTCGGCTTCAT
TATTGAACAATTTACAATTATCTAAGAAAGAAGCAACAGATAAACTTGCGAGTGATCGTCTGAAGA
GCAAAGGATTCACCAACACAATGATTTACATATTTGGGTTTGTATCCAACAGGTACATCTTTGAACC
AAAATAGTACCCTGCTTGGCAGCAAGCTGATGGAAAAATCTCGAGCACGGGAATTGCATGATTTGA
GTGTTGAAACATCTGGTCATAAGTCGTTGTCTTCGTCTAAACAAGATCGCCAGTCGAAAGTTGCAA
AATGGAACACGAATATCAGAACTTTACAAAATTACGATCGACGAGTTGCCAGCCACTCCTTGAGTA
CCTCTCGTCCGTTACAGAATCTTGTAGGAAAGCAAACACACGCTACACTAGTAGATAAAAGGAAAA
GAGTGGTTGTCTCAGATGATGAACAACCGGGGATGGAAGAAGATGAAGAAGACATTGAAATCCAGT
TTGACGACGAAAAGTCTAAGATGTCTTACATGAAAATGACTGGAGCCAGGTAA

YIL150C_homolog 598aa (SEQ ID NO 374)
MNDPRDEQIDSDDVLTEDSSDELKDLVQEFELKYAELKKNKALKKKRRSQSPSEDMSNKQKPHQPEV
PRTPEKAKVHLDKVVEEPKQRIFTKKEPRDSKIKESNFLNKLKLYETSNKHDKEDAHKIDFSKRRFEF
QLDKYTFTPKDVVDDLEPISKLYLRRRYLAQSQIADIIAETDSNMKFLKIDKFLAKTHKSNNYAEP
KYCNWCLVAFVVRKDPVQVAANNSKYIKLVGNFMNSVDLMLFDKAFQKNGKIQPGDLLFILNPLI
NKYEIQVGKGQFQSGFNLKVENTNVSSILEIGSLRDFGFCFKFTRKLDNSRCKRAINTRTQEFCDIH

LDMKFKSSTRMELNGSVSIRSPQKNKKKMYMNKNGSGFIKQYNEESTVIGTSYGSPLDPKRYQDPK
VLQNQIKRRKLIDDKAKEMLEQKLSKLGSAASLLNNLQLSKKEATDKLASDRSKSKGFTNTMISHIG
FDPTGTSLNQNSTSLGSKSMEKSRARELHDL SVETSGHKSLSSSKQDRQSKVAKWNTNIRTLQNYD
RRVASHSLSTSRRLQNLVGKQTHATLVDKRKR VVSDDEQPGMEEDEEDIEIQFDDEKSKMSYMKM
TGAR

YIL167W_YIL168W_homolog 1499bp public: 1..1499; CDS: 501..1496
(SEQ ID NO 375)

TTTCTTCATCAACTTGCTCAAATGTCTTTGAAAGTGAAAGCTTACTTTTTTGGTTTCGTTTAGGTG
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TATAACAGAACTACCAAAAGTGAGCCCATCTGTAACTCTGAAAAGCAAAATTGAGAAAACCAT
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AATATAACAAAATGTTTCAATGTAACTGATGGTTAAGGGATTATAAATCAAACGAGTAGTGCTT
TTGTTCTTAAAAAACCATCGTGGTGGTAACGTCAGGAGACCGCGACATCAAATGGAATTCACACA
ATCAGTCTCCGAATTTATTACCTTGAACCTTAACCTTAATGAAAGAGCCTTCCATCACTACTACCT
TTGTTGAGGTTACAGACAACTTCTTACAAAGCCTCCGTGCAGGGTGTTTTTCAAGAATGAGTATG
AGCAGCCCTCCGGCAGTGTCAAATTAAGAGGCATGGGACACTTGGTTGGCCAGTCTATAGATGTGG
CCAGAAAACCTTGGCAAATCGAACGTAGCAGTTTTTTCGTCATCTGGTGGTAATGCAGGATTAGCAG
CTGCTTATGCCAGCCAGTTTTTTGGAGTATCGTGCACGTGGTGTGCTGAAAGTTCGAAGCCAA
CTGTTATAGAAAAGTTGAAATCCTTGGGTGCAGATGTCATTATTCATGGGAAACATTGGGGAGAGG
CCGATAACTATTTAACTGATTTTTGTTATTAAAAATCTTGACAAAACAGTCTATCCGGTCTATTGTC
ACCTTTTTGATGACCCATTGTTGTGGGAGGGTCATAGTAAGATCATCACGGAAATCATCGATCAAA
AGCAATTACCCAACCTTTGATAAAGTTAAGGGGGTCATTTGTTCCGTAGGAGGGGGTGGCTTATACA
ACGGAATAGTTGAAGGTTTGAAAATCATAAGGAGATACCAGTGTGGCAATTGAACTAAACAAG
CGGCCACGTTTCACGAGGCGGTCAAAGAAGGTAAAGTTGTTTACAAAAAGTGCAAACCTTTGG
CCACTTCTTTGGCTTCGCCGTACCTTTCTTCCAAGGCATTAGCAAACCTATATTGAGCGTCTACAG
TTCTTGCTGAAATTGATGACTTGGACGCTGTTAAAGGTGTTGTTGATGTATACGACCATTTCCGAT
ATATGGTTGAGCCTGCATGTGGTGCATCCGTTGCATCAGTGATGCACAGGCAAGATTTATTGAATA
AATTTGGTACATTAAGTCCAGATGATATTATCATTGTTGTCATATGTGGTGGATCGGCTATCAACA
AGTATATTATAGACGAATATAGAAGTTTATTAGAAAAAGACTCTTGA

YIL167W_YIL168W_homolog 332aa (SEQ ID NO 376)

MKEPSITTTFVEVTDKLPKPPCRVFFKNEYEQPSGSVKLRGMGHLVGQSIDVARKLGKSNVAVFS
SSGGNAGLAAAYASQFFGVSVTVLPESKPTVIEKLKSLGADVIIHGKHGGEADNYLTDFVIKNL
DKTVYPVYCHPFDDPLLWEGHSKIITEIIDQKQLPNFDKVKGVICSVGGGGLYNGIVEGLENHKEI
PVLAIETKQAATFHEAVKEGKVHLQKVQTLATSLASPYLSSKALANYIERPTVLAIEDDLDAVKG
VVDVYDHFHYMVEPACGASVASVMHRQDLLNKFGTLPDDIIIVVICGGSAINKYIIDEYRSLLEK
DS

YJL034W_homolog 2564bp PathoSeq: 1..806/1401/2504, public:

807..1400/1402..2503/2505..2564; CDS: 501..2561 (SEQ ID NO 377)

TTTTTGAAAACAGAGAATGAATGAACAATTGATGACCATAGAAATGAAGTGAGAACACATAAATCT
GCGACACTTCACGTGATAACAACAAAGTGACATGAACAACAAATGTCGTTTGTATAATTTGCGACA
TTTGTTGTTCAAGCCAAAAAAGAAAGACAGAAACAGAAAAAAGAAAAATCTCAAAGTTGCCACGT
AAGCACAATTAATCTTTTTATGGTTGTAACCTTTCTAGTATATTCTACGTAATAGGTGAGGTCCT
ATATGCAGTACACACAGGTTTTTTTTCACAGATGTTGACACAGTGTGAAAATTATTCACGTTGATT
TATAAATATACAACCTTACCTTCCACGGTTTTTTTTTTGATTTTTTGATTTTTTGAATTCTTCTTCT
TTTTTTTGTCAATTTATTTATTTAAACATTCTCTTGTAACTTTTATTTGATAAATTTTACAAGATT
TAATTAGATCAATTAGATTATAGAATCATTTCAATATAATGAGATCATCACAATCTTCTTGGTTAC
CACGTATTGGTTTATTATATGTGGCGTTAGTTATACTTATACCATTTTTTGGTTTCACCGAAGCAG
CATTTGCGGTTGCTGCAGTGAGCGATGATGAATCCTCGACAGATAATTATGGTACAGTCATTGGTA
TAGATTTGGGTACCACTTATTCCTGTGTTGGTGTATGAAAACGGTAAGGTTGAAATTTTGGCCA
ACGATCAAGGTAATAGAATCACTCCATCATACGTGTCGTTCAATGGCGATGAAAGATTGGTTGGAG

ACGCTGCCAAGAATCAAGCTTCCTCTAATGTCAACAACACTGTTTTTCGATATTAAAAGATTGATTG
GTTTGAAATATAATGATGACACTGTGCAAAAGGAACCTAAACATTTGCCTTACAAAATTGAAAATA
AGGGTAACAAACCAGTTGTTAAAGTTGAATACCAAGGTGAAGAAAAAACTTTCTCCCCTGAAGAAA
TTTCATCTATGGTTTTTGGGTAAAATGAAGAGTATTGCTGAAGATTACCTTGGCAAAAAGTTACTC
ATGCCGTTGTCACTGTTCCAGCTTATTTCAACGATGCTCAAAGACAAGCTACTAAAGATGCCGGTA
CTATTGCTGGTTTGAACGTTTTTGAGAATTGTCAATGAACCTACTGCTGCCGCTATTGCCTATGGAT
TAGACAAAGGCGACCAAGAAAAACAAATTATTGTTTACGATTTGGGTGGTGGTACTTTTGATGTTT
CTTTATTGTCCATTGAAGGTGGTGGTTTTTCGAAGTCTTGGCTACTGCTGGTGATACTCACTTGGGTG
GTGAAGATTTTGATTTCAAGATTGTCAGATACTTGGCCAAACAATTCAAGAAGAAGCACAATATTG
ATATCACTGCCAATTCTAAAGCCATTTCCAAATTGAAGAGAGAAGCCGAAAAGGCCAAGAGAAGCTT
TATCTTCTCAAATGAGTACTAGAGTTGAAATCGACTCCTTTGTTGATGGTATTGACTTTTCTGAAA
CTCTTTCAAGAGCCAAGTTTGAAGAATTGAACATTGCTGCTTTTCAGAAAGACTTTGAAACCAGTTG
AACAAGTGTGAAGGATGGTGGTGTCAAGAAATCCGATATTGATGATATTGTTTTGGTTGGTGGTT
CCACCAGAATTCCAAAAGTTCAAGAATTATTGGAAGGATTCTTTGATGGTAAAAAGGCTTCTAAAG
GTATTAACCCAGATGAAGCTGTTGCTTATGGTGCCGCTGTTCAAGCAGGTGTTTTGAGTGGTGAAG
AAGGTGTTGATGACATTGTTTTGTTGGATGTTAACCCATTGACTTTAGGTATTGAAACTTCTGGTG
GGGTTATGACCACTTTGATCAAGAGAAACACTGCCATCCCAACCAAGAAATCTCAAATCTTCTCAA
CTGCTGCTGATAACCAACCAACTGTTTTGATCCAAGTCTATGAAGGTGAAAGAACCATGGCTAAAG
ACAACAACAGATTGGGCAAATTCGAATTGACTGGTATTCCACCAGCTCCAAGAGGTGTCCACAAA
TTGAAGTCACTTTCTCATTTGGATGCCAATGGTATCTTGAAAGTTGAAGCTGCTGATAAGGGAAGTG
GTAAATCTGAATCCATTACTATCACCACGAAAAGGGTAGATTATCCAAGGATGAAATTGATAGAA
TGGTTGAAGAAGCTGAAAAATACGCTCAACAAGATCAAGAATTGAAAGAAAAGATTGAAGCTAGAA
ACTCATTAGAAAACATATGCTCATGTCTTGAGAGGTCAATTGAGTGATACTTCTGAAACCGGTTTAG
GTTCTAAATTGGATGACGATGACAAGGAACTTTGGATGACGCTATCAAGGAACTTTAGAATTTA
TTGAAGATAACTTTGATACTGCTACTGCTGAAGAATTTGAAGAACAAAAACAAAATTAATTGACG
TTGCTAACCCAATCACAGCAAAATTATACGGTGGAGCTGCTGGTGAAGGTGCTGGTGGCGCTGGGG
ATGCCAATTCGGTGATGATGATTGATGATGAATTCGATCACGATGAATTGTAG

YJL034W_homolog 687aa (SEQ ID NO 378)

MRSSQSSWLPRIGLLYVALVILIPFLVSPKHAFVAVAVSDDDESSTDNYGTVIGIDLGTTYSCVGV
KNGKVEILANDQGNRITPSYVSFNGDERLVGDAKNQASSNVNNTVFDIKRLIGLKYNDTQVQKEL
KHLPHYKIENKGNKPVVKVEYQGEKTFSPPEISSMVLGKMKSLAEDYLGKKVTHAVVTVPAYFNDA
QRQATKDAGTIAGLNVLRIVNEPTAAAIAYGLDKGDQEKQIIVYDLGGGTFDVSLLSIEGGVFEVL
ATAGDTHLGGEDFDFKIVRYLAKQFKKHNIDITANSKAIKSLKREAEEKARTLSSQMSTRVEIDS
FVDGIDFSETLSRAKFEELNIAAFRKTLPVEQVLKDDGGVKKSDIDDIVLVGGSTRIPKVQELLE
FFDGKKASKGINPDEAVAYGAQVLSGEEGVDDIVLLDVNPLTLGIETSGGVMTTLIKRNTAI
PTKKSQIFSTAADNQPTVLIQVYEGERTMAKDNRLGKFELTGIPPAPRGVPQIEVTFSLDANGIL
KVEAADKGTGKSESITITNEKGRLSKDEIDRMVEEAKEYAQDQELKEKIEARNSLENYAHVLRGQ
LSDTSETGLGSKLDDDDKETLDDAIKETLEFIEDNFDATAEEFEEQKQKLIDVANPITAKLYGGA
AGEGAGGAGDAKFGDDSDDEFDHDEL

YJL035C_homolog 1346bp PathoSeq: 1..125, public: 126..1346; CDS:
501..1343 (SEQ ID NO 379)

GCCCCATGGTGACAGAAAAGTATTGATCCAGGTTTCTTTGAAGGTTTGTAATACGTTTTAACTTG
TGACCTAACTCATTTTCATAAAATTCCTTGATAAAATTGGTTTCTTTGAATTGTTTGTAATCTCTT
AAGATTGTCTCGTCTTCAGTGTTCGAGTGGAGCTGCTATTGCCAGTCGGCGGCATAACAGCAGGT
TCTGGTATGTCATCTTCATCTACTAAGCCGGACAATCCCAAAGCCGTCTCTTGTTCTTTTATTCTT
CTAAGGAATGCTTTATGTAGTTCTGACATTCTTGCGTAAAGGAAGTACAGTATTAAAGCTCGAAA
CTCAATTGCAACAAAAGTCTTAATTTTTCTTCTATAAGTAATTGATCTTGGTCCCCCAACAAAA
AGATACAGAGGAGAAAGGAGGGCCTTAGGCTGACAGAAAAAAAATTTAGTACCTGCCACACCAG
TAGCTCCAAACCCATATATGATTTGATAGAGTTGAAGTATGCTGACAGATCTTACTTCACACTTTC
AGTACATGGCTATAAGCTTGTTTGTGCGTTACAAAGCCTTACTAAATAATGAGACACCAGTGTCAT
GTATAGTCGTGGATTCAAAATCAGATAAAATCATTAGCATAGGCTACAATTATACCAACCCTCTC
TAAATGGTACACAACACGCAGAATTTATTGCTTTACAACGATTGCGGGAACAAAACCTGAGTATTG

ACTATAATGATTTAATTTTGTATGTGACAGTGGAGCCTTGTATTATGTGTGCATCTTATTTACGTC
AGTTGGGCATCAAAAAAGTAATATTTGGTTGTGGGAATGATAGATTCGGAGGAAATGGTACCATT
TATCAATACATAGTGACATCACCTTGCCCTAACGCAGCTTATTCCAGTATCGGGGGTATATGTAGGA
CAGAAGGAATCCAACCTATTACGAAATTTTATATTCAACAAAATGAGTCGGCACCAATCCAAAA
TCAAAAAGAACACAGATATTGAGAGTAAGGAATACCCAGAGAATCAGTTTTGTAGCATTTCAAAGG
ATGAATTTATAGAGTTTTACGGAAATGAAAGAGTGCATATTTACGATGGGAAGATTTTTGAAATCA
CTCCATTACAAAACAAGGGTTATGATATAAAAGAATTGATATCGTTGGATATGATGCAAAAAGTTC
CATTTCTAGAGGATGAGTTGGGACAAATTACAGATGAGCAAATAATTGAATTCACAACTTATTTT
TCAACATAAATGATGATGGAACGGTTAATTATAAAAAACCAATAGGCAAATATAACAGTAAAAAGA
GACACTTTGCAAACGATGAAGAATAG

YJL035C_homolog 281aa (SEQ ID NO 380)

MSTDLTSHFQYMAISLFVGYKALLNNETPVSCIVVDSKSDKIISIGYNYTNHSLNGTQHAEFIALQ
RFGEQKSSIDYNDLILYVTVEPCIMCASYLRQLGIKKVIFGCGNDRFGNGTILSIHSDITLPNAA
YSSIGGICRTEGIQLLRNFYIQONESAPNPKIKKNTDIESKEYPENQFCSISKDEFIEFYGNERVH
IYDGKIFEITPLQNKGYDIKELISLDMMQVPFLEDELGQITDEQIIIEFHNLFNINDDGTVNYKK
PIGKYNSKKRHFANDEE

YJL180C_homolog 1504bp public: 1..938/940..1504, PathoSeq: 939;

CDS: 501..>1502 (SEQ ID NO 381)

CTTTATCTAATTGATTTAAATAATTATTAACATTAGTACCAATAAATGCTTTACCACAACCTTGCC
AACTTTTTTCATTTGATTGGGTATTACATATTTTATTTAATTTAGCATTGTAGTATCAATTATTG
TTAAATTTGTCATGGCTCGATCAAGTTGTAAATTACCCATGGATAATTCTGCTTGAGATTTATTTA
ATTGATTATCCATTTCAAGTAGGACTTTTTGTAAATGCTTCTTGATTCATGATTAAATGAGACGAGT
GTGTGTGTATGGGCGATGAAGCTGAAGGTTTTGCAGATGTGGTGTCTATAAGAGTAATTTGATGTG
AAAAATATACAATCTATAATCAGTATGTTTCAGTTTTGGAATGGAAGCCCCAAGAAGAACAACAGGG
AAATTAATAAATAAAAAGGTGTTGGAGAAAAAATAAATTGAACAGAAAGATTCATCCTTTTAGA
TCAAACGAAATATATCTTACCATCCCCCCCCCTCCAAATGCTTAGATTTACTAGGACTACTGCTT
GGAAATTAAGATCTATTCCAATTGCCACTATTCAATATAGACAATTTACTTATTCCACTATATGTT
ATCAATTAATAAACCTTACTCCATCTTTAGGAATAAATAATACCATTGAATCCAATATACCTTCAG
AACTAATAGATTAGCTAAACTGGTACTAGATTTTGGAATAAAGGTGAAGTTAAATTCAATAATG
AACTCAAAAATATGAAATTCAATTAGATGGGAAACTCTACGCACACCACTTGGATTCCCATTAG
AATTACCAATCAATAAAAAACAATTGGCATATTTAATTGCTCATGAATGGACTCATTTACCTGATA
TTAAAGTGAAATCAAGTACTTTACCATTAAACAGCTTTAGCCACTAGAGCTATAGATTTGAGTCAAC
AACATTTGAGTGATATGAAGACAGAAAAAGCTGAAGAAATGTTAGCATTGGAAGATATTAAATTAC
AATGTTAAGATATCTTGATACTGATACTTGCTCTTATATTTGCTACCAACAAAGAATGTGATGGTA
AATTAAGAAAAAGACAAGAAGAAATTTATCGTCCATTAATTAATGAATTTAATGAATTTTTCACAA
TTTATGCTCATAATAAAAATTTAATCCCTCGACAAAAATCTATTGAATTGAAATATTTAGATTGTG
AACTGATGGATTAAAGAGGTAATAACAAGATGAAACCACTCAATTAGTTGTATTGGATTGGTTAA
ATCAATTACCAATTTATGATTTAATTGCCTTGGAGAAAAACAATCTTAATACTACTAAATCATTTTAT
GTGGAATTACTTTATTAAGATCAAATGTTAATGATATTGAACTTTAAAGAATTATATCAATTTA
ATAAAAATTCATTGATGAAGATTATTATCATAAACTTTAGAAGAATTAGTTGAATTAGGAAATT
TAGAACTATTTATCAAACCTGAAGAATGGGGTGAAGTAGAAGATACTCATGA

YJL180C_homolog 334aa (SEQ ID NO 382)

MLRFTRTTAWKLRSIPIATIQYRQFTYSTICYQLKTLTPSLGINNTIESNIPSETNRLAKTGTRFW
KKGEVKFNNETQKYEIQLDGKTLRTPPLGFPLELPINKKQLAYLIAHEWTHLPDIKVKSSSTLPLTAL
ATRAIDLSQLSDMKTEKAEEMLALEDIKLQMLRYLDTDTCLIFATNKECDGKLKRQEEIYRPL
INEFNEFFTIIYAHNKNLIPROKSIELKYLDCETDGLRGNKQDETTQLVVLDWLNQLPIYDLIALEK
TILTTKSFLCGITLLRSNVNDIETLKLKYQFNKNSIDEDYHKTLEELVELGNLETIYQTEEWGEV
EDTH

YJL187C_homolog 3689bp public: 1..452/3414..3689, PathoSeq:

453..3413; CDS: 501..3686 (SEQ ID NO 383)

TATTTATATATAATCTAACACAAGTACTATCCCTTAACCTATTAGCTCAATGTCATTCTTCATTA
ACAAGAGATATGGTAATTGTTGATTAGACAACAGTTGGGTATCCATTTGTATTGGAACGCTTTTT

TTAAACTGCTGTTTTATTGTAAAAATTATTGTCGTCTTTCTTCATAACATTATTTGTAACAGTCTC
TAACTGTATTGTTGGGCTGACAGTAGAGTATTGCGGTCATTTTTAGGAGTGATTATAATTCTCTGT
GAGAAACGCAAGCAACAAAAAAGAACAAGGAAACACAATCATGATTAATTATATTAATAGTAGA
AACTCAAGGGTGAGCTAGATGACTGAGCGTGCGAGAAAAAACAATCATCCAAAGTTTAAA
CAAAGTATTCTTTTTTTTTTTCAATTTTACAACCAAAGATAAATAACTACACAACACCCAACATTA
CAGCCAAAACCACATATCTGTGCAATATTTACGCTCCAATGGATTCAAACCCGTGTCAAGACGTAT
CGGGTGATACCAGTAGCACACCAATGGCCAACAATAATCCCACATAATGACAGCACAATCTCCTCTC
AGAACCATTCTAAAACTGGCTTGAGAAAACACCAACAACAACACTACCACCAACACCTGCACCTGC
AAATGCATTCTCATTACAGCAGTCACCTTATATTAATCAATTGGAATACCTTACCAATAACCAGT
TTTCACGCTCTTTCAATAGTTTAATTTTGGAGGATGCCAATGATGCCAACCAACAATAGTTCAA
CAACAACCTTAAATAAGAAAACCATTAACAAGTCACCACCATTCAATATCAAGCAGGACTTATTAA
ACGATAGTATCGACACGTTTCTTGATAACTCCAACACGGAAACGATAGAAGATGGAGACGTCACAA
CAACAGACGACGATCACGATTTTGATGATGAAGATATTGAAGATCCTGAAGCAGTGCAGTACACCC
CAACTTTGAATATCTTGAAATCCAAAAAAGTCGATAGCTTCAATATTATCTAGCAAGCATAGAA
AGAGCAATAGTCAGATTACCTACAATCTGCACGTACGGAAGCCATCCGAAGAAGATACGTCATCAT
CGATGGCTACAATAAGGTTATCTAACAACCTCACAAAGTTCAATTAAGAGATCGTCAAAGTATTTGA
ATTTATCTATTGATTCCAATTTGAAAACGGTTGATGGAGGTAATAATCCCGATGAAATAGATGACA
TTAGTTTGAACGAAATAGATGTTGCAGTGGCACCTAACGATTTTTTCATCACCCTATCAGCAAGAA
AGCCGGACATATTTGCTGCTATAACTGCAGCAAACGGGAATTCCAATAATCAATTTAAAAGGCCAC
ACAAGTTGGTTAGTCAATCGCCTTCCCCGTCGTCAAAGAATAAGTTTCGCATATCATCATCAACCA
CATCTTCGCCACAGTCTAACTTGCATTACCTTCCAAGTTGGGACTGAAAGGATTCAAAATGTTTA
AAAATGCAAATAGAGACGCGATAATGTCGTCAAGCAGAGTTATGACTCCAGAAAAACCGAAAATGG
TATCTAAAATATTTGGCAAGTCAGCAAAAATAAGGCGAGCTTATACCCCAACCCATACATCTACCC
CAATGGCTGTCTCATCACTCAACCCTCCTTCATCATCTACACTGAATTCAACAACGGCAGCAATAA
CATCTACAAGTCCAGCAGCTGATGAGCATTTATGATATTGACAATGACTGTGACAGTCCGTCAAAAA
ATAGAAAACGTGCTAATATTTCTGCATCTTCAATTATTATTTATCAAGATGAAAATCATATCAAGT
CAAATCATGCTAGAAAATCTAGTAATCCAATACCATAACCTCCGACCGAACCCTACCGACAAATA
TTTCTGCTTCTGTGGCTGAAACAGGGAAAGGGTCAACTACAATAAAAGCAACCTATCTAAGGGTT
GTCCCTTATTTGATGATAAAGAGAATAAAGCTTCTTATCAGTTTGTAAACCATTGCAAACAGCTT
TCAATTCCTCGGGGTTGGTCAAAAAGAATAGCATAAGTGGTCTGCTGGACAGGAACTACCTCCAG
AAACACCAATCAAAAGAAATCCATTAATGATTTTAAATACCAACAAGTTGTACCTCCATATAGCA
GTGGATTGTGCTGAAGGAAAAGATGTAATGGGTGATCAACATGATATATATTCCCATATTCCATGTC
AAAATCAACGTTTTCTTGGCAGCGTGAATCCCAACACTACTACGAACAACAACAACACTCAACAGC
ATCATGATAGTGATCTTTCTATTGAAGTTGGAAGGAATAATTCTTATGATGCCAGTAGTAGCACTA
TCAATAACACAAGTTATATCAAAATTTTCCCTTCTTCGGAATTGAAAAAGGAGCAGGTGCTTCAGC
GACCACAAGAAGATTTAGAATTAGTTTTCAATTCTGACATTGAACTAGATGATAACATAATACCAG
AAACACCAACAAAGAACTGCTACTACCGAATCAGCACCATCAACATCACTTACCCCTTTACACGC
AATCCAAGAGTCCATTGTTGAAGTTTGACACTGAGAAAGATGGAAGAAGGAATTTGTCAATAGTCT
TAGATAAATCAAATGCAACTAAACGAGAAATTAGCGAACCACCTTCAACACCAATCAATATGTCAT
TTGCAAAGAATAGTTTTAAGAAACCTATGAATAATGCTGAAAGAGGTGATGACCCTGATAGTATAA
TTGCTCAACGCATAGATATTATGCCATCGTTAGATGAAGTTGACTCAGTGTCTGTTTATCCTTCAA
AGATAGATGAACATTTAATTGAAAAGTTTGGAAATGAAGAATATCAAGTATATTGGATCGGGAGCAT
TTTCCATTGCTTTTGAATGTTTATTTAATAACGAAAAGTTTGCTATCAAAAGAACTAAAAAACAC
TTATTGGAAAATTGGAGAAACAACTATAAAACGAGAAATTGAAGCATTGAGAGTGTTGACAAGCA
TTAAAGAAGATGAAGCAACTAATATGCAAGAACAAGAAGGAAAGAGTATCTAGTTTATTTCA
TTGAGGCCTGGGATTTTAAATAATTACTACTATATAATGACAGAATTCTGTGAAGGTGGTACATTAT
TTGATTTCTTAGAGGAAAATAAACATTACAAAATTGATGAATTTAGAATTTGGAAGATCCTAATTG
AAATTCTAAATGGGTAAAATTTATTCATCTGAAAATTTATTTACATTTGGATTTAAAACCAGCAA
ACATTTTTTATCACTTTTGAAGGGTCATTGAAAATTGGTGATTTTCGGATTGGCTACTAAATTGCCTA
TACTAGAAAAGGACTTTGATCTTGAAGGAGATCGTAATTATATTGCCCCGGAATTGATTAATGACA
AAATTTTATACTCCGTTTGCAGATATTTTCAGTCTTGGATTGATTATATTGGAGATCGCTGCTAATA
TAATTTTACCAGATAATGGAACGCCATGGCGTAAATTGAGAAGTGAGACTTGAGTGATGCTGGCC
GATTATCAAGTGATAATATTTCAATGTTTTTACAACACAATCCAAATACCAATAGCAATATCAGTG
GCAGTGGAAGTAGAAGTGGTAGTGGCAGTACAGGAGGCAATGGTAGTGCTGGTGATTGA

YJL187C_homolog 1062aa (SEQ ID NO 384)

MDSNPCQDVSGDTSSTPMANNPTNDSTISSQNHSTGLRKHQQQHYHQSHSQMHSQSQQSPYIN
QLEYFTNNQFSRSFNSLILEDANDANTNNSSTTTLNKKTINKSPPFNIKQDLLNDSIDTFLDNSNT
ETIEDGDVTTTDDHDFDDEDIEDPEAVQYPTLNILKSKKVDSEFNISSKHKRSNSQITYNSHVR
KPSEEDTSSSMATIRLSNNSQSSIKRSSKYLNSIDSNLKTVDGGKIPDEIDDISLNEIDVAVAPN
DFSSPLSARKPDIFAAITAANGNSNNQFKRPHKLVSQSPSPSSKNKFRISSSTTSSPQSNLHSPSK
LGSKGFKMFKNANRDAIMSSSRVMTPEKPKMVSKIFGKSAKIRRAYTPHTSTPMAVSSLNPPSSS
TSNSTTAAITSTSPADEHYDIDNDCDSPSKNRKSSNISASSIIYQDENHIKSNHARKSSNPIPY
PPTEPLPTNISASVAETGKGSTTTKSNLSKGCPLFDDKENKASYQFVKPLQTAFNSSGLVKKNSIS
GSSDRKLPETPIKRNPLMILNTNKVVPYSSGFAEGKDVMGDQHDYSHIPCQNQRFPQSVNPNT
TTNNNTQQHHDSDLSIEVGRNNSYDASSSTINNTSYIKIFPSELKKEQVLQRPQEDLELVFNSD
IELDDNIIPETPTKSLLPNQHHQHHLPLYTQSKSPLLKFDTEKDGRNLSIVLDKSNATKREISE
PPSTPINMSFAKNSFKKPMNNAERGDDPDSIIAQRIDIMPSLDEVDSVSVYPSKIDEHLIEKFGMK
NIKYIGSGAFSIAFECLFNNEKFAIKRTKKPLIGKLEKQTIKREIEALRVLTSEIKEDATNMQEQE
EGKEYLVYFIEAWDFNNYYYIMTEFCEGGTLFDFLEENKHYKIDEFRIWKILIEILNGLKFIHSKN
YLHLDLKPANIFITFEGSLKIGDFGLATKLPILEKDFDLEGDRNYIAPELINDKIYTPFADIFSLG
LIILEIAANIILPDNGTPWRKLRSGDLSAGRLSSDNI SMFLQHNPNNTNSNISGSGSRSGSGSTG
NGSAGD

YJL189W_homolog 887bp public: 1..666, PathoSeq: 667..887; exon 1:
501..506, intron 1: 507..737, exon 2: 738..884 (SEQ ID NO 385)
AGTCAAGAATTTTATGATGACTTTGGAGGATGGTCTGATTAAGACTTGTCTTTTACCAGTTTTTTC
AGCATTTGTTGATGGCGTTTAAAGCATCAGCTAAGACGGAGGTTCTAGTCATGGTTGAATTGTCTGT
TGATAAAAAGAAACCGTGAAAAGGAAGTATTGTGAAAAATCGATTGATATTTTTTTTTTCTCCTCCT
TCCTCACTGTAACAGTAGTAAACACACTAGTTACAACCTGATGACCTGCATATTATAAATCTTTCTG
AAAAAATTTTTTCCCTGTATTTTTGTAAATCTTTTCGCTCTTTCTCACTCACTCACACTTATTAAT
GAATGAAAGGTTTGGTGTCTACAAACTCCACTAACAAAATCTCACTCCTGTGCCTAACACACACA
GACCCACACGCAAACCTTTCTCTCAGAAACAGAAAAAAATTTCAAGCAAAAATTTTTTCCATC
TAGATTTTCTTTCTTCAAGTATCAAGTAACTTTAAAGATGCCTGTATGTACAATAACAGTGTTAT
AATGATGTCTTTCACTCTTTTATTGGGTGATTATTATAATAAATGGCAGATGAGAAATATATTGGA
TAATAAACCTTGCAAATGAAATCAGTTGACCATTTTGAAATAATGGACCATTAGCAATACCCAGAT
TGCTGGAACAAAGACGAGAGAACTAGACAACCTCAGATATAATAGAACATCCATACTAACTTCACTC
ATTTCTTATAGTCTCAAAAATCATTCAGAACTAAACAAAAGTTAGCTAAGGCTCAAAAGCAAAACA
GACCATTGCCAATGGATCAGATTGAGAACTGACAACAAAATCAGATACAATGCTAAAAGAAGAC
ACTGGAGAAGAACTAAGTTGGGTATCTAA

YJL189W_homolog 51aa (SEQ ID NO 386)
MPSQKSFRTKQKLAKAQKQNRPLPQWIRLRTDNKIRYNARRHWRRTKLGI

YJL190C_YLR367W_homolog 893bp public: 1..893; CDS: 501..890 (SEQ
ID NO 387)
GATTTCAATTTGCAAGGTTTATTATCCAATATATTTCTCATCTGCCATTTATTATAATAATCACCCA
ATAAAAGACTGAAAGACATCATTATAACACTGTTATTGTACATACAGGCATCTTTAAAGTTACTTG
ATATTCTGAAGAAAGAAAATCTAGATGGAAAAAATTTTGCTTGAAATTTTTTTTTTCTGTTTCTG
AGAGAAAGGTTTGCGTGTGGGTCTGTGTGTGTTAGGCACAGGAGTGAGATTTTGTTAGTGGAGTT
TGTAAGACACCAAACCTTTTCATTCATTAATAAGTGTGAGTGAGTGAGAAAGAGCGAAAGAATTACAA
AAATACAGGGAAAAAATTTTTTCAGAAAGATTTATAATATGCAGGTCATCAGTTGTAACCTAGTGT
GTTTACTACTGTTACAGTGAGGAAGGAGGAAAAAATATCAATCGATTTTTCACAATACTTC
CTTTTCACGGTTTCTTTTATCAACAGACAATTCAACCATGACTAGAACCTCCGTCTTAGCTGATG
CTTTAAACGCCATCAACAATGCTGAAAAAAGTAAAGACAAGTCTTAATCAGACCATCCTCCA
AAGTCATCATAAAATCTTGACTGTCATGCAAAACACGGTTACATTGGTGAATTTCGAATACATTG
ATGATCACAGATCCGGTAAAATTTGTTGTTCAATTAAATGGTAGATTAAACAAATGTGGTGTCTATTC
AACCAAGATTCAACGTCAAAATCAACGACATTGAAAGATGGACTGACAACCTGTTGCCAGCTAGAC
AATTCGGTTACGTTATCTTAACCACTTCTGCTGGTATCATGGACCACGAAGAAGCTAGAAGAAAGC
ACGTTTCTGGTAAAATCTTAGGTTTCGTTTACTAG

YJL190C_YLR367W_homolog 130aa (SEQ ID NO 388)

MTRTSVLADALNAINNAEKTGKRQVLIRPSSKVIKFLTVMQKHGYIGEFYIDDHRSRKIVVQLN
GRLNKCQVIQPRFNVKINDIERWTDNLLPARQFGYVILTTTSAGIMDHEEARRKHVSGKILGFVY

YJL197W_homolog 4619bp PathoSeq: 1..3041/3260..4619, public:
3042..3259; CDS: 501..4616 (SEQ ID NO 389)

CAACGACAACAACAATAAGAAGAATCTTTTCCAGATATTGTAAAATCCTTATATTAAATGTTAATA
GAAGCCTAAAAATTGCTTGAATTGATAGATTGCTGATTCTTTTGCTAGAAACACGCGTTATATTA
CTTATCCTTTCTGTAATTTCTTGATCTCTGTTTGAATCAACAACGCTTTGTTTTCTCTTTCTGCC
TCCCTCTGCCACCCCAAGTTTATTTGTTTGCTTGTGACGCTGCTGCCAAAAAATAATGAGTTC
TCTCTCTCTTTTACAAACAGAGAAGAGACAAAGAAAAAATAACATCAAAATTAAGATTCAAGC
TTTTTTTTTAGTTTTTTTAAACAACAAAATTGAAATTACAATCCTTGAATTTACAACCTCATATTC
AGCTCTAAATACTAATAATTATAACAATAATTAATTGAATTATTCTATAAACCACTGATATTTGAT
TTTATCTTTTTATTTTTGTTTGTCCATAATTGTGTCATGCCTGACAATATAGAAGATCGATCCG
AGATACCTTCTGATGCAAAGGAAATTGTGACTACAAATGAAATTGAAGCAACAGATTTCAGAACATA
CAACAAATGTCGATAATGAACTCCCTCAAGGTGAATCCAATGAACAAACAGGAGATGACTCAAATG
ACAACCTTGCATCCAAACGTCAATTAATCAATGATTTATTACACAATGATCATTTTGAAGAAGGAA
CAGAACGTTACATCATCCCTCAAAATTTCTTACATGAATTTTGAATTTACCAATCGATAATTTTA
GTGATTTGAAAGATCAACTTGGTCTTATTGATTTCCACTCATTACTTAATGAACAAGGTAATTTAT
ATCCCGAGAATGAAGAACCAGTCACCTTTTGTGTCATGTATCGCCAGAAGTATTTCAACATTTGGGTG
AATGGTTTGAATATTGGGCCAACCAATTATTAGAGCTATCATTATTAATCCAGACACCAAAGAAA
AACAGATTGAAAGATTCCCGCCATTATTTTGGGTTTCATCAATTAGGTAAAAAGACGCAACCAACAT
ACTTGCAGACACCGTCATAATGGAAGCAACCACAATCATCATCACCATGGTCATCAGATTACCAA
TACCAGTATTGCTTTCCAAAACAAGCACTTTTCATAGATTAATGGATGTTATACGTTATAATGTTT
TTAAAGCACCACGAAAATCGACGAAAGATTTTAGGATTTGGTTTATTGTCCCAAGATAAAGGCT
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YJL197W_homolog 1372aa (SEQ ID NO 390)

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PISDIIRDITDDVIVYIVPHNPAVDIIVPVFNAVEDADSSYQMVNFFGIPLFVVMNKEVDVNSFGFI
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YJL198W_homolog 2693bp PathoSeq: 1..899/1285..2693, public:
900..1284; CDS: <3..2690 (SEQ ID NO 391)

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CTAAACATGAATTGATATTACAACAAATTTTGAATTCTAATGATGAATCATATATTAATCCTAAAT
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YJL198W_homolog 896aa (SEQ ID NO 392)

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NYDLEKQNNTTVAIHDDDDSEDEEEEEETHSHSDSVLLNHTFNVKQQLKITLKRKAITLFINLS
ELKSFIELNRIGFTKICKKFDKTCGYSIKQDFINEFLPQYSRVFENDTIEELDYKLNQIIKIYAFL
SNKLTQSTTKEDLDNIKFEIERSYLRDHIVFERNVWKDLSLEKSYNIDLDNSVQNNKMGDEG
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CLAVLVAAAMLWASEALPLYTTALLIPLLVVTCKVCKTPGTDPMDATKASQYIFGTMWNSTIMIL
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RSIPTDSPVAKALVLGIALASDVAGMASPIASPQNVIALESMPNPNPGWGKWFVAVALPVAIISLILI
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YJR049C_homolog 2279bp PathoSeq: 1..839, public: 840..2279; CDS:
501..2276 (SEQ ID NO 393)

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YJR049C_homolog 592aa (SEQ ID NO 394)

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YLR048W_homolog EMBL_entry 1042bp public: 1..1042; CDS: 28..786
(SEQ ID NO 395)

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YLR048W_homolog SWISS-PROT_entry 253aa (SEQ ID NO 396)
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IKESSYVNIPVIALTDMQSPSEYVDVAIPCNNGKHCIGLIWWLLAREVLRLRGIIPDRTTTEWSVM
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YLR088W_homolog 1335bp public: 1..80/494..776/821..1335, PathoSeq:
81..493/777..820; CDS: <1..1332 (SEQ ID NO 397)
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YLR088W_homolog 444aa (SEQ ID NO 398)
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DLLNTANVMTYHEQIPCAMQMSDRVINYSTRLQTLFRGILKLTVLVGLTDEVHGCFAFSGWQIQAF
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ALLAVALLITALLIVHFALAFSIGILALPLTFVPTLMKNKSRLTAFCLAVSNPFFVIFVAGKVLGH
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YLR167W_homolog 1190bp public: 1..1190; CDS: 501..1187 (SEQ ID NO
399)
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AA

YLR167W_homolog 229aa (SEQ ID NO 400)

MQIFVKLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTLSDYNIQKEST
LHLVLRRLRGGMQIFVKLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFAGKQLEDGRTL
SDYNIQKESTLHLVLRRLRGGMQIFVKLTGKTITLEVESSDTIDNVKSKIQDKEGIPPDQORLIFA
GKQLEDGRTLSDYNIQKESTLHLVLRRLRGGF

YLR234W_homolog 2390bp public: 1..2390; CDS: 501..2387 (SEQ ID NO 401)

TCCAGAATAGTAATTAGGGACTTTAATTTTATTAGGAGTGGATTGCATAGAATATGCTATCTAATA
GATACATCTTATTATATTCTTATTCATGGGAAAGCACCAGTATATGGAAATGCTGCCCAAGGTAGT
GCACACAACAACTAGTTTACAAAGTAAATTCGAAGTTACGTCAAAGCTTAGAATGGTTCTTATA
GTAGTTGTCCTACTCTATCAAAAAACCCATAATTTGTCTATATAACGTAAGGATCACTATATGCTGT
TGAGTAAGAAATATGTTGCGAGCCGTACCGACAATGGATTGGCTGAAACTTGTTCATCAAACCTT
GCAAAACACTTGGAGACGCGCGCGCGTTTCAACACACAATAAACAACACGAAAAATAAGGTAGAAA
ACAAAAAATAAAAGGAACCTTTAAACAAGAAGTAATCCCCATTAAACTTGATCAACACTTTT
AGGGTTTCCGATTTCCCATTTTCTTGACTAAAATAATATGAGAATACTATGTGTTGCCGAAAAAC
CATCGATTTCAAAGAGAGGTGGCAAACATTTTGGGAGGAGGGCGAAAAAAGTAAGAACTCACGAG
AAAAATTCATCAAAACTACGATTTACCTTCACTTTCAACTCTGAAGATGGGCCATGTCAAGTAA
CCATGACTTCGGTGGCTGGACATATCACAGGACTTGATTTTGGGTCTGCCTTTTCGTGGGGAAATT
GTGTTCCCGGGCGACTATTTGAAGCAGACATCAAGACCATTATCACCAAGAAATCTATTTATGAAA
ATATTGCAGAAGAGGCAAGAAACGCTGATAAGTTGATGATCTGGACAGATTGTGATAGAGAAGGAG
AATACATTGGATTGAAATTATGAATGCTGCAAGAAATACAATAGGAACCTTGGGTAAACAATA
TTTGGCGAGCTAGGTTTTCACATCTTGAACGAAATCACATTATTCGAGCAGCAAAAAATCCCGTGA
ATTTGGATATGAGTGCAGTTTCTGCAGTTTCTTGTCGTATGGAAATCGATCTTCGAGTGGGTACCA
GTTTTACACGTTTGTGACTGATCAATTGAGACAAAAGGGGATAATTGAAAAGAAATGAAGTAGCTT
CTTATGGTACATGTCAATTTCCCGACATTGGGGTTTGTGTTGATCGATACAAACGAGTCAAGAGTT
TTACACCGGAACCATTTCTGGTATATTGAGATTGAAACTAGGAAAGAGAATAAAAAGACAATTTTCA
ATTGGGTTCGAGGTCATTTTTCGACAAGATGTATGTGGTTATGCTTTATGATCGATGCTGCAAAA
GTGGAGAATTTGGAACCATATCAAAAATAGAATCAAAACGGAAACCAATTTCCGTCCATTCCCAT
TGACAACCGTGGAGTTACAAAAGATTGTGCTAGATTTTAAAGATGTCTGCTAAGACGGCGTTGG
CAGCTGCTGAAAGACTTTATAACCTAGGGTATTTGTCGTATCCTAGAACTGAACTGACAGGTTTG
CCAAAGAAACCGATTTCAAGAGCTTACTAGAGGTGCACAAACAAGATCCGCGATGGGGAAGCTATA
CAACAAAGCTTTTGAACGAAGGTTTCGAAACTCCTCGAAGCGGTTCTCATGATGATAAGGCGCATC
CTCCAATCCATCCTATCAAATATGTTTCTTTGGACACCCTAAACACCCTCGATGAAAAGAAAGTGT
ATGAATACGTTGTGCGACGCTTTATTGCCTGTTGCTCCAAAGATGCTGTTGGTACGCAAACCGTGG
TGACTTTAAATGGGGAGATGAATTTTCAACCGCAAGTGGATTAATGGTGCATGAAAAAATTATT
TGGAAGTGTATACTTACAAAAAATGGGAAAGCTCTAAACAACCTACCGAAATTTACAGAGGGAGAAC
AGGTCAAGTTGTGAGTGGAATATTGAAAGACGGTAAACAAGTCCACCCAATCATATGACCGAGC
CCGAGCTAATTGCATTGATGGATGCCAACGGTATTGGAACCGATGCTACTATCGCTGAACATATTA
ACAAAATAGAGACTAGGCACTATATTAATAAATTGAAAAAGGGGAAAAATGAATATATTCTTCCTA
CTCCTTTAGGAATGGGGCTTATAGAAGGCCTTGAAAAATGGAATTTGAAGATGTATCACTATCGA
AACCATTTTTCGGAAGTCGTTGGAACGATCACTTGAGGACATAGCAACCGGGTCCCGGCCAAAAG
TGGATGTTTTGAATACAACAATAGGCGTATATGTTGACGCTTATAGTGTGTTCTCATCAGATAC
TTGTTTTGTGCAATGAATGTAGGAGAATTATACTTGGAATAGCAGTAACAACAACAACAATA
ATAATAATACGTAA

YLR234W_homolog 629aa (SEQ ID NO 402)

MRILCVAEKPSISKEVANILGGGRKKVRNSREKFIKNYDFTFTFNSDGPQVTMTSVAGHITGLD
FGSAFSGWNCVPGRLFADIKTIITKKSIIYENIAEEARNADKLMIWTDREGEYIGFEIMNAARK
YNRNGLNLIWRARFSLERNHIIIRAAKNPVNLDMSAVSAVSCRMEIDLRVGTSFTRLLTDQLRQK
GIIKKNELASYGTCQFPTLGFVVDYKRVKSFTPEPFWYIEIETRKENKKTIFNWVRGHFFDKMYV
VMLYDRCCKSGEFGTISKIESKRKPNFRPFPLTTVELQKDCARFFKMSAKTALAAERLYNLGYLS
YPRTEFDRFAKETDFKSLLEVHKQDPRWGSYTTKLLNEGFETPRSGSHDDKAHPPIHPIKYVSLDT
LNTLDEKKVYEVVRRFIACCSKDAVGTQTVVTLKWGDEFFTASGLMVHEKNYLEVYTYKKWESSK
QLPKFTEGEQVKLSSGILKDGKTSPPNHMTEPELIALMDANGIGTDATIAEHINKIETRHYINKLK
KKGNEYILPTPLGMGLIEGLEKMEFEDVSLSKPFLRKSLESLIEDIATGSRPKVDVLNTTIGVYVD
AYSVC SHQILVLCNECRRIILGNSSNNNNNNNNNT

YLR241W_homolog 3098bp public: 1..827/2190..3098, PathoSeq:
828..2189; CDS: 501..3095 (SEQ ID NO 403)

ATATATAGAATTATGGCTTAGTGCCCTTTATTAACATAATTAGAGGTTACATTAATACAACCTTAAC
AAACAAGGAACTAACATCCACGTATAGGGCTTCTTATATTAATATACCTAATTCAACCTGATTAT
ATTGCCCTTATATACAGCTTGTAACAAAAACACATAAGAAAGTTTACATCTCAAGATGAATTATCCCC
CTATTGTAACAAAGTACATCGCCTAATGATAGACATCATAGAGTACTGGCGACTCCTTACATGATGG
TAACGACAACAACATAACAAAAAACAATTATCTTGACGGTATAATTAGTAGTGTGCGAGAGG
CACACGATAAGATTTATCAGTTTTCCTTTTCTCGGTTGACCTTAATCTGTTTTTGTATAGACTTTAT
TTTTTTTGTTTTTGACCACACCCACTTTTAAATATCACAGATATTTAACTGATTATAGAAAACAA
CAACAATAACCCAAATACGTTAACCCTTTTATTACATATGATAGACAATATAATCAATAATTTGC
AAATCATACTACAGCAAAATGATGATAATTTTACATCCCCTCACGACGATGTGATATATCGACCAC
ATTCTGCTCGTGTAGCACGATATCAAGTAATAATTGCATCTACATTTGGGACTCACTGCCCTATTAC
TATTTTCTATCTTACGATTAAATATCCCAAAATATATGTGGCAAACCTTTAATCATTGTGAATTTCA
GTCTACATTCGACCTCAAGAAGGAATTTACCTGAATTGCCTTCAAATTCATTATTTGGTTGGATTC
CTACAGTTTACAAAATTACTGAGCAAGAAATTTTGGAAATGCTGGATTAGATGCAGTTGTGTTTT
TGGAAATTTTTTAAATGTGCATTTCGAATAATAAGCATATGTTTAGTATTTGCCATTATTATCATAT
CTCCTATCAGATACAAGTTTACAGGGAGAGTAGATGAAGATTATCCCGACGATGATAGTGACAACG
ATGACGATGATGGAAGTAATAATAATGGTACCACAATAATTAAGCATATAGTGTGACGCTGGAATTC
TGGTGGCAAGTAAAAATAACGATGGAGAACAGTATCAACAATTTCTTTGGTTATACACTATTTTCA
CCTATGTATTTACATTTGTTACTGTTTACTTTCTATTCAAACAACCAATAGGATTATTTCTATGC
GTCAGAAGTATCTTGGATCGCAAAATTCAGTCACCGATAGAACGGTAAAAATATCTGGGATACCAG
GATCATTACGAGATGAAGTGGCACTCGCACGGCACATTGACCGTTTGAATATTGGTGAAGTGGATT
CTGTGTTGATTGTCAAGGAGTGGCAAATCTAAACAACCTATTTCAAAGAAGGAGAAGAATAGTTC
GAAAATTAGAGGAAAGTTGGGTTGAATATTTTGAACAAAATGGGATAACCAATAAGAGCGATTGTA
TATCGTTGCATCCCCAAGTTGGCGAACTGTATCGTTTTTCCAATAGGTATACTGATGATGCAGAAG
AATCACCAGACTGGGGATCTCAAAATTCGAACCTCTGCACAAGCTTCAATAATAGATCAAGACTCAG
AATCTGTTGAAGGAGATTCTTCTGACACTTTGAATCGCTTGTGTAATGATGAACGAGAACAAGAC
CAAGTCTTCGGAAAGGTTGGTTCCGATTGTTTGGACCTAAAGTGGATTCAATAAACTACTACACCG
ATAAATTGGAGGTCATAGATAAAGAGATTACCAGGGCCAGAAGTAGAGAATATCCCGCCACTTCGA
CTGCATTTCTCACTATGAAAACCGTGGCTGAAGCACAAATGTTGGCACAGGCAGTCTTGGATCCAA
AAGTCAATCATCTTATCACCAACTTGGCCCTGCTCCTCATGATATCCGATGGGATAATTTGTCAT
TAACTAGACAAGACAGAAATACAAAGATCCTTGCTGTCACGATATTTATTGGTATAATGAGTTTGT
TGTGTTGTTTATCCAGTCAGATTTATGGCTAGTTTTTTAAACACTAAAAGCATTTCTAAAATATGGC
CATCATTTGGGGAAGCTATTGAATCGCATAAATGGGCCGAACTTTGATTACTGGATTATTGCCAA
CTTATTTATTTACAATTTTAAATATTGTGATTCCGTTTTTTTATGTATGGATTTCTGAAAAGCAAG
GTTATTTATCTCATAGTGATGAAGAGTTGTCATCGGTATCCAAGAACTTTTCTATATATTTGTGA
ACTTATTTTTGGTTTTTCACAACCTTTTGGTACCGCCTCTTTTGTGATACGACCAAAATTCGATTG
ATTTAGCAAGATCACTCAGAGATTTGTCAATGTTCTATGTTGACTTAATAATTCTACAAGGATTGG
GTATATTTCCCATTCAAATTATTATTGGTGGGGAACCTTACTTCGCTTTTTAGTGAATTCATTATTA
GGTGCAAGACCCCAAGAGATTACTTGAATTTGTACAAACCGCCAGTTTTCAATTTTGGTCTACAAT
TACCACAACCAATATTGATATTTATTATTACGTTGGTATACTCGGTAATGTCTTCGAAGATATTAA
CTGCAGGGTTACTATATTTTATTATTGGTTATTTTGTGAGCAAATACCAATTGCTTTATGCTTGTG
TTCATCCTCCACACTCAACGGGCAAAGTTTGGCCAATAATTTTCCGAAGAATCATATTAGGGTTAT
TTCTTTTTCAAATACAATGGTTGGCACATTAGCATTACAAGATGCAATCACATGTGCTACTTTCT
TGGCACCATTGCCGTTTTTTGACACTTTACTTTTGGTGGAGTTTCCATAACAATATATTCCTTGT

CAACATTCATTGCCTTGAGAGCAATTGAAAGCAATGAAAATATCAACCCTACTGATTTGGAGCAAA
TCATTGAAAACAACAATAATAAACTCTTGACGAAAGAAGGGAATTGAACACTAAATACGAATACC
CCAATCTAGTTAATGATTTAGACGGGCCAATGATTGCATTGGATGGTGAAGATGTATTGATAGTTA
ATCGAGATGGTACAACCTGTACGGAAACCACCTCAATATTTTCAGTTCAGAATGGGACTATTAA

YLR241W_homolog 865aa (SEQ ID NO 404)

MIDNIINNLIILQQNDDNFTSPHDDVIYRPHSARVARYQVIIASTLGLTALLLFSILRLKYPKIY
VANFNHLNFSLHSTSRRLPELPSNSLFGWIPTVYKITEQEILEHAGLDVVFLEFFKMCIRIISI
CLVFAIIIIISPIRYKFTGRVDEDPDDSDNDDDDGSNNNGTTIIKHIVSAGISVASKNNDGEQYQ
QFLWLYTIFTYVFTFVTVYFLFKQTNRIISMRQKYLGSQNSVTDRTVKISGIPGSLRDEVALARHI
DRLNIGEVDVSVLIVKEWQNLNKLFRRRRIVRKLEESWVEYFEKNGITNKS DLI SLHPQVGESYRF
SNRYTDDAEE SPDWGSQNSNSAQASI IDQDSESVEGDSSDTLNRLLNDESRT RPSLRKGWFGFLGP
KVDSINYYTDKLEVIDKEITRARTREYPATSTAF LTMKTVAEAQMLAQAVLDPKVNHLITNLAPAP
HDIRWDNLSLTRQDRNTKILAVTIFIGIMSLLLVYPVRFMASFLNTKSISKIWP SLGKAIESHKWA
ETLITGLLPTYLFTILNIVIPFFYVWVISEKQGYLSHSDEELSSVSKNFFYIFVNLFVFTTFTGTAS
FVDTTKIAFDLARSRLRDL SMFYVDLIILQGLGIFPKLLLVGNLLRFLVNSLFRCKTPRDYLNLYK
PPVFNFGQLPQPILIFIITLVYSVMSSKILTAGLLYFIIGYFVSKYQLLYACVHPHSTGKWPI
IFRRIILGLFLFQITMVGTLALQDAITCATFLAPLPFLTLYFWWSFHKQYIPLSTFIALRAIESNE
NINPTDLEQIIENNNNKTLDERRELNTKYEYPNLVNDLDGPMIALDGEDVLIVNRDGT TVRKPPQY
FSSEWDY

YLR321C_homolog 1559bp public: 1..947/1189..1559, PathoSeq:
948..1188; CDS: 501..1556 (SEQ ID NO 405)

TTCCAGAATTAGTAGATATTTCTGATATCAAGTTGGAGATAGGGATATCGAACTGGGATTCTATAT
TTTGTTTTATCTTGAGAACCTGTGTTGTTGTTGGCGTTCTATCTCTTTATATATTTTCTCTATTA
ATTCAATTGAAACATTTGAAGGAAATCTTTCTTAAAGCATCTAGTGACACATGATCTCTAATCT
CCAGTCTTTTGATTAAATATTTCTTTTAGAATATCAGGTGAAGAAGTGTGGTAGTCATAGCTAGTA
GATACTGTGTGGTGTCTGGGATAATAATTATAATGTAAACAAAACAAAGTCGTGTCAGTGTATATT
TTTCTTTTGTCAATTCCATCTTTTTTTTTTTCTCTTGAGAAATGTATAACAGAGGATCCATCCATT
TGCTTGACAGAGAAATACAGAACACTAAACAAACATTTTTTTCATTCCTTTCTTGTTTTGTTCTGTT
ATACCCCAAAGTTTGAATAAGTCTTCAGATATCTAGCATGGCAACTTCTCAAGAATTGACAGCAG
ACATACAAGCTCTTGCAACTAGTTTCCCCAAGCGATTAGCTAATGATAGTGACAATTCATTACTTA
TTAATGTTGCACCAACTGGTCGACAAGCCAAAAGACATATTCAACAGATTAATTA TACTCCGAAGAGT
TTGGAGATGACCTTGATTTTGATGAATTTCCCATCTTCGACACCCGGTACTAGAAGCTTAAATGAAA
ATAAAGCTCAAATAGAAGCACAAAGATATTCTCTTGCGAAAAACACACCAACGCCCAAGAGAATCT
TAGAAAAACCGGTGTTATCTGAGTTGGTTGAAAAACAGTGGTGCTTATTCCTATCAAAATAATGA
TTGAGAATTTGAACACAAACCAAAAGTTGATTGATTCCTTTATGTGGAACCTGAATGAAAGCTTGA
TTACACCAACTGAGTTTGCGGAAATTGTTTGCAGTGATTTAGATTTACCATT CAGTATGGCTGCAC
AAATAGCAGACTCCATTAATCAACAGATTGAAGAGTATTCCTATGCATCTAATTTACA ACTACCAA
ATAAGGGCCCTTACAATGTTACCATTGATTTATCAGTAAACTTAAATAAACAATTATACCAAGATA
GATTTGAATGGGATATGAATCAAAATGAAGTTACACCAGAAATTTTGCTGAAATAGTTGTTGCTG
ATTTGGGGTTATCGTTAGAATTTAAGAATGCCATATCACATGCATTGCACGAAATAATTATCAGAG
TGAAAAAAGAAGTAATAGATGGTACTTTTGACAATGAAATGCACAACTTG CATCTAGTAAAAGGTA
TAATGTTTGAAACAAGGAATTAGAATTTTCACTGAAAACAGTGTTCAA AATGGAAATGACCGTTGGG
AACCTTTGGTCGAAGTATTGACTTCTAGTGAAATCGAAAGAAGAGAAAATGAAAGGGTTAGAACT
TGAGAAGATTAAAGAGAGAGAATATGAGAAGAGATTACGATGATCATAGTAGGAGAAGGCAAGCAG
GAAAAAGAAGGTATGATGAGTTAGAAGGAGCCTGGGTATAG

YLR321C_homolog 352aa (SEQ ID NO 406)

MATSQELTADIQALATSFPKRLANDSDNSLLINVAPTGRQAKRHIQQINYS EEFGDDLD FDEFPS
TPGTRSLNENKAQIEAQRYSLAKNTPTPKRILEKPVLS ELVEKPVVLIPIKIMIENLNTNQKLIDS
FMWNLNESLITPTEFAEIVCSLDL PFSMAAQIADSINQQIEEYSYASNLQLPNKGPYNVTIDLSV
NLNKQLYQDRFEWDMNQNEVTPEIFAEIVVADLGLSLEFKNAISHALHEIIIRVKKEVIDGTFDNE
MHNHLVKGIMFEQGIRIFTENSVQNGNDRWEPLVEVLTSSEIERRENERVRNLRLRKRENMRDY
DDHSRRRQAGKRRYDELEGAWV

YLR325C_homolog 737bp PathoSeq: 1..737; CDS: 501..734 (SEQ ID NO 407)

AAGAAAAGTATAGTCAAATTGTTATACAAGCTAAGGAGCCATAAACTTTCTTTGGACATGCTAATA
TCGCTCCTGACCATTGTTTACTATATTCAACAAAACGAATTCAACAAGGCAAACGAAAGCTACATG
AAACTAAGTATCGGCAACGTCTGTTGGCCAATTGGGGTGGTCAATGTAGGTATTTCATGCAAGAAGT
GCAGCACTGAAAATAACCGGTGCCTCTAACGTCAGTAACATAATGCTAAGCGAGTCTACACGAAGA
TGGATTATAAGTATAAAGAGGTTGATTAGTTTTTAAAGAGAGAGTATATAATAATGCACGTGATTAG
TTTAGTAATTTTTTGGGAGTTAGGGCTATAGCCCTAAGACATTCACACAACCTAACAAAAAGGAAGT
TCTCACGCACATAACGTGTAACCCACATAAAGAAAGAAAAAAATTTCTTTGAAAAAATTCACA
TCACGCTTTAACCACCTCAACCTATAACAACCTCCAACCATGGCTAGAGAAATCAAGGATATCAAAG
AATTCGTCGAATTGGCTAGAAGATCAGACATCAAATCTGCTATTGTCAAAGTTAACGCCAAGGTCA
ATGCTAACGGTAAAAAATTCAAACAAACCAATTCAAGGTCAGAGGTTCAAGATACCAATACACTT
TAGTTGTCAACGATGCTTCTAAAGCTAAAAAATTACAACAATCTTTACCACCAACCTTAAAAATCA
CCAACCTGTAA

YLR325C_homolog 78aa (SEQ ID NO 408)

MAREIKDIKEFVELARRSDIKSAIVKVNANANGKKFKQTKFKVGRSRYQYTLVVNDASKAKKLQ
QSLPPTLKITNL

YLR344W_homolog 1348bp PathoSeq: 1..1348, exon 1: 501..515, intron
1: 516..979, exon 2: 980..1345 (SEQ ID NO 409)

ATACCATGACAAGCAAGCTCAGGGTCGCGGGTTCGAGTCCCGCGGGGAGCTAATTATACCCTCATT
TTTGAACCCACCAAATTTTCTTTCACATTATAATGAAATAAGAGTATTCCTTGGCTTCTTTTTTTT
TTTTTTTTTGGCAATATAGAGAAGACTGTAATAAGTATAGCTCACTAAAAGTCTTTTTTTTTTCTATT
CGTTTTATATTTTTTTAAGAAATTTGATGTTGATTGTTGTAATGCCAAATTTTAAATGTGTGTTAG
GGCTATAGCCCTAATGTACTGTATATGCAGTATCAGAAATACTTTTGTACGCACAGTTTGTCTTA
CCAAATACATTATATATATATATTTTTTTTTTTTTTGTAGTAGAGGAGCTACACTAGACCACAGTGCG
AAAAATTCATCTCTCTATACACTTACTCAATTTGAAGATATTCAAATTTTTTTTCAAAAAAAATTC
CTTTTGGATCGATACTAGATAGCATATAATCATCAAAAATGGCCAAGATCAGTCAAGGTATGAAAT
AGATATTCAATTAGATATGGAGAAAGGAAGATAAAAGGAAAAGAAAAAAAGAAAGAAATAA
AGGAATATATACATTGAAAAGGAGATAGAACATCAAACAACAACCATTAAGAATTAAGTTTAATAC
AGTTTCAATAAAGAGGGTTTTTTTCTCAGAACAAACCATTGACTGAAGTACTACACCAAGAAAGGTA
TAATGATTTACGATTTACCTGAATATAAAGAACATCCTTAATATTGAATTTCAATATTAATAATA
CAATTTGGGGATATTGATGAAATTATGTATAGGAGATTCCATTTTTTCAAACCTGTTGAATGGAAAA
CTTGAAAAATCAAATCAAATCAAATCATAACCCTTCAATATATTCCTTCCTTATCTTACTTTTCTCT
ATTAAAACAAAGACTAAGAAACATTCAGTAAAATACTAACAAAAATTCATTTTATATAGACGTTTC
TTCATCTCGTTCTAAAGCTAGAAAAGCTTATTTCACTGCTTCATCAGTTGAAAGAAGAGTTCTTTT
ATCTGCTCCATTATCCAAAGAATTAAGACAACAATACAATGTCAAATCTTTGCCAATTAGACAAAA
TGATGAAGTTTTAGTTGTTAGAGGTTCTAAAAAAGGTTCTGAAGGTAAAGTTAATTCTGTTTATAG
ATTGAAATTTGCTATTCAAGTTGATAAATTACAAAAAGAAAAATCAAATGGTGCTTCTGTTCCAAT
CAACATTCATCCATCTAAAGTTGTCATTACTAAATTACATTTGGACAAAGATAGAAAAGCTTTGAT
TCAAAGAAAAGGTGGTAAAGCTGAATAA

YLR344W_homolog 127aa (SEQ ID NO 410)

MAKISIDVSSSRSKARKAYFTASSVERRVLLSAPLSKELRQQYNVKS LPIRQNDV L VVRGSKKGS
EGKVNSVYRLKFAIQVDKLQKEKSNGASVPINIHPSKVITKLHLDKDRKALIQRKGGKAE

YLR393W_homolog 1631bp public: 1..1207/1209..1631, PathoSeq: 1208;
CDS: 501..1628 (SEQ ID NO 411)

TTCATCTTTTCGAAATCTTCCCTCTTGGAACGACCAAGAGTTGGATTTCGGTGCCCTTGACTAGCAC
AACTTTGTTCAAATCTTTATTGAATAATGCAACACCACGAACCGGTATGGTCGATTTATATTTTCC
GAATTTAGATAATGCTTCCCTGTGGGTCACCCCATTTCCAAATAAGCGGGCATTTCTCTAAAATCTT
TGTAAGTGAACGTCTTCATCTTCATGCTTTGCAAATCGGGATTCAACTGACGAACAAAGTCAGCATA
AAACCATTTGTGCTTCCCTCAATCTGAAACATTATCTTTCAATGGAAGATAAATCCTCTTCGGGAAC
ATTCACCACAAATCTAACTAACAAATCTTCCAACACCCGATCTAGAGTTTGATTAGCTAAACCAT
CGGTAATTGGATCGACATATCTTGTTATTTTCTATGATTAATCTTTCTTTTTTCTTTCTTTTTCAC

TGAATATTCGTAATTAAAATTGATTCAAAATTGTATTGATGTTTGTATACTGGATAAAACAACTTGT
GTGAGATCATTCAATGTATTTGCTGGCGGAGAAGGAGGCAAGGACGAACCTTTTTTTCCTTCATACT
TTTTTTTTTCTCTCTCTCTTTTCTTTCAGTCACATTGTCTGAGTGTTAAAGGCTGGCTTTTCTGTG
CTGAACCTTGTGGACTGGTAAACGCACGACATAGAGTAATATTTGGAGAAACCAAAGAATTTTGA
AAAACCGTGGTTTGAATTCGACCACAGATTGGTTGGACGACAAAATGCAAAGTGTATTCATCCGGA
CTTTTGCTACCTCAAGAATAGAGTTCCAGCGGTACCAGCCGCGTTTGTAAATACCATTAAAGAAA
CGGTCAAATCGGCACAAGAAAAGTCGTACAGTATTACTAGACCATTGGGGTTGTCAAACCAAGTTT
TGTTAAATCATAAATTGTCAGACACATACTCATTGTCCAATATATACGAGGAGTTGTTTGGTCAAA
AATCCAAAGAAAGAAGACAGAAACAACTAGACTACGATTGAAACACTCGCCAATTTATGAAGTCA
AGTCATTTGAGAATACAAAGGGGAAATATTTACTCCTCCTGTTTCGTACTTTCGACAAGACAAAT
CTTTGTATTTCCCGGATTTTATAGCGAAAACATTGGCAGGTAATCAGAGAAGTTTGTACGACTCAT
TAGACAATAGATTAAGCATAGTCAAATTGTTTTCTTCTGTTGCTGGTGAGCAGTGTACCCGTTTCGT
ACTTTAAGGTTGAAAACAAAGATTACTATTCCCAGGATTATGATACCTTTGTGGAGGAATATCCCC
ATACCCAGATACTTGATGTGAATATGCCGCAAAGTTGGATCAAGGGGTTTGTGACAAACTTGAGCA
CAGGAAATTTAAGAAAGACTTTGAAGCCAGCTCTGAGATACGAGAATTATTTTCATCTTGCCTGGCC
ACATAATGTCAGCGGAAATTAGAGAACAGTTGTACTGTGATAATCAATGTTCCGGGTATATTTATA
TTGTTGATTTCGATGGGGAAGATAAGATGGGCGACAAGTGGGTATGCAACTCCTGAGGATTTGAAAT
TGATGTGGAAGGTTGTGAAAGGGGTGCAAAGAGAAATGACCAAGTAA

YLR393W_homolog 376aa (SEQ ID NO 412)

MFVYWINNLCEIIQCICWRRRRRQGRFFPSYFFSLSLFFQSHCSSVKGWLFCAEPCGSVNARHRV
IFGETKRILKNRGLNSTTDWLDDKMOSVFIRTFATSRIEFQRYQPRFVNTIKETVKS AQEKSYSIT
RPLGLSKPVLNLNHLSDTYSLSNIYEELFGQKSKERRQKQLDYDLKHSPIYEVKSFENTKGKIFTP
PVS YFRQDKSLYFPDFIAKTLAGNQRSLYDSLNDRLSIVKLFSSVAGEQCTRSYFKVENKDYYSQD
YDTFVEEYPHTQILDVNMPQSWIKGFVTNLSTGNLRKTLKPASRYENYFILPGHIMS AEIREQLYC
DNQCSGYIYIVDSMGKIRWATSGYATPEDLKL MWKVVKGVQREMTK

YML063W_homolog 1271bp PathoSeq: 1..773, public: 774..1271; CDS:
501..1268 (SEQ ID NO 413)

CCAGTGCGTTTGTGTTGTTTCCACATCATACTTCACTGAAACTAAATAAGTTTGTGTTACATTTT
GAGACTTCAGGTACGACCCAGGGTTGCGACAAAGTTTAGGTAGTTTGTCTGCTGAATGTCGCAACA
AAATAGGGCTGTAGCCCTAGTCATGTGATGTGAATTAACATAACAAGAAGAAATTGCTGGTGCGCAA
AAAGATTATGTGTATTTTATGTGCGTTGTTATCCTGCACACTAAAATTGAGCAGTGTACACACACA
CATATTGGGCTGTATTTTATTTCTTGTTTTTCTGCTGTTCTCTCACTGTTAAGCTCTAAGTGAATT
TGTGTGTGCTGTAATAGTGTGTGTGTTCCAAGTCCCAGCTCTCACAGATACTCACGCACGCCATA
CTACTGAAAATTTCTGACTTTCTGTATCTAAAAATTTTTTACTAGGAATTTTTTTCTTTTACGTT
TTTCACTTGTTTCATATAATCACC AACTCAAGTACAACATGGCTGTGCGTAAAAACAAGAGATTGT
CCAAAGGAAAGAAAGGATTAAAAAAGAAGGTCGTTGACCCATTCAACCAGAAAAGATTGGTTTGACA
TCAAAGCTCCAACCACTTTTGAAAACAGAAATGTTGGTAAAACCTTTGATCAACAGATCTACCGGTT
TAAAGAATGCCGCTGATGGCTTGAAAGGTAGAGTTTTCGAAGTTTGTGTTGGCCGACTTACAAGGTT
CCGAAGACCACTCTTACAGAAAAATCAAATTGAGAGTTGATGAAGTTCAAGGTAAAAACTTGTTGA
CCAATTCCATGGTTTGGATTTCACTTCTGACAAATTAAGATCATTGGTCAGAAAATGGCAATCAT
TAGTTGAAGCTAATGTCACTGTTAAACTTCCGACGATTACGTTTTGAGAGTTTTTGCCATTGCTT
TCACCAAAAGACAACCAAACCAATCAAGAAAAC TACTTACGCTCAATCCTCTAAATTGAGAGAAG
TCAGAAAGAAGATGATTGAAATTATGCAAAGAGAAGTTTCCAAC TGTACTTTAGCTCAATTAAC TT
CCAAATTGATTCCAGAAGTCATTGGCCGTGAAATTGAAAAATCCACCCAAACCAATTTTCCCATTAC
AAAATGTCCACATCAGAAAAGTCAAATTGTTGAAACAACCAAAATTCGACTTGGGTTCAATTATTGG
CTTTGCACGGTGAAGGTTCAACCGAAGAAAAAGGTAAGAAAGTTTCTTCTGGTTTCAAAGATGTTG
TTTTAGAATCTGTTTAA

YML063W_homolog 256aa (SEQ ID NO 414)

MAVGKNKRLSKGKKGLKKKVDPFTRKDWFDIKAPTTFENRNVGKTLINRSTGLKNAADGLKGRVF
EVCLADLQGS EDHSYRKIKLRVDEVQGNLLTNFHGLDFTSDKLRLSLVRKWQSLVEANVTVKTSDD
YVLRVFAIAFTKRQPNQIKKTTYAQSSKLREVRKMKIEMQREVSNCTLAQLTSKLIPEVIGREIE
KSTQTIFPLQNVHIRKVLLKQPKFDLGSLLALHGE GSTEEKGKKVSSGFKDVVLESV

YML128C_homolog 1517bp public: 1..1499, PathoSeq: 1500..1517; CDS: 501..1514 (SEQ ID NO 415)

TGATATGGATTTTTCAAAAC TAAGAAACAATACCAACTACAACAACAAGAACATAAGTGTTTGCT
TAATTCAATGACCTCGAGTCATATCCCACGTTTAAAGTATGAGTGTTTACGAAGTTGTGGATCC
TATTTTAAATAAAACAATAAGTAATAAAAAAAAAAACCTTCTTTGCTTTTCGAGAATTTGTAAC
ACATTGTTTCTTTCTTCCACAGCAACCAAATTTTATTTTATTTTCTTTTGGGACTTACCCACA
GTTGCTCAATTATGTATAACAAGGGTAGAACTCTGTGGGATTCCCTCCTTAAAAATATAGCAATC
CTTTTCTTTCACAACGATTGCTATATGACCCCCCCCCCTAAGCATTCATTGCTTTTATATATATTTA
ATAATGTATTTCTCTTGTTCAGGATAATTATCACTATTTGTGACGTTTAAATTTTACATTTCTTCT
TCTTCTTCTTCTTCTTATTTCAACATTAAAGAACATTTAATATGTATTTCCCAATCATTGTATGGTTAT
ATGTATCTATCACTTTTGTGGTTGCCAATTATGGTTTGTATCAATGGACAAATGATGATTTAAAC
AATTTTAAAGAAGCTAAAGTTGCATTCAATGATGCCTTGGAGAATCCAAAATTAATTAGTTTGG
CTAATGAAGAAGCTAAGAAATTAGAAAAAGGTTACAAGAAAGTTACTGAAGAATTAAATAACAATT
TGAATCCTCCAGATGATTCATTAAATGATTATTTGAATTTTGATTACTTATTTGGGAAAAGAAAAG
AAAATTATTCAATTAAAGAATGGATTTTGAAGTTGGCCAGTAACCAGTTTGCAAACCTTTTAA
CTCAAAATAATATCCAATATAGTGCAAAGGATACCAAAGATGATTTAATCAATAAGGTTAAAGATC
AATTTGATTCTATTTCTAAGAAAAATCATGGGTCTAGTTTATCCTGGCAATTGGTTATATGAAT
CTTGGTCAGAAAATGATTTGAAAGATTGGTTGAAATCTTATGGCATTGAATTTAATCCTAGTTCAA
CAAAGGATCAATTGGTTGAAAAATTAAAGAATTTAGTTATCAAGCCACTCATTCAATTAGAGATT
CCAAAGAATCTTTATTTGATTCAATTGGATTTATTTGATAAAACCATTTTGGATAAAAAAGGTCAA
TTGAAGATGAATTTTCCAACTTGGTCATATTCTCAATTACGTGAATGGCTTTATTTACATGGAT
TTATTGACACTAAACCAGGAATTTACGTTGAAGATTTGGATAAGGAAAAATTAGTCAAGATTGCCC
AAAGTTATAAGAAATGTTTGTGAGTGACATTCATACTTGGTTGGCAAACACTGAAAAGAAGTCTC
AACCTTGGATCACAAAGGGAGAACAAAAGTCTCAGAAAAAGAAGGGTAGTAATTTGATTAATGATA
CATTCCTTGTGTTGGTATTAATAATTGGTCCAAGGATAAATTGCGTGAATTGGGCAATCTTGACTAA

YML128C_homolog 338aa (SEQ ID NO 416)

MYFPIIVWLYVSITFVVANYGFDQWTNDDLKQFLKERKQVAFNDALENPKLISLANEEAKKLEKGYK
KVTEELNNLNPPDDSLNDYLNFDYLFGRKENYSIKEWIFESWPVTSLOTFLTQNNIQYSAKDTK
DDLINKVKDQFDSISKKNHGSSFPYGNWLYESWSENDLKDWLKSYGIEFNPSSTKDQLVEKLKEFS
YQATHSIRDSKESLFDSDLDFDKTIFDKKGQIEDEFFQTWSYSQLEWLYLHGFIDTKPGIYVEDL
DKEKLVKIAQSYKKCLLSDIHTWLANTKKSQPWITKGEQKSQKKKGSNLINDTFFVGINNWSKDK
LRELGNLD

YML130C_homolog 2243bp public: 1..829, PathoSeq: 830..2243; CDS: 501..2240 (SEQ ID NO 417)

ATGAGTTCATAGATGATCTGTTTCACTTTCAAATAACGTGTCAACAAAAATAAAGTTAGAGCATAG
ATTTTGCCGCCACTTGTACAGATGGATAGAATTGAATGCAAATTCTGCATAAAGATTAAAGTGAAA
AACAAATTTCCGAAAAAAGAAGAAAATCGAACACATTAGAAAAAGAAACGAACAAAAGAAAAAAAT
TTCAAATTGTAGTTGCATGTATATAAAATAATATAAAAGATATATCACCAGCACAACTGATTACTT
TTTATTTATATCACCTGTCAACAACAAATTTCCAAATAAATACAACCTCAGAAAAACACTTACTAT
CTTTTCTTAGTTTGGTTTCTATAATCTTATTAACATTCTTGCCTTTCATCCTTGATTATCATATT
AGATCTTATCTTTAATTTGTTTGAATAAATAATACCAATAATCTTCCCATTAGAACTTACAACACA
ACAACAAAAAAACCCATTCTAAATCACTATTCTCCATTATGAAAATTTTCAGATTATTTTCACTAC
TAATCGTACAATTTATCATAAATACCACTGTTGCAGTATCACCTGTGTCAGCAGTTTACCAAAC
TGAGTTTTCAGTCCATTTGATTCACCAGAATTTTGTTCACAGATCATAACTCCCCTTGTAATACAA
CTTTCACCTACATTGATGAATTGAATAAAGATATTCGTCCCTACTTGTGGAATTAGTCAAGACCC
TGTATTTCCGTTATTTTAAAGTCAATTTAGATAAACAATGTCGTTTTTGAATGCTCAACATTTT
GTGCTAGTGAAAACGTGCTGTTGAAATATTGGAAGATTCAATTGGAGTCAAGTCACCAATGAAA
GTTTGAAACCTTCAGGATTAGGTAAGATTTCAATTACCTGACAAATCATCAATTGATAATTCATTG
AAACCGAAGAAGTTCAAACCTTGTGAAGATTTAGATTATAGTGAAATAGATGACCATCATTGTG
TTTATGTCAACTTGGTAAATAACCCAGAAAGATTTACTGGGTATGGTGGTAATCAAAGTTTGTATG
TTTGGAAGGCTATTTACCTGGAAAATTGTTTCCCTAATACTAATCCAATGTCAGTGACAAATGATG
CCGACAATGGTGGTGAACAATGTATCGAAAAGAACTTGTTTTATCGTGTGTTAGTGGTATGCATG
CTTCAATTGCAGTACATTTATCAAGAGAATATTTGAATTTCTGAAACTGGTGAATTTTATCCTAATT
TAAAGGTGTTTATGGAAAGAGTAGGTATGCATAATGACAGATTATCTAATATTTATTTCAATTATG

CCTTAGTGTCCCAAGCTATAGTTAAATTGAGTGAAATTTTACCATTGAGAGAGTTCATTCAACTGG
GGTATGATGACATTACTCCAGCTCAAAAGCAACATTTATTGGCTAATAATGATGTCGAATCAGTCG
AAGTTTATGATCGTTTGTGTTAGATGACATTATTCCTAGTTTGGGAAGCAAATGTTGTGTTTAATA
CTTCCAACCTTGTGTTGATAATAGCAATTTGAGGGATGAATTTAGATCAAGATTTAGAAACATTTCTG
CCATTATGGATTGTGTTGGTTGTGATAGATGCAGAATGTGGGGGAAAATCCAAACCATTGGTTATG
GTACCGCTCTCAAGATTTTATTTGAAGATGACAACCTATGATAATCACAATTTGAAATTTAGAAGAA
TTGAAATTGTTGCCTTGATTAATACTTTTGATCGTTTATCTAAATCTATTGAAAGTATTAATATGT
TTAAAGAAATGTATTTGCAACACCTTAAAGATATTGCTGAAGGATTAACCCAACCTGGTGTTTACG
ACAAAATACAAAACAACAAACCAGGTAACGGATTTGCCTTCCCATTTGTTAGTCCATTACCTCAGA
AAAAACCTGACCAACCAACACCCCCCAAAAATCAACAACAAAACAACCTCAAGAACTGACAAAA
AAAGACTTACATTAGAAGAAATTGCCACACAAAACCTGAAGATCGAACTTTTATTGAAGACTTCA
GATTATCCTTTGATGAAGTTTGGCAAGCATTAAGATTTGTTTTAACTAGTTATCAAAGATTCCCAG
CCGTATTGAGTAGATTACATTGGTTCAATTGAATGAATGGTGGAAATAAATTGCTTGGTAAACCAA
CAGTTTATGATTACCAAAGTTCTTTTGATGTTGATGCCCTACAATACAGTCAAGTCCTTGGATAA

YML130C_homolog 580aa (SEQ ID NO 418)

MKIFRLFSLLIVQFIINTTVAVSPVSAVLPKSSFSPFDSPEFCSQIITPTCNTTFTYIDELNKDIR
PYLSELVKTSYFRYFKVNLQCRFWNAQHFCASENCAVEILEDNFWSQVTNESLKPSGLGKISLP
DKSSIDNSIETEEVQTCEDLDYSEIDDDHHCYVNLVNNPERFTGYGGNQSFVDVWKAIYSENCFPN
TNPM SVTNDADNGGEQCI EKNLFYRVVSGMHASIAVHLSREYLNSETGEFYPNLKVFMERVGMHND
RLSNIFYNYALVSQAIVKLSEILPLREFIQSGYDDITPAQKQHLLANNDVESVEVYDRLLDDIIP
SLEANVVFNTSNLFDNSNLRDEFRRFRNISAIMDCVGCDCRMWGKIQTIGYGTALKILFEDDNY
DNHNLKFRRIEIVALINTFDRLSKSIESINMFKEMYLOHLKDIAEGLTQPGVYDKIQNNKPGNGFA
FPFVSPLPQKKPDQNTNTPKNQQQKQPQETDKKRLTLEEIAHTKPEDRTFIEDFRLSFDEVWQALRF
VLTSYQRFPAVLSRFTLVQLNEWNNKLLGKPTVYDYQSSFDVDALQYSQVLG

YMR022W_homolog 1004bp public: 1..507/668..1004, PathoSeq:
508..667; CDS: 501..1001 (SEQ ID NO 419)

TGTGAAAAAAATTTGTGGTGTGGATGTTGTTGTCGTTGTTGCGTTGTCCACAACAAAAACAAGT
AACAATTTCAAAGTTGGGCTTGGAGATCGATTTTTTTTCCCGCGTCTGTGTGGCAGAGACAATTG
AGTCGACCAGTACGTTTTAATTGAATACGAGAGTCGACGCAATTACATCAATCCAACATTCCACTT
ATTCTATATCAATGTAAAGTCATTTTTTGATAATATCGTAATTTACACATTTCTGATATCTCGGCA
ATAGGGGGGATAAAAAATAGTATTGACTAATTAATATATCTTGTATTATCAAATCAGGAGTATAGAA
TTCCACCCAACAACCTAGATTTTCCGAATGCGAAACGACGAGGACGACACAACAACGACTAAAGAAG
AAGAAGAAAAAAATATAAATAAATTGATCACGCACACATTAGAAACACAATATTGGATCACTTTT
TTCGATAATACTACCACCACACAGCTCATTCACTCATGCCCCGAAGTTCTACTGCTCAAAAGC
GTTTACTAACAGAGTATCAACAATTATCGAGGGACCCACCACCTGGGATAATCGCAGGACCAGTGA
GTGAAGATAATTTATACAAATGGGAATGTTTATTAGAAGGACCATCCGATACTCCATATGCAAATG
GAGTATCCCCAGCAGTATTGACTTTCCCTAAAGATTACCCATTATCACCACCTACATTAAAGTTTG
ATCCACCATTGTTACATCCAAATATTTATGCTGATGGAACCGTTTGTATTTTCGATTTTACATCCTC
CTGGTGAAGATCCAAATCAATATGAACGACCAGAGGAAAGATGGTCACCTGTGCAAAGTATTGAAA
AGATCTTGTGAGTGTGTCATGTCTATGCTTGCAGAACCTAATCCTGAAAGTGGGGCTAATATCGATG
CTTGTAATTATGGAGAGATAATCGTGCTGAATATGACCGACAAATTAGACAACATGTCAAGGAGT
CATTAGGATTATGA

YMR022W_homolog 167aa (SEQ ID NO 420)

MPRSSTAQKRLLEQYQQLSRDPPPGIAGPVSEDNLYKWECLLEGPSDTPYANGVSPAVLTFPKDY
PLSPPTLKFDPLLPNIYADGTVCSILHPPGEDPNQYERPEERWSPVQSIEKILLSVMSMLAEP
NPESGANIDACKLWRDNRAEYDRQIRQHVKESLGL

YMR118C_homolog 1031bp PathoSeq: 1..1031; CDS: 501..1028 (SEQ ID
NO 421)

CTACACAAAGCTTCGAGAGTTTTTTTTTCGTTGCAGGGGTGGGACAGGTGAGTAACGAATAAAACGT
CGATTGTCTTTCCTTTATGATTGTTCTTTAACGGAATTGTGTTCCCTTAAAACAAAATCAGTTCTGC
ACGTGATATAATCTCCTATCGCTAGTAGTAAGTTTAAATTTTTTTGATCAAAGTACACTCATCAG
TCTATTGTCGTAGATTTTCGCATACTTGTGATAATATCTGGTGTGTACACTACTTTTTTGGTTTGTA

TTGTAAATTACAATTTTTCTATTGGTTAAAATGATAATTGTTAACAAGTCTTTTTTTTCCCCGGGA
TTGAATCCGGAACTACCATTAATTCATCTACTCTACTCACCTTACACCCTCACTCACTCAA
ACAATTATATCAACCCAAAAAATAATCTTCACTACACCAATAACAAAGAACCAATAGTTCAAT
CTAATAAACCATCCTTCCCCCTAGCCTGCCACAACAACATGATTTCTCGTATTGGATTATTGAAAA
GACCTACCGTGTCCACTTTAAACAACATATGTCAAATTACAATCGACATTAGCCCTTAAAAGATACA
CATCAACCGTACCAGCAACTTCAAATCAAGAACAAGAAATATTGGTTGCCCAACGTAAAAATAGAC
CTACATCACCTCATTTACAAATTTATGAACCACAATTAACCTTGGATCATGTCATCATTCATAGAA
TCACTGGTGTGCTATGGCCGGTGCCTTTTATGCTTTAACTTGTGGATTGCTGCTACTTCAATTT
TAAATATTCCATTTGATACTACTACTTTAGTATCTGCATTCACCACATTACCAACATTTGCTCAAT
ATGGTATCAAAGCTATTTGTGCTTATCCATTTGTTTATCATATTGGTAATGGGATTAGACATTTGG
TTTGGGATTTTGGTAAAGAATTAACCATCCCTGGTGTTTATAGAAGTGGGTATGCTGTTTGGCTG
CTACTGCTGTCATTGGAAGTTATTTAGCTTTCTTATGGTAA

YMR118C_homolog 176aa (SEQ ID NO 422)

MISRIGLLKRPTVSTLNNYVKLQSTLALKRYTSTVPATSNQEQEILVAQRKNRPTSPHLQIYEPQL
TWIMSSFHRITGVAMAGAFYALTCGFAATSILNIPFDTTTLVSAFTTLPTFAQYGIKAICAYPFVY
HIGNGIRHLVWDFGKELTIPGVYRTGYAVLAATAVIGSYLAFLW

YMR230W_homolog 1176bp public: 1..1176; exon 1: 501..551, intron
1: 552..870, exon 2: 871..1173 (SEQ ID NO 423)

AAAAGCAAGAAGAGAAGGACTCGTTGGCCAATTTCTTCGGCAATTTCAAGAAGAAAAGAGTAGCTG
TTTAGAACTATATATATATGTACTCGCGCTTTAATGTTTATAGCAATAATGAAATGTTTAAATAAT
TATTTAATCAAACCTTGGTTGTAACCTTATGATTATGGTAGTGATCTAAGAACACAACCTTGCAAAGCA
ATGGTAGTTTCTTTGATTTTGTGTTTCTATTAGATTCTGTCTATTAGATTCCCGCTTTTTTTT
TTTTTGCAGACATTAAACCTCAGGGCTATAGCCCTAATGGCAAAACATGCACGTGTATGTTCTTG
ATTTTCTACACTACTAGTAAAAAATTTCTTTCCGCTCACTATTCACACATACACTCTTTTTCG
CACAATTACAGTCTACCAACAGGAAAAGAAAAAAGGAATCTGGTAATTGAAAAATTGAAGTT
TGTTCTTTTAATACTATCAATCAACTAGAGTCACAGCATGTTAATTCCAAAAGAAGACAGAAAGA
AGATCCACCAATACCTCTTCCAAGGTATGTAAATATGAATTATAAACTGGAACAGAATATGGCATT
TCAAGGGATGCACGATAAGTCAAGAGTTCATGAAAAAGCACAGATTATAACAGTCGTAAAGAAAAA
TTTCACTACCAACAACAATAAGAAGATATCAAAGAGATTCAGTAATCACTACTTACAAGAAACATA
TAACATCATGGAGAGTTTAATTTGAAATACGAATGAATATACAAATGAACATAACCTTTTATGG
CCATATCACGTTTCAAGAAATATTTAAACAAAAATAAAATGAAGAATAAACTTGGATATACTAAC
ACATGTATTATAGAGGGTGTCTGTTGCTAAGAAAGACTTCAACCAACCAAGCACGATGAAATT
GATACTAGAACTTGTTCGTCATCAAAGCTTTACAATCTTTGACTTCTAAAGGTTACGTCAAGACT
CAATTCTCATGGCAATACTACTACTACACCTTGACTGATGAAGGTGTTGAATTCTTGAGAACCGAA
TTGAACATTCCAGAAGGTATCTTGCCATTGACCAGATTGAAGAATGCTCCAGCTGAAAGACCAAGA
CCATCAAGAGGCGGTCCAAGAAGAGGTGGTTACAGAGGTAGAGCTAGAGACTAA

YMR230W_homolog 118aa (SEQ ID NO 424)

MLIPKEDRKKIHQYLFQEGVVAKKDFNQPKHDEIDTRNLFVIKALQSLTSKGYVKTOFSWQYYYY
TLTDEGVEFLRTELNIPEGILPLTRLKNAPAERPRPSRGGPRRGGRGRARD

YNL054W_homolog 2840bp public: 1..2197/2199..2840, PathoSeq: 2198;
CDS: 501..2197 (SEQ ID NO 425)

TGTTGGGAGTATTCTGGCACAACAAATACTTACTTTTAGGTTACTAACATTATTTTCTTCAGCTA
ACTAATTATCTAGTTTATATCTATATCCATTATTGTTGAAATCACTATCGTGAGGTAAATAACAAC
TACAGAGTTGTCACAGTATCCAAAAAACTTTGTACCTATCAATACATTTTAAGCAATAGGTCAT
TTATTGCTGTAATCAAGTGTTACCAGTATCTCTAGTTAATGTTGAGTTTATACCTAAAACATGAAC
TATATCAACTTTAAATGCCCCATAACACGTGATACAGCACATGGGAATTTGCTGATCTTGCTTCCT
TGCACGTACACGGCACATGTACACGACTTTTTTTTCTAAATATTTTTTTTTTTGTTGTTGTTGTTA
TTAAACAATATTATTTTCATATATATAATTGCTTAGTTTACTTGCTTCTTACACCCTTTGCATATT
TTTTTTTTTTTCTTTTCTGCCAACTTGATCAAATTCGATGCTACATCCTAATAATTCAGTAGTCG
ATATGTCTAGCACTGGAAACATGAATGAAAATACAGATGCTCCACCGAAACAGCAGACGAAAAAGA
AAATATCAAAACAGAATTCAACCAAAACCGATTTTTTTTGCTGCACGATTGGCTAGTGCAGTTGACG
ATATAGAAAGCAGTGATAGTGATGAAACGTTTATATATGAGAATAATGATACTGAACTTGATGATA

ATGCTAGTAATATTAACAATAACAACAATAACAGCACCAATAACATTATCAATTTAGATAATGCTA
GTGTTAACGGAAGTATGATTGCTTCATCCAATGCAATGGTGACTGGTCCTCCCGGAACATCGATAG
CGTTAGGATCGGGCCTTCGATCGCCATCCATACTAGAGGGGGAACAGCTTCAATATTTTCATGACC
CAGTGAGGCAACAACAGTTCAAACCTCCTTCTACCAAGGCTCCGTCAATTTCCAACCTCCATCAGCA
GTTCAAATAATATAGATTCAATACTTAAACGACCTGTACATCTACGTGAGGCATCAACGTATTTCAG
TGAATGATAATGACCACCGAAATCTTGTGCTACCAAACCTCAACTGAAAGGTTTACTGCTTCACCTT
CGAACAATATTGGTAATGAAAATATACCTCAATACCAGAAAACCTAGTAGTGTGCCCCACTCAATCA
ATGAAGGATACAATGATGATACATTTTCATATAATGAAGTTGAGGATAATTTAATTGATGAAGATT
CCACGGACGATGGGGATTTGACAAAAAATACCATTACTAATAACAACAATCCACCAACCACGTCGA
GCCAACAGCAACCACAACCGCAACCACAGCCGCAACCACAGCAACCACAACCTACATACTCTGTCTC
CTCTAAATCAGATACAAGCAGCGACATCAGCAACACCTTCTGTGTCCACTAAAAACGCGTCTAAAA
GAAATTACAAAACCTCATCCACTTCCTCAAAATTAAGATCAACTACATCAAAACTTTTCGATAAAA
AAGGGTCACAACCAAGAAGATACAGTACCATTTCCTGATGATATTGACATTGAAGATTTTCGATGATG
AGCTTATATACTATGACAACACAGCTAGGTTCCAGCGAACGAATCAACTTCATTACTAAATCAAA
ACCAAAGAATCCCCCATTTATAGATCACTTAATTTGAATTTCCCTCAGGTGAAGCGCCAAAGCAAGC
GTTATTTGTCAACTGGCCAACCTTTAGAGAGTTCTGATCGTGGCTCTAACAAAGATGGTACTGATA
ATGGAAACAACAGTGATCACAATATTAATTTCTCCTTTGACTGCTAATAATAATAATAAACGTCA
ATCACAACGATCATGGTGATAACAAAAAGAGTAATACCAACAACAACATTTGCTAATAATAGAG
CATTTCCATTTCTTATCAAGATCAACAACATCATTATTACTACGACTACGATGATTTTGACCAAG
AATCACAATCAATGGACCCAATTTTGATTTGCCAGACCTCCCTATAAACAGATCAGCTTCACGGA
ATTTTAACAACAACAATAACCCCAAAAGATTTGGCGACAGTCATTTTTTTCTACCAAGAAAGACAG
ATCAGTATAGTCAAAGAACAAGCTTTCTAAAGTCATGCATTTTATACCTTTGTTTGTATATTAATTG
TGCTTACCATAGGGTTTGTATTGGGGTTTGTTTTGGCCACAACAAAAGATTTAACTGATGTAGGTA
TCACATCCATTGAGAACCCCATTTGTTAGTAAAGATGAGTTAGTTTTCAATGTTGTTATTGAAGCAT
TTAATCCAGGGTGGTTTTCCGTTGACATCAATGAAGTAGAGTTGGATTTATTTGCAAGAAGTGGCT
ATCTACCTGATACAGATAATCTGAAAATATCTAACATGGGAGGGTCACAAAAAGTAGAGACGGTTA
AATTAGGAACGATTTTGAATTTTGAATCGGTTCTCAATTTCAAAGGTGGGTTTCTCTCTCGAGAAC
CGACAATTCAAAGGGAGGAATCCGATTATTATATCCTGGCAAAAATGTTACTGCCGAGGCTAAAT
TGGTTGTAAATATGGCTGATATTAATAAGCTGCTTCCAATAGCATTGCTAAAGAAAGCACTACTA
GTAATGACACCAACGATAATGACAACCTCAAGAAGTGGGAAATCATATCAAGCAATCCATTTGATT
TGATTATAACTGGAGTATTGAAGTATGATTTACCATTTTCAAGAACCTCAAGATCAGTCGTGGTTA
GAAAAACTGGGTATATTGATCCTACCTTATTCGTAATACCACAAGGAGAGAATAATATTTCAATTT
AG

YNL054W_homolog 779aa (SEQ ID NO 426)

MLHPNNSVVDMSSTGNMNNENTDAPPKQQTKKKISKQNSTKTDFFAARLASAVDDIESSDSETFIY
ENNDTELDNDNASNINNNNNNNSTNNIINLDNASVNGSMIASSNAMVTGPPGTSIALGSGLRSPSILE
GEQLQYFHDVPVRQQQFKLPSTKAPSISSNSSNNIDSILKRPVHLREASTYSVNDNDHRNLVLPN
STERFTASPSNNIGNENIPQYQKTSSVAHSINEGYNDTFSYNEVEDNLIDEDSTDDGDLTKNTIT
NNNNPPTTSSQQQPQPQPQPQPQPQLHTSSPLNQIQAATSATPSVSTKNASKRNYKTSSTSSKLR
STTSKLFDDKKSQPRRYSTIPDDIDIEDFDELIYYDNTARFPANESTSLLNQNQRIPHYRSLNLN
FPQVKRQSKRYLSTGQPLESSDRGSNKDGTDNNGNSDHNINSPLTANNNNNNVNHNHDGDNKKSNT
NNNNNIANNRAFPFPYQDQQHYYYDYDDFDQESQINGPNFDLPDLPINRSASRNFNNNNNNPKRFGD
SHFFLPRKTDQYSQRTSFLKSCIYTFVCILIVLTIGFVLGFVLATTKDLTDVGITSIENPIVSKDE
LVFNVVIEAFNPGWFSVDINEVELDLFARSGYLPDTDNSKISNMGGSQKVETVKLGITILNFESVLN
FKGGFLSREPTIQKGGIRLLYPGKNVTAEAKLVNMADIKIAASNSIAKESTTSNDTNDNDNSKKW
EIISSNPFDLIITGVLYDLFPFSRTSRSVVVRKTGYIDPTLFVIPQGENNISI

YNL075W_homolog 1352bp public: 1..136/138..1352, PathoSeq: 137;

CDS: 501..1349 (SEQ ID NO 427)

CCCACAGACCAATAACGTTTTACCAACCAAAACCTCTGATATCAATGATTTCGAAAAGATTCATTCA
ACCCCGGTTAGCTGTTTGAGTATTGGATAGCAACACTTTCAATTAGTGCAACACAATCAAATTACC
AATACTTGTTTACCTTTTCATCTGATTCTAATTGGTTCATAGCAATATAGTCTCTTCTGTTGTTTGA
TATTAATATAAATAAACTTATTTATCACGTTGTTTAGTAGTCTCGCAAATTTGAAACCATGGATG
AGTAAACTTGTTGTGTTAGATGAGCTCAAATATCTGGTGGAACAATTTGTGTAGTAGCTCTTTGATA
AATATCCAAGAACAGTCGTGCAAGTTTCAAATACCATCGCAAAAATCCTAACAAAAAATAAAT

MIRKQARERREYLYRKALQLQESSLTEKRQQLKAALASGKSLSKELAEDEKLQRDFIYDESEQIEI
DDEYSRLSGISDPKVVITTSRDPSPVKLLQFSKEIKLMFPNSLKLNRGNYIIISDLVSTCNRVQVSDM
ILLHEHRGVPSSSLTVSHFPHGPTAIFTLHNVKLRHDLPNLGNVSESYPHLIFENFQSDLGKRUVKI
LQHLFP PGVKKDSSRVITFVNNDYISVRHHVYVKT KDSVELSEIGPRFEMRLYEIRLGLPDNKDA
DVEWQMRRFIRTANRKNYL

TCCTTTTGTTTTATTTTTGTCTGTGTTACTCCAGAAATGTGCATAATAATGATAAATAGTAATTTGT
GACTAATATGAGATGATCGTATGTGGGTGGGTGGGGAGGAAGGGACCCGGAATTC TAGGAACAGGA
AAAATAAAAACGAATAAACAAAAACCCCCAATCGGCATGCATCGGAATTC TTTTCAGCCCAATTAC
TTTATTTTGTCCACTTCTTTTGGATTAGGGCAATAGCCCTAAAGCTCGTGT TTTTAGCCCTTTATA
TGCAGTCTATTTTATTTTCTCTTTTTTTTTTTGGCTGTTGGTAAACTTTTTTTTTTTTCGCAGGTG
TTGAAAAAAAAATCATTTTACAGTTTACATTTCTCTAACCTGCAAAAAGCTCTCGTTTTTTTGTA
GTGAGAGTTACTCGTTCACAATAGTATACTTTACAGGGGAGTTCTTTTCTTTTGGAATAGTCAACC
AACAGCAAATAGCCAAGGATCAAGCTTCATCATTAATCATGTCCTCTAAGATCTTATCAGAAAACC
CAACTGAATTAGAATTA AAAAGTTGCTCAAGCTTTCGTTGATTTGGAATCTCAAGCTGATTTAAAAG
CTGAATTGAGACCATTACAATTCAAATCTATCAAAGAAATTGATGTTAATGGAGGTA AAAAAGCTT
TAGCTGTTTTTCGTTCCACCACCAAGTTTACAAGCTTACAGAAAAGTTCAAAC TAGATTA ACTAGAG
AATTAGAAAAAAATTC C CAGATAGACATGTTGTC TTTT TAGCTGAAAGAAGAATCTTACCAAAC
CAGCTAGAAAAGCTAGAAAACAACAAAAAAGACCAAGATCAAGAACTTTGACTGCTGTT CATGATA
AAATTTTGGAAGATTTAGTTTTCCCAACTGAAATCATTGGTAAAAGAGTTAGATACTTGGTTGGTG
GTAACAAAATCCAAAAAGTCTTGTTGGATTCTAAAGATTCAACTGCTGTTGATTACAAATTGGATT
CTTTCACAACAAATTGTACTCAA AATTGACTGGTAAACAAGTTGTTTTTGAAATCCCAGGTGAATCTC
ATTAG

MSSKILSENPTLELEKVAQAFVDLESQADLKAELRPLQFKSIKEIDVNGGKKALAVFVPPPSLQAY
RKVQTRLTRELEKKFPDRHVVFLAERRILPKPARKARKQQRPRSRTLTAVHDKILEDLVFPTEII
GKRVRYLVGGNKIQKVL LDSKDSTAVDYKLDSFOOLYSKLTGKOVVFEIPGESH

TGTTTTGTTTTTGCAATCAACATAATAGAAGACCAAACAAATAATTTCTATTTTTTTTGA CTCTCC
CGTAGTTTTACACTTCTAGCCTCTCTTGTA AATATACACCTAATTGACAGTACCATTAGGACCCCA
TCTTATTGTTAAGGATAATACTTCTTCTTCTTCTTCTTGTTTAATCAAATTTGCAATAAATA
AAAAAAAAAAAAAAAAACAAAGCCGCACAAGTTTTCCTAAAATGACTTATTTTGTGTAACGCATTAC
GTGATCATAATTTTTTTTAAATTCAAAAAC TGAACCAAATTCCTGCATATTGAGGTTGAAAAAAAAA
AGAAAAAGAAAAATTTTTTCAATCTTGTTTGAGGAGAGAGAGGTGAAAAATTTTTCTCTCTCTTT

CTTCTTTTCATTCTCATATACCATAAACTTAAACAACCTCTTTTACTTTTTCTTTCTTTTCCTTT
CAAACCTCTACAACAGATCCAATTAATTAACAAAAAAATGGTTAACGCTATCTTATCTAAGAAAA
AGAAATTAGTAGCTGACGGTGTCTTCTACGCTGAATTGAACGAATTCTTCACCAGAGAATTAGCTG
ACAAGGTTATGCTGGTGTGAAGTTAGAAAACTCCATCTAAATTGGAAGTTATTGTTAAAGCTT
CTAACACTCAAGGTGTTTTAGGTGAACAAGGTAGAAGAATCCATGAATTAACCTCATTGATTGTTA
AAAGATTCAAATTATCTCCAGAAGGTATTGCCATTTATGCTGAAAGAGTTGAAGAAAGAGGTTTAT
CTGCTGCTGTTCAAGCTGAAGCTTTGAAAGCCAAATTAATTGTCTGGTTTACCAATTAGAAGAGCTG
CTTATGGTGTTTTAAGATTTGCTATGGGTGCCGGTGCTAAAGGTGTTGAAGTTGTTATCTCTGGTA
AATTAAGAGCTGCTAGAGCTAAATCTCAAAAATATGCTGATGGTTTTATGATTCATTCTGGTCAAC
CAACTAGAGATTTTCATTGATATTGCCATTAGACATGTTTTAATGAGACAAGGTGTTTTGGGTATCA
AAGTTAAAATTATGAAAGATCCAGCTGCTAATAGATTTGGTCCAAGAGCTTTACCAGATGCTGTTA
AAATTGCTGAAGCTAAAGATGAAGATGAAGTTATTCCAGCTCCAAGTGTAAATCTTATAAACAAA
CTGCTGAAGATGAACTGAACTGATGCTCCAGTTGAAGCTGAAGCTGAAGTTGAAGCTACTGCTT
AA

YNL178W_homolog 251aa (SEQ ID NO 432)

MVNAILSKKKLVADGVFYAELNEFFTRELAEQGYAGVEVRKTPSKLEVIVKASNTQGVLGEEQRR
IHELTSLIVKRFKLSPEGIAIYAERVEERGLSAAVQAEALKAKLLSGLPIRRAAYGVLRFAMGAGA
KGVEVVISGKLRAARAKSQKYADGFMHSGQPTRDFIDIAIRHVLMRQVGLGIKVKIMKDPANRF
GPRALPDAVKIAEAKDEDEVIPAPTVKSYKQTAEDDETETDAPVEAEAEVEATA

YNL182C_homolog 2105bp public: 1..728, PathoSeq: 729..2105; CDS:
501..2102 (SEQ ID NO 433)

AACTTTCTGATTGAATAAAGTGAACCTCAAATCACATTCTTCGGCATATATCAAACCATTTAGT
TTTATCACGTAAATCTTCAATATACTCAGCCACCCATTGATCATTGGTTCTTCTAGTAAGTAATAT
TAGTTGTGCTCCTCGTTGTCCCAATTCATATGCTATTTGAGCTCCAATACCACTGGTCCCACCACT
AATCATAAACACTTTCCCATGCATGTCTCGCTCCCACGTATTGGTGGCACCATGGAAATAATACTT
GGCTCCAGCAAGAGTTAATAGAATGGGAAGAACGGTAGGTCCATATTCTTTAATTTGGTCCCAATA
TGGAATCACCTCTGGCCCATCAAACACAACACTAGTTAAAAAATTCAGTGGCATAATTGGTATATC
AAGAGTGAAGAAAAATGCTGTATTGGAGGTTGGAATTTGTTACAAATTTGGTTGCCTTTTTATTCT
TCTTGTCTTTTTTTTTTTCAGTGCTAACATAAATTTGGGATGTATGTATTGAAAAAATAATTTTG
TACAATTTCTTGTCTTGTCTCTCCACTCATCTCATCGCTCTCTTATAAATTCACAAACATGGATG
AAGTAGTATTTTACATAGCTCAAGGTGATCCAGCTGATAAACACAGTCAAGAATCATATGGATATG
TTACATCAATCCATTCTTCCAAACAATATGCATCTTATCGACAAGCAGACTCGCATATAAACGGTA
CTGCCATAACTGGTATTGGCCCAGGAGAAAGATTTTCACTGCTGTTCCCTAACAAAGGCATTAATCA
ATGTATATTCATGGGGAAAAGAAAGTGTGATCAACGTATACCGATACCAGAAGCATTGACTTGTA
TCACGTTGATAAACCATCCAAATGGCAGTAACAACAACAGCGACAATGATGACAACCAAGTTATACA
AATTACCAAATTACCGAGTTCCTTGGTTGTTAGCAGGTGGATCAAAGAGTGGGAAATTGTACATTT
GGGAATTAAGTTCAGGCAATTTATTATGTGTGTCAGAGACGCCATTATCAGGGGATCACTACCATCA
AGGGTTCAAGCTGTGGAACATTTTAAATTACTGGAGGAGAGGATGCCAGATGTCTTGTATGGAATT
TAGCAGAATTAATTAGTATTTATGACAAATCAGACCATCAAGTGAAACCATATTGGCAAATCACTG
ATAACACATTACCACTCACTGATCTTTGTTTAAATGATACTCATAACATTAATGATCTAAAATTAT
ATACAACCTTCAGAAGACAGCACGGTCAGGATTTATGATATAGTCACAAAGAGTTTGTAAACCAT
TTATTTTACCCAGTTCGCTGAATGTATCACCAAGGATCCAGCTAATAGAGCGTTATATGTCCGGT
TGAATAACGGTCTTGTAAGATCAATTCCTTTATATTCTATAAATAGCCATACATCAGTGTGGA
GTATTGGCGGCATGAATAAGATAATCACGGTTGATGCTGATCAAAATTTAAAAGAGACATTTGTTG
CACATCAACAAAAGACGAAAACAGGAGACGATAAGCCTGTTGTTGTACGAAATTGACAATTTCTT
TTGATGGTACAAGTATAATATCTGGTGAATCTGAAGGCAGAGTGTGTTGTGCTGACATTGTAACGA
AACAAAGTTGTGAAATCATTACACCTTGTAACCTCCAATAGCTTATATTGCTGTTGAACTATCC
CTGATGACTTTGTCAATAACTTAGCTACTAGTACTACCACTAATAAAGCTGACAAGAAACATAGAA
TGATACCTCAATTTAAACGAGTACTAGCAAGCACCAATCTGAAGAACATCAGATATTCTTGGACA
TTCTCTGGTAAAACCAACCGCAACCAACGCAACCGGCAATATTGACTTTGCAACTTGGTTACAAG
GCAACAATCTGAAGAATTACAATTCAAAAACCTTTCTGGAATAAACTCTATTGTCAAACAAGTTG
GCAACGAGAATGTATCGGATCTCGAAGAGAGATTACAAAGAGTTTCTCAAGCATACACTGAATTAA
GAAACAAACATGAAGAATTAATTAAGAACATGCCAAATTATTAGATAAATTAGAATAG

YNL182C_homolog 534aa (SEQ ID NO 434)

MYVLKKKNFVQFLVLVPLISSLSYKFTNMDEVVFYIAQGD PADKHSQESYGYVTSIHSSKQYASY
RQADSHINGTAITGIGPGERIFTAVPNKALINVYSWGKESVDQRIPIPEALTCITLINHPNGSNNN
SDNDDNQLYKLPNYRVPWLLAGGSKSGKLYIWELSSGNLLCVRDAHYQGITTIKGSSCGTFLITGG
EDARCLVWNLAELISYDKSDHQVKPYWQITDNTLPLTDLCLNDTHNINDLKLYTTSEDSTVRIYD
IVTKSLLTFFILPSSAECITKDPANRALYVGLNGLVRSIPLYSINSHTSVLESIGGMNKIITVDA
DQNLKETFVAHQKTKTGDDKPVVVTKLTISFDGTSIISGDSEGRVVFVSDIVTKQVVKSFPCNSP
IAYIAVETIPDDFVNNLATSTTTNKADKKHRMIPQFKRVLASTNSEEHQIFLDIPGKTTATTNATG
NIDFATWLQKGQSEELQFKNLSGINSIVKQVGNENVSDLEERLQRVSQAYTEL RNKHEELIKEHAK
LLDKLE

YNL190W_homolog 896bp public: 1..896; CDS: 501..893 (SEQ ID NO 435)

TTTCTGCAAGTATTGCGTGTGCTGCACAACTTTTTATATCCGAAAATTTTTGGCCGGGAACGAAA
CGGCAAGAAAAACAGAAACAATACCACCAGCACGGACAAAAAGATTATAAGCTTTGTGTAATAAG
GTTATGTCATCGGGTATTACAGATTGCAGGGCCATCTTGTCTTCATCAGTTATAGCATTTCATAA
AAATAAGCCACATATGTGTACAGCGCTGAGTCTACTCAACATGTGTAAATAGAATAAATCAATTGA
CACAGTCTTTTGAGATCTGTTATTCTGGCCTATAGCGTTT TAGGAAATTGCGGTATTTTCTTGCTCT
GTTTTTCTTTTATCTATTTTCGCACGACTTGGGGTGGTTTGTGTGACTTTTTTAGCAAATTAATTT
TGTCGGTCTTCGCAGTAAAAATAAAAAATTCAAAAAAACAATTGACTTTTTTTTTTACTTT
CTTTCTTTTCTATCAACAATACTAATCACAAGCCAACCATGAAATTCACTACTGTTGCCACTGTTT
TTGCTATTTCTCATTAGCTGCCGCTAAAGGTGGTGAAAAAGATCACGGTAAAGCTTCTACTGTCA
CCAAATATGTCACTGAAACTACCCACAGATACGGTCGTTT TGACAAAACCAGTAGATCTAAAAAGC
CAAAGGAAACTGGTACTCACAGATACGGTAAATTCACAAGACTCCACGTCCAGTTACCACAACCTG
TCTTGGTCAAAGAAAGCGACCTTCCAAAGAAAGAGATGCTGTTGTTGCTAGAGATTCTAAAAACG
CTTCTTCCAACCTCTACCACCTCTAGTGGTAACAATGGTGTGCCACTGGTGTGAGCTTGGGTCTTG
CTGGTGTCTTAGCTGTTGGTGCTGCTTTGGTCATCTAA

YNL190W_homolog 131aa (SEQ ID NO 436)

MKFTTVATVFATVFAISSLA AAKGGEKDHGKASTVTKYVTETTHRYGRFDKTSRSKPKKETGTHRYGKFN
KTPRPVTTTVLVKESDLPKKRDAVVARD SKNASSNSTSSGNNGVATGVSLGLAGVLAVGAALVI

YNL208W_homolog 1076bp PathoSeq: 1..1076; CDS: 501..1073 (SEQ ID NO 437)

TTTTTGATCAGGCCTTTTGT TTTTTTTTTTTTGGGTGGTGCTGTGGTTCGTTGGGTAGTTGGCTCTTG
TTTCGGTTC TACTTGTTCCTTTTTTTTATTCTCCTCGTTAATCCTAATTTTGTGTAACAAATTAAT
TATAGGGAGTTGGA AATTA AAGCTTGAAAAGAAAGAAAGAAAGAAATACCAACGTGGAATTTCT
ATTACGTAAGTCACTATAACTTGCATAGAAATTT CAGGTTTTCAATTTAAGAAAGTATTAATCAAC
TGAATTAAGCAATTGAAACGAATTGAACCAGCTCAGCATTATTTTTTCGTTTTCTTTTTTTTCAA
GGGGTGGGTGAAAGAAAATCTAAAAATATATAAATACTCCACTTATCTCCTCTCTTCTCTCTT
TCTCTCTCTA ACTCAATTTCAATTTTCCCAAACCAAAATTTCTTTCTTTCTTTCTTTCTTTATT
TTTTACTCAATTGAATCAATATTA AACAATAAAGCCATGTCAGCTAACGATTTTTATTCATCTG
GTGATCAATCCAATTATGATCCAAAAAGATCCTCGAATCAAGGATCATCATCAATGATGAAC
AACAAGACAGAGGGTTATTATCTACTGTGCGCCGGTGGTGTGCTGGTGGTTATGGTGGTCACAAAT
TAGGTGAAAAGGCACAACATGGTACTTTGGGTACTGTATTAGGTGCCATTGGGGGTGCCATTGGTG
CCAATAAACTAGAAGATGCTTATGAAGACCGTAAAGAACATAAAAAACACGAGCAACAATATGGTG
GTAGTGGTAAACACGAAGGCGGAAGACATGAAGGTGGTTTTGGTGGTGGTAGACCAGATGATCGTT
ATGAAGGCGATAGAAGAAATGATAATTACGGTGGTGGTTACAATGATAGAAGAGATGACGGTTATG
GTGGTGGTTACGGTGGTGGCAGACCAGACGATAGAAGACACGAAGGTGGTTTTCGCCGGTGGCAGAC
CAGATGACCGTTTTTGGTGGCGGTAGACCAGATGACCGTTTTTGAGGTGACAGAAGAGATGATAGAA
GAGATGACCGTAGATGGTAA

YNL208W_homolog 191aa (SEQ ID NO 438)

MSANDFYSSGDQSNYDPKRSSNQSSSSNDEQQDRGLLSTVAGGVAGGYGGHKLGEKAQHGT LGTV
LGAIGGAIGANKLEDAYEDRKEHKHEQQYGGSGKHEGGRHEGGFGGGRPDDRYEGDRRNDNYGGG
YNDRRDDGYGGGYGGGRPDDRRHEGGFGGGRPDDRFGGGRPDDRFGGDRRDDRRDDRRW

YOL031C_homolog 1745bp public: 1..1342, PathoSeq: 1343..1745; CDS: 501..1742 (SEQ ID NO 439)

TTGGTATTGAAGACACCGAAGACTTGTTGAAAGATATTGAACAAGCTTTACAAAAGGCTGCTTCTG
TTTGAGGGGATGTTTCATTAGCAATGTATATAATTATTGTATATTATGACAAAGAAAGAAAAAGAA
AACCAGAAAAGTGGTTTATACAGGAATATTTTAATAGAAATATCGCTTATATTGTGATAAAAAATT
TGAAAGACAATCCGAATGTAGTGCTTGTCTTATTCTGCTTGGGAATACTGTAGTATTAGCATCAAT
TGAGGAAATTCCAGATAGCTAACGGTTTTGCGATTACGAATTTTCGCAACCAAATAAATATGTGACA
AGGAATACACTACTGATCAAGGTTATTCTTAGTACAATGGAAAAAAGAAAGCAACAAAA
AAACGAGAAATTAATGAACACGACTTCACCTTCTACAACCTACTGGGAAAAAAGGCAGAGAGTTA
TTGAAAAAGGATCATATCAAGTTCTTATTGTATATTATATGAAGTTTTCTGTTTTAGTATTACTTG
CCAGTTACTTAGTTGGTGTGAATTCCTGATTGTTGATACTTCAGAGGAATTAATTTGTCCAGATC
CAGAAAACCCCTTTAGATTGTTATCCAAAATTGTTTTGTTCCAACAAACGAGTGGCAAACCATTAAC
CAGGTCAAGATATACCACCTGGGTTACACGTTAGATTAAATATAGATACGTTGGAAAAAGAGGCCA
AGCTAATGAGTGCTGACGAAAAAGACGAGCCAGTTCAAGAAGTAGTTGTTGGTGGCGAATTGCAGG
ATCATTCGAGGGAAGCCATCACTGAGAATCTACAAAAGTTGCATGAGCTGAAACATCCTGAAGTAA
AACAGGAGCACGCTCATCGTACAAAGGTTAGCCAGGGAGATTTGAGTAATTTTGACGCAGCTTGTC
TGGAAATTGAGAGTTTCAAGCCACATGAGAGTGATGTGGAAAGGTTGCATTTGGCACTAGATACTT
TAGAGGAATTAAGTCATGATATCGAATTTGGGGTGAAATTGACCTCAGACAAAGCCATATTTTCAGA
GTTTTGTCAACATTGCCAATGGTGCTTCTGATCCAAAAATAACCGAAAAGGTATATCGTGTAATGG
GGTCTAGTTTGAGAAATAATCCTGAAGCGATTAGTAATATCTTGACCAACTTCGACAAGAGCTATG
TGGATAATTTGTTTGAGCAATTAGCGAATGAAATGATGTTCTACAAAAGAGGATTTTGGGTATAA
TTCAAGCTTTAGTCCAAAATAGCCATTTTGCAAGACAATATTTTTCATTTGACCACAGTTCCGGGT
TAAATGATTTAATAGCGATTTTTCCTCAAACTTGGTCCAACTCAAAGTCCAGGGCAAGTAACATTT
TAGAGGATTTACAATTGTTCCAGTAACAAACGATAGAAGATCACTTGAAGATCAAGATCCTGAAT
CACAGGTTTCAAAATTTATTCAGAATTCCTTTGTTGGAAATAAACTTGACGAGAAGAATTTCAAGT
CTTATTTTGATCAACTAGTAAATTTGCATCAGCTGAATAAGAGTTTGCGACCAAGTGGTGACTTTC
TCAATTGGTTAGCTGAAGAAGTGGAGTCGCGTAAAGAGAATAAAAAAAGAGACGATTATTCACAAG
AAGACAAAGACTTTGATGAGTACATGTTGCGAGCACGTCATGAAGTATTTGGCAATCCAATGGGAT
TAAGAAAGGCAATTGCCGACGAGTTGTAG

YOL031C_homolog 414aa (SEQ ID NO 440)

MKFSVLVLLASYLVGVNSSIVDTSEELICPDPENPLDCYPKLFVPTNEWQTIKPGQDIPPLHVRL
NIDTLEKEAKLMSADEKDEPVQEVVVGELQDHSREAITENLQKLHESKHPEVKQEHHRTKVSQ
DLSNFDAACSEIESFKPHESDVERLHLALDTLEELSHDIEFGVKLTSDKAIFQSFVNIANGASDPK
ITEKVYRVMGSSLRNNPEAISNILTNFDKSYVDNLFQLANENDVLQKRILGIIQALVQNSHFARQ
YFSFDHSSGLNDLIAIFPKLGPNSKSRASNILEDLQLFPVTNDRSLEDQDPESQVSKFIQNSFVG
NKLDEKNFKSYFDQLVNLHQSNKSLRPSGDFLNWLAEVESRKENKKRDDYSQEDKDFDEYMLRAR
HEVFGNPMGLRKAIADL

YOL048C_homolog 1244bp PathoSeq: 1..27/985..993, public:

28..984/994..1244; CDS: 501..1241 (SEQ ID NO 441)

ATGATTTTTTTCCTTGATTTTAGAGCTGTTAATTATACCTTTTTTGTTCCTCAAATAAGCGCTAAAAA
TGATTGAAATTAAAAATACTAATTTCCAGGTCAAAGTAAACACTATAAAACAATATATTTCAAT
AACAGGAGCAGTAATTAGCTTCAACATCAAGGTACTCTTTTATTTTTCTACCAAAAACACATCTGA
AGTAGCTCTTATCCATAGATCCAAATATTTTAACCTTTTTTTTTTCTACTCTCATCTACTTTTTT
TTGCAACACTTACTGCTCACAACGCCAATGACCATAACCATTAATTTCAATAATCAAATCAAGAGCT
TATTTGTATCCTCTCAAGGTATGTTAATGTATTAACAACACCGATTCTATTTACCAACTAACACG
ACAGAAAGGGGTGTACTATTTTGTAACACATCCCACCGTTTGGCCCTTTTACATAACCATATTGA
TACCTCAATTGGTCCTTACACTAGTCATTTACCTGATTATGTTTTCATTGTTCTTCCCACCTCAAG
CTATTGTATATACATTGTTAATGGGACCATTAGGGGTGATTGGTGCGTGGTATAGTTTGATCCTGC
AAGCGAGCACATTGTCTATATTTGTTGTCACAATATCCTTAATGCCTCACATACAACGAGTGGCAT
ATGATGCAATATTGAGTAGAGAGTGTGCAAATGATGTGGTACTAATGGGAAAACCTTAGGAGGTATA
GAAAACCTACCCATTAGAGTAAGGGCCAGAGAATACCTTAAGGCCATTCCAGATTTTTTCGATCTTTC
CCTTCTCTTTGCTCAAGCTACTTGTGTTTTTCGGTATTTACTTCATACCCTTTGTAGGTCCAATCA

TTGTATTGTTTTTCCAATCTTCCAAGCGTGGACTAAAGGCACATGCAAGATACTTTAAGTTGAAAG
GGTTTCTGCGTAGTGACATAAGAACAATCCACAAGCTAAACAGACCAGCATATATGGGGTACGGAG
TGGTTGCGCTTTGGCTCGAGCTGTTTCCATTTATCAATATGTTTTTTATGTTACCAATACTTTGG
GAGCTGCTTTGTGGGCAGTTGATATTGAACAACAAGAGAAGGCCGTCACAGAGAATGTGGCCGCAG
CTACTACCACCGCCACAGATACGAATAGCGTCAATCAACAAGGTCTAGTTATACCCGTACACAATG
AACCAGCAACTAATATACCTGAGGCTACCCCAAAAACCTGCTACAAATACCATCTAA

YOL048C_homolog 247aa (SEQ ID NO 442)

MFSLFPPQAIVYTLMLGPLGVIGAWYSLISQASTLSIFVVTISLMPHIQRVAYDAILSRECANDV
VLMGKLRRYRKLPIRVRRAREYLKAIPDFSIFPFSLLKLLVFFGIYFIPFVGPIIVLFFQSSKRGLK
AHARYFKLKGFSRSDIRTIHKLNRPAYMGYGVVALWLESFPFINMFFMTNTLGAALWAVDIEQQE
KAVTENVAATTTATDTNSVNQQLVIPVHNEPATNIPEATPKTATNTI

YOR027W_homolog 2270bp PathoSeq: 1..947/1781..1828, public:

948..1780/1829..2270; CDS: 501..2267 (SEQ ID NO 443)

GCATTTTACTTATTTAGATATTACTTCATATTGCTTTTATTTAGATTGATTTTGTTTAACAGTGAA
AGTTTTTATTTTTTTTTTTGTTTAAAGTTTTTATTTTTTTTTTTGTTTAAAGTTTTTGTATTATACAA
TATTTAAATTATAGTAATCATCCTATAAATTTCAAAGTCAAAGACAGATCTTAAGGTCTAATTAA
TAACTCTCTATGGCCTTCTGTGTCAAATTGTTGTCGTTTGATAACAAGTTTGGAACGGTAATGGTT
GAAATTAGAAAAGAAAAAATTACACATGGTAGCAGCTGATGTATAGAACTTTCTAGCAAAAAAAA
AAAGAAAGAATTTTTTTTCTTCCATTTTTTCAAATTTGAGAGATCGAAATAATTTCTTGAATTTA
TTAAAAGGGAACCCCTTCCCGAAAAATCCAAAACCAAACCTTCCACCCAAATATCAAATAACTAAC
TTATCATTCCAACAGATAATATTTCCCACTTCAATAACAATGACAACAGCTGACGAATACAAAGCAG
AAGGTAACAAATATTTTGCTGCTAAAGATTTTGAAAAGGCGATTGAAGCATTCACTAAAGCAATTG
AAGCATCACCTGAACCAAACCATGTTCTTTATTCAAATCGTTCTGGATCTTATGCCTCTTTAAAAG
ATTTTAACAACGCATTAAAAGATGCTCAAGAATGTGTCAAGATCAATCCTAGTTGGGCCAAAGGGT
ATAATAGAATTGCTGGGGCTGAATTTGGTTTAGGTAATTTTGATCAAGCCAAATCCAATTATGAAA
AATGTTTGGAGTTGGATCCAAATAATGCCATGGCTAAAGAAGGTTTAAAATCAGTTGAATCTGCTT
TATCATCTGGTGGTGGTGAAGGATTTAGGATTTGGTAAAATTTTAAATGATCCTAATCTTT
ATACTAAATTGAAAAATAATCCTAAAACAAGTGAATTTATGAATGATCCTCAATTTGTTGCTAAAC
TTGAACGTCTTAAACTAATCCACAATTGGGTAATCCTGATATGTTTAGTGATCCAAGATTATTGA
CGGCTTTTGCTGCTTTAATGGGTATTGACATGGATTTACCAAATATGGGATTCAGTCTCCAAACG
AATCACAATCCAATGCATCAGAACCAAACCTGGAACCAAATCAGTACCAGAATCTAAACCAGAAC
CAAAGCAGAACAAAAGGAAGAAGATCAACCTCAGCCAAAGATGAAGACACTCCAATGACTGATG
CCCAAGACGACACTAATGATAATGATGCCAAAACCCAAGCTGACAATGCTAAAGCTGAAGGTAATG
CCTTATACAAGAAACGTCAATTTGATGAAGCAATTGCCCGCTATAATAAGGCTTGGGAATTACATA
AGGATATCACTTATTTAAACAATCGTGCTGCTGCCGAATATGAAAAGGTGATTATGATGCTGCTA
TTGCTACATGTGAAAAGGCCATTGATGAAGGTAGAGACATGAGAGCTGATTATAAATTGATTGCTA
AATCATTTGCTAGATTAGGTAATATTTATTTGAAAAAAGATGAATTACCCGAAGCAGTGAAAAATT
TTGAAAAATCTTTAACTGAACATCGTACCCCTGATGTTTTTAAATAAATTAAGATCAACTCAACGTG
AAATTAAACTAGAGAATTAAATGCTTATATAGATCCAGAAAAGGCTGAAGAAGCAAGATTACAAG
GTAAAGAATATTTACCAAAGGAGATTGGCCAAATGCCGTTAAGGCTTATACTGAAATGATTAAAA
GAGCACCAGAAGATGCTAGAGGATATTCTAATCGTGCTGCTGCATTGGCAAATTTGTTATCATTTT
CTGATGCTATACAAGATTGTAATAAAGCCATTGAAAAAGATCCAAATTTTCATTAGAGCTTATATTA
GAAAAGCTAATGCTCAATTGGCAATGAAAGAATATAGTCATGTCATGGATACTTTAACCGAGGCAA
GAACTAAAGATGTTGAATTGGGTGGTAAATCAATTCATGAAATTGATGAATTAATGAATAAAGCTA
CTTATCAAAGATTTCAAGCCATTGAAGGTGAAACTCCTGAACAAACTATGGAAAGAGTTTCTAAAG
ATCCAGAAATTGTTCAAATTTTACAAGATCCAGTAATGCAAGGAATTTTAGCTCAAGCTAGAGAAA
ATCCTGCTGCTTTACAAGATCATATGAAAAATCCTGAAGTTTATAAAAAAATTAATATGTTGATTG
CTGCTGGTGTATTTCGTACCAGATAA

YOR027W_homolog 589aa (SEQ ID NO 444)

MTTAD EYKAEGNKYFAAKDFEKAIEAFTKAIEASPEPNHVLYSNRSGSYASLKDFNNALKDAQECV
KINPSWAKGYNRIAGAEFGLGNFDQAKSNYEKCLELDPNNAMAKEGLKSVESALSSGGGDDKDLGF
GKILNDPNLYTKLKNPKTSEFMNDPQFVAKLERLKTNPQLGNPDMFSDPRLLTAFALMGIDMDL
PNMGFTAPNESQSNASEPKSEPKSVPEKPEPKAEQKEEESTSAKDEDTPMTDAQDDTNDNDAKTQ

ADNAKAEGNALYKKRQFDEAIAAYNKAWELHKDITYLNNRAAAEYKGDYDAAIATCEKAIDEGRD
MRADYKLIAKSFARLGNIYLLKKDELPEAVKNFEKSLTEHRTPDVLNKLRLSTQREIKTRELNAYIDP
EKAEEARLQGKEYFTKGDWPNNAV KAYTEMIKRAPEDARGYSNRAAALAKLLSFPDAIQDCNKAIEK
DPNFIRAYIRKANALAMKEYSHVMDTLTEARTKDVELGGKSIHEIDELMNKATYQRFQAI EGETP
EQTMERVSKDPEIVQILQDPVMOGILAQARENPAALQDHMKNPEVYKKINMLIAAGVIRTR

YOR312C_homolog 1019bp public: 1..1019; CDS: 501..1016 (SEQ ID NO 445)

CCACTAACAACTTTTTTTTGTACTATACACCACTGAAAAAAAAAAAAAAAAATTTTTGTAAAAATCT
TAAGAATTTTCAGTTTAGAAGGTATTCAACAACAACCGAAGAGTATGTTCAACATCGTTATAATAGA
ATAGAATAAGAGCATGACAACAAAGGGATACAAGCTTGAAAAAGAAAAAGGGTGGGATATCTTAA
AATTATTAAAGAGTTTTTTTTTATAACATGTCATTGAGATTGAGATTGGGAATACTGAATTCGATTT
TAAAGTCATTGGATGGGAGAGTTAATTATTCGTTTTATTATTAGGATTACCAATGAATAGTAATGA
AGTGATGGAGAGATAGAATGAAAGTATTCAGAAGAGCATCAAGTCCCTTATAAGTTTGTGAGACAT
AATATGTCTACCCCCCTGTCAACTTGTCAATAATTTATTGCTCGTCCTTTAAAAGAAATGAATAA
AAAGATTTACTAACTTAATTTCAATTATTTATAGAAAGATGTCTAGATTAAACGAATATCAAGTTA
TTGGTCGTAATTTACCAACTGAATCCGTTCCAGAACCAAGTTGTTTCAGAATGAGAATTTTTGCTC
CAAACACCGTTGTTGCCAAATCAAGATATTGGTATTTCTTGCAAAAATTGCATAAAGTTAAAAAG
CTTCTGGTGAAATTGTATCTGTCAACATTATTTCTGAAGCTAAACCAACTAAAGTTAAACTTTTG
GTATTTGGTTAAGATATGAATCCAGATCTGGTATTCATAACATGTACAAAGAATACAGAGATGTTA
CTAGAGTTGGTGCTGTTGAAACCATGTACCAAGATTTAGCTGCTAGACACAGAGCTAGATTTAGAA
GTATCCATATTTTGAAAGTTGTTGAATTAGAAAAACTGATGATGTTAAAAGACAATACGTTAAAC
AATTTTGTACTAAAGATTTGAAATTCCTATTACCACACAGAGTCCAAAAATCTAAGAAATTGTTCC
AAGCTACTGCTCCAACCACTTTCTACTAA

YOR312C_homolog 172aa (SEQ ID NO 446)

MSRLNEYQVIGRNLPTESVPEPKLFRMRIFAPNTVVAKSRYWYFLQKLHKVKKASGEIVSVNIISE
AKPTKVKTFGIWLRYESRSGIHNMKEYRDVTRVGAVETMYQDLAARHRARFRSIHILKVVELEKT
DDVKRQYVQFLTKDLKFPLPHRVQKSKKLFQATAPTTFY

YOR369C_homolog 932bp PathoSeq: 1..228, public: 229..932; CDS:
501..929 (SEQ ID NO 447)

TGTTTACTTTTTCTGTAGTTTTTAAAGTTTCCTAATTTAACTTCCAAAAGTTTCATTAACAACAATA
TTAACATACCTTTGTCACAAGCAATTATATTGAAGTTTTTTGATACAAGTGTGTTGTTTTTTGTG
TACATGTGAGATATATAATTGTGTATATACAGTCACGTGAATAGAGCAGAAAAATTACGAAGTAGA
AATATTGGTAGCGCGTTAGGGCTATAGCCCTATTTAGTTTGTGCACCACACGACTTACAATTTTTT
TTTTTTTCTTTCTTAGAATCCTTGAGGCACTGACACTGTACTCTCTCTCTCTCTCTCTCTCTCTG
TAGGTAGTGAAAAATTTCCACTAGTCTTCCATAACCCACCTAGGTTCTTTCTTTTGGAACCACT
GAGCAGTAAATCAATTTACTTGACGAAGAAGTCTATACATAAATATAAACTTGTCCCCTCCCCCCC
CTTTTTTTTAACTAACTAAGAAGAAAAAATTAATAAATGTCTGACGTTGAACAAGAACAATTTG
TTGAAGAAGTTGTTGTTGAAGAACAATCCGGTGCCATCACCATTGAAGATGCTTTAAAAGTTGTTT
TAAGAAGTTCTTTAGTCCATGATGGTTTAGCTAGAGGTTTAAGAGAAGCTTCTAAAGCTTTATCTA
AAAGAGAAGCTCAATTATGTGTTTTGTGTGACTCTGTTACTGAAGAATCAATCATCAAATTGGTTG
AAGCTTTATGTAATGAACCAGAAGAAAAATCCCATGATTAAAGTTTCCGATGCTAAATTATTGG
GTGAATGGGCTGGTTTATGTCAATTAGATAGAGATGGTAATGCTAGAAAAGTTGTTGGTGCCTCTT
GTGTTGTTGTCAAAAAGTGGGGTGCTGATTCTGATGAAAGAACATCTTGTTGGAACACTTTTCTC
ACAATAA

YOR369C_homolog 143aa (SEQ ID NO 448)

MSDVEQEIVVEEVVVEEQSGAITIEDALKVVLRTSLVHDGLARGLREASKALSKREAQLCVLCDSV
TEESIIKLVEALCNEPEEKIPLIKVSDAKLLGEWAGLCQLDRDGNARKVVGASCVVVKWNGADSDE
RNILLEHFSQQ

YPL047W_homolog 881bp public: 1..811, PathoSeq: 812..881; CDS:
501..878 (SEQ ID NO 449)

AAAATTTCCAATCTTGAATTTTCATCTTCAACGTCATAAACTTGTCTGTTTGAAATTTATCGTCCT
CATTATCGTTGTCATTTTCATTGTCAATATTACGGTTACGATTTTGTTCCTTTGAAG
TCTTTGACTCTAGCTGTTTCATCTGTCATTACCCTTGGCTTGGTTTGTCTTACTGTTGAGCGATGAG
ACAAACTTTTTGATTGATTGCAACTGAACAAAAAAATACGACAGACACACACACACACACAC
ACACAATTTTCAGCTCCTTCCAAGTCGTGTTTTTTTGGGAAGAAAAAAAACAACTTGGCCCTAAA
AACTCTATGCTCTAACCGACAACATTAGATTACTTTGATAACTCACAACCTTTAATTAACACTATC
TACAAAATATGACAAGTACACCAATAACGTACAAGACACTAGTATGAAAGGCAAGCACAACTTGC
AAACAAAAAACCCCTAACTTTTATTATAGTTTTTGTGTTGATGTTATTTTGTGTTTTATACTAACTAAAA
TCTGTTTTTTTTTTTTTTTCAAAGGCCGATTCTATATTTAATGATCTAATCAACAATATCATTAAAC
AACATACATTAACAGTTTAACCAATATTAAAGATCATTCCTCATTATTAAATTCATCTAATAGCA
ATACTAATAGCAATACCAACGGTACAATTGCCAGTAATGGTGGAAATGGGACTACAAGTGATGAAA
ATAATGAAATTGAAAATTCAACAATTCAAGATAAATCAAATTTAAACAATTAGAACTTCAAGGT
ATTTCCGATGTCTTAATTGTGGTAGAAATATTGCCGGTGGGAAGATTTCATCTCATATAAGTAAGT
GTTTAGAACGGAAACGGAAATGA

YPL047W_homolog 126aa (SEQ ID NO 450)

MLFCFILTKICFFFFSKADSIFNDLINNIKQHTLTSLTNIKDHSSLLNSSNSNTNSNTNGTIAN
GGNGTSDENNEIENSTIQDKSKLKQLETSRYFRCLNCGRNIAGGRFASHISKCLERKRK

YPL137C_homolog 5344bp public: 1..3342, PathoSeq: 3343..5344; CDS:
1250..5341 (SEQ ID NO 451)

CTCTAGAAGTAGGACATCGTATAGTGTATAAACTCAATAAGTAATGAAGAAACACGTTTTGTTG
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TGATGGATCGTTATTAATGGAAACAGCTGAAAAATTATTAGTTGAAATAGAAAAGGGTAAGAAAGA
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ACATGCCAACGGATTATTATTAACACCAACGACCTCCACGGACGATCTCAGAAGTAGAGCCATGTC
GCCATCGGTCACTGTTGATACAATCCATGAAAGTGCAAATGAGTTGATTACTGCTGGACCAATTTT
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ACCAGAGTTGAGAGATGCTATAATGGCAGCTAAGGGAGTAGCAAATGTTACTGAATTAATTGATCG
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TGGTGACGATTTACATCAACTTGGTGACGGTAAACATAATGGTAATGGTACGGTTGATCCCATGGT
TAGTGAAGTTTATGACAAGTTGTTAAATGATGCTGAACGAGTCAGACTGAATAGAGATATATAA

YPL137C_homolog 1364aa (SEQ ID NO 452)

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SSSASSKQPQSHSSSTPSTTTNNGGNSSAAPKSSHHSKFNPSLVGPVSKHNREAEDLVSLTNLT
PAGSGIPIKRKPSISGNSIFKDSFLDDASSPSSSLNSDGLKFFRRRSSVASTPSTHASTPRVIL
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GNSQCVGVDFIAFNDLSKGQLRPFINAFNTGKVNVLVFFSLNSTNLSNIEETSDLIKSLINVKTLRF
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ILSPHVNRKAEQSSYFPVFANNDNLTPHQVVESNDEGRDVPIDKMTGRPVLIRSISQTSVHAKEQ
EIEEGELHKFGFFIQKERQKQQQQQQQQQNSHHQHQPASIQQENQSPSPQQGKYEDLPILNTLP
SGPELRDAIMAAKGVANVTELIDRINNHRVKIDAPSTKHHHELNKPNSDKVVEDEVEVSDNASIDS
TNGDDLHQLGDGKHNGNGTVDPMVSEVYDKLLNDAERVRSNRDI

YPL175W_homolog 1859bp public: 1..393/395..1859, PathoSeq:

394;CDS: 501..1856 (SEQ ID NO 453)

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TTATAATGAAGTAAAAACATGTAAGTGTGTAATTTTATTCAAGTCCAAAGGTATTGATTAATATTG
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GGCTAGGAGGAATAAAATCTGAGTAGAGAACTTTCGTTTATATCAGTTTTTTTGCAAGAAAAAAGG
AAAACAAAACAAAATAACACCACAAACGAATTACACAAGCACATCCTAAACACCACTCTGTTGGAG
CACCAATCAACCTGAGAAATGCAAACCTTGTAATAAAATATGGGATACAATATAGCAATGGTAACAG
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YPL175W_homolog 452aa (SEQ ID NO 454)

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IYRSSVFPTVFSFPILRNIFIRENIEIIHGHSFSTLCHEAILHGRTMGLKTVFTDHSFLFGFAEI
GSIMGNKALKFTFSDVGHVICVSHCKENTVLRGSIDPIKVSVIPNAVISKDFKPKSHCVNKNYTK
EITIVVITRLFPNKGADLLTAVIPKICQLKPKVKFLIAGDGPKFLDLEQMREKYFLQERVTLVGAI
KHEEVRDVMVQGDYILHPSLTEAFGTVIVEAASGLYVVTTKVGGIPEVLPNEMTSFAEPEENSLI
DAAIDAINKIESNEIDTSKFHDAVAKMYSWNDIARRTENVYNSLDLKLNESLLHRLQRYCCGII
AGKLYALCVIVDIFIFVILEWLYPADHIDKATKWPSAIKEEDESEETFIKPNKVN

YPL218W_homolog 1231bp PathoSeq: 1..407, public: 408..1231; exon 1: 501..518, intron 1: 519..676, exon 2: 677-1228 (SEQ ID NO 455)
GATACAATTCACGACCTCTAATTTCTTAGTGATAGGTTAATCATGAAATATATAAAATGTCTAGA
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TCAAGTGTTGTTACACTCTTGTTATTATTATTATTATATCGTTTACAAGTAGATTTCTCATTTTGA
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YPL218W_homolog 190aa (SEQ ID NO 456)
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VPTAVGEMELKNALGLYNTTGKDTGKLPEGTRPIEVFMVSVVMRSGYGEAFKWLSQYI

YOL127W_homolog 429 bp, public: 1..429, CDS: <1..429 (SEQ ID NO 475)
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AAATACCAAAGAAAATCAGTCCCACACTACAACAGATTGGATGCCACAAAATCATTTGTTGCTCCA
ATTGCCACTGAACTGCTATGAAAAAGTCGAAGATGGTAACACTTTGGTTTTCCTAAGTTGACATC
AAATCCAACAAACACCAAATCAAATCTGCTGTTAAAGAATTATACGATGTTGATGCCTTATACGTT
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TTGGATATTGCTAACAGAATCGGTTACATCTAA

YOL127W_homolog 142 aa (SEQ ID NO 476)
LIATTKASAAKKAALKGVNGKKALKVVRTSTTFRLPKTLKLTRSPKYQRKSVPHYNRLDAHKIIVAP
IATETAMKKVEDGNTLVFQVDIKSNKHQIKSAVKELYDVDALYVNTLIRPNGTKKAYIRLTSDYDA
LDIANRIGYI

YJL188C_homolog 117 bp public: 1..117, CDS: <1..>117 (SEQ ID NO 477)
TTAGATACCCAACCTTAGTTCTTCTCCAGTGCTTCTTTTAGCATTTGTATCTGATTTTGTGTCAGT
TCTCAATCTGATCCATTGTGGCAATGGTCTGTTTGTCTTTGAGCCTTAGC

YJL188C_homolog 39 aa (SEQ ID NO 478)
LDTQLSSSPVSSFSIVSDFVSSQSDPLWQWSVLLLSLS

YGR183C_homolog 198 bp public: 1..198, CDS: 1..198 (SEQ ID NO 479)
ATGTTGACAGTCCTTGGTCGTTTACTTGAAAGAACTCAATCTACGTTGCCACTATCTTTGGCGGT
GCTTTTGTCTTTCCAAGGTTTTTTCGATGTTGCAGTGAACAAATGGTGGGAGGAACACAACAAGCT
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YGR183C_homolog 65 aa (SEQ ID NO 480)

MLTVLGRLLERN SIYVATIFGGAFAGQGFDFVAVNKNWEEHNKAKLWKNVKGKFLEGE GEEEDDE*

YDR529C_homolog 457 bp Pathoseq: 1..457, CDS: 1..457 (SEQ ID NO 481)

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TTAAATTATTCAAGAAATTTTAGAATTCTTACTGCTCATCAATTAGCTTTATCTCATCAATTATTA
CCAGCTGAAAAAGCTGTTAAACCTGAAGAAGATGATAATTATTTGATTCCTTATATTTTAGAAGCT
GAAAAGGAAGCTTTTGAAAAAGCTGTATTGGGGAATATTGACGCTAGTGCGATTGTAATTAATACG
ACGAATAAGAAACCGACGAGGAAGAGGAAGAAGATGAGAAGGTCAAACATTGAAATATGAA

YDR529C_homolog 151 aa (SEQ ID NO 482)

MVQSMTSVVKAANFILARPTLSKIITPLAQKFTAYAGYREMGLKFNDLLLEETPIMQTAIKRLPSE
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TNKKRTRKRKKMRRSNIEI

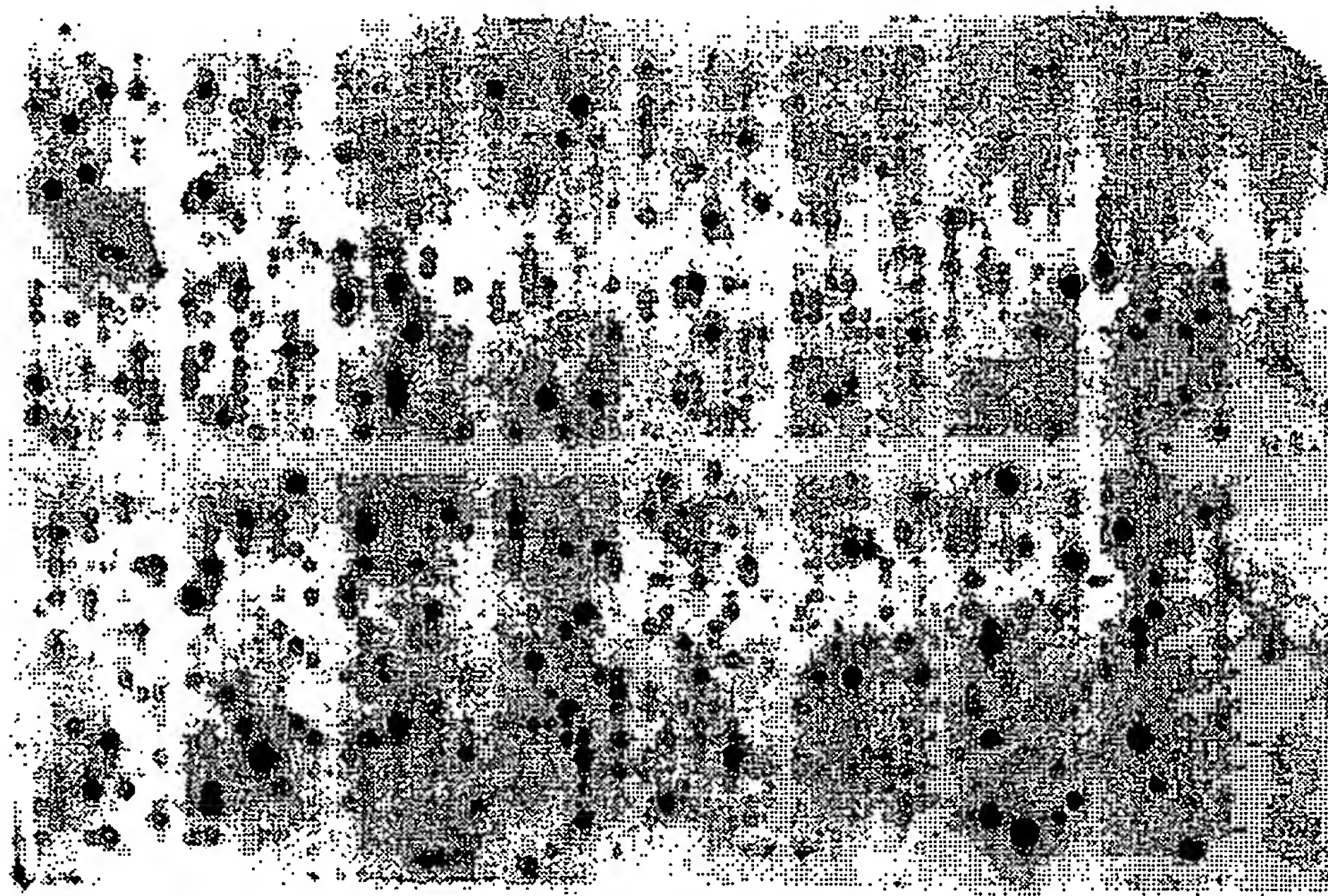
YBL003C_YDR225W_homolog 399 bp public: 1..399, CDS: 1..399 (SEQ ID NO 483)

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CAT

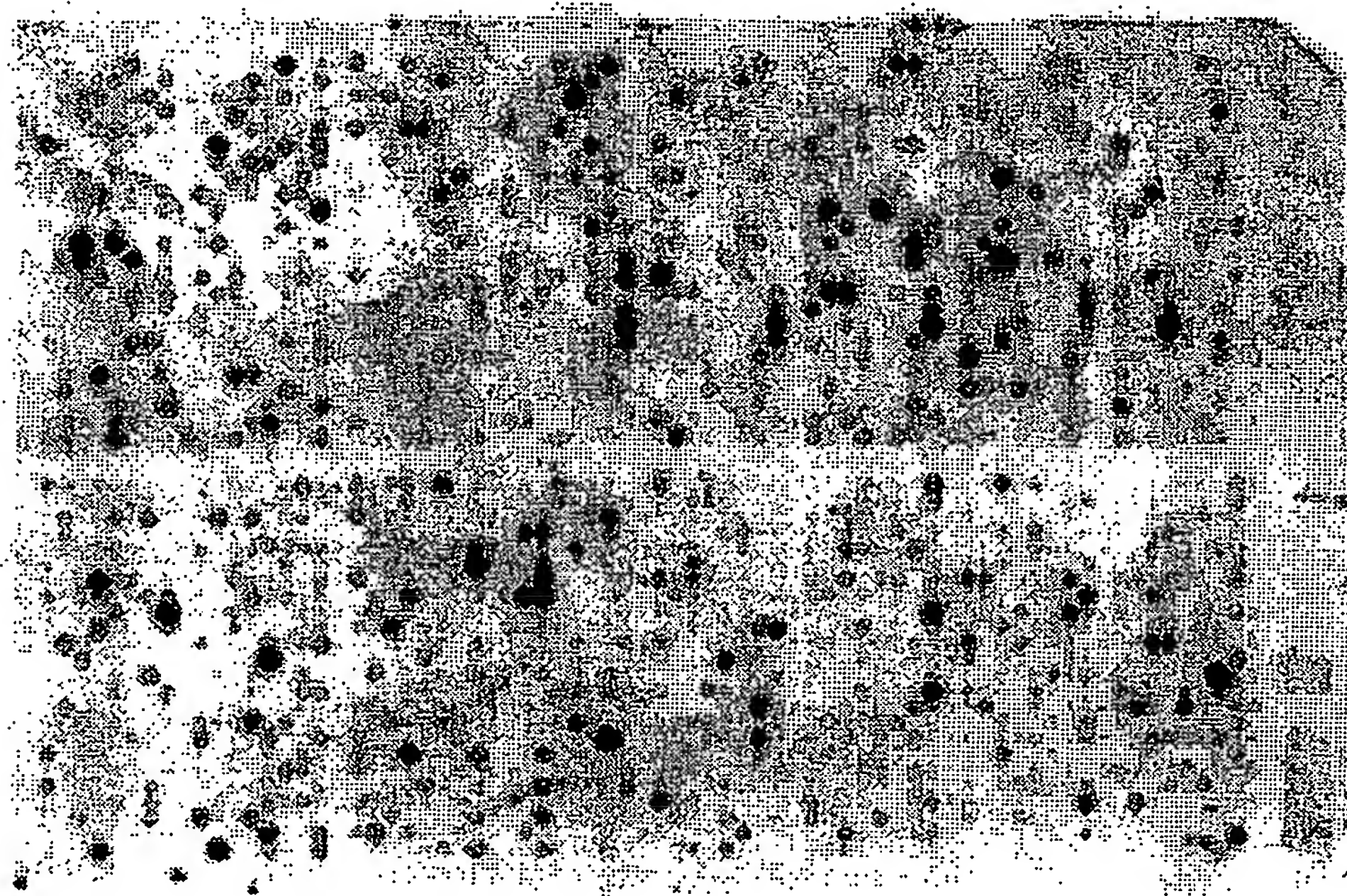
YBL003C_YDR225W_homolog 132 aa (SEQ ID NO 484)

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158/161



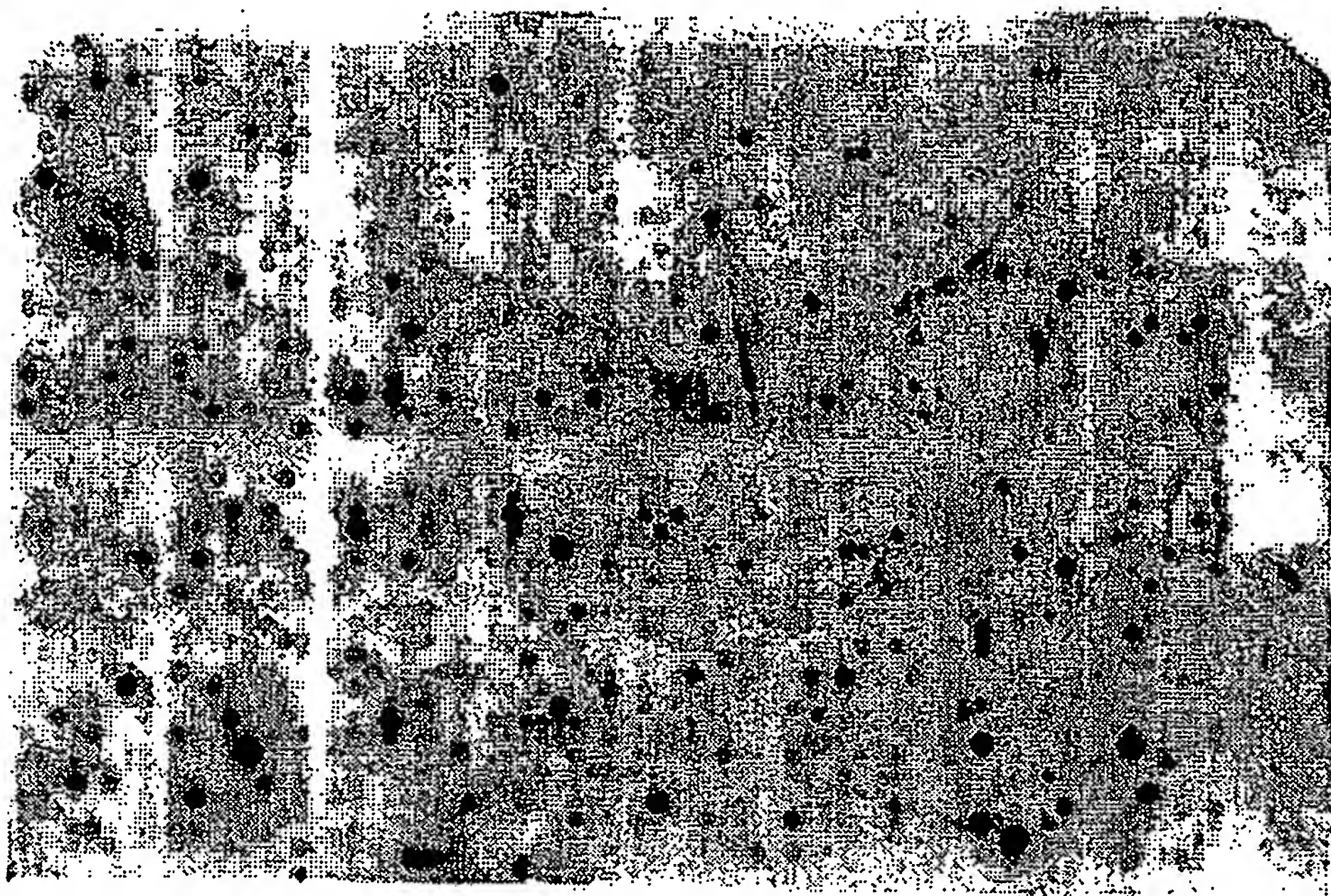
Filter I



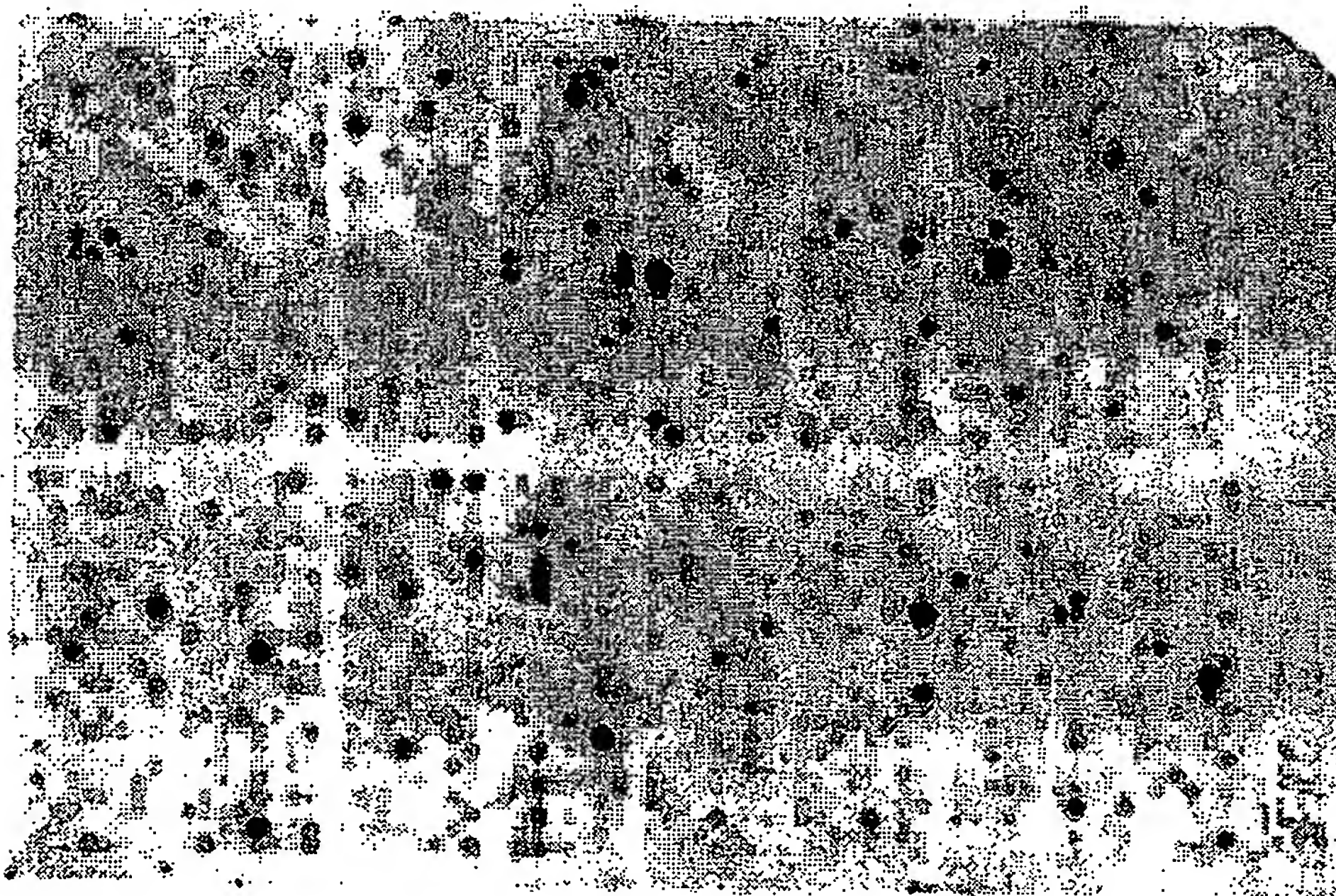
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FIG. 3A

159/161



Filter I



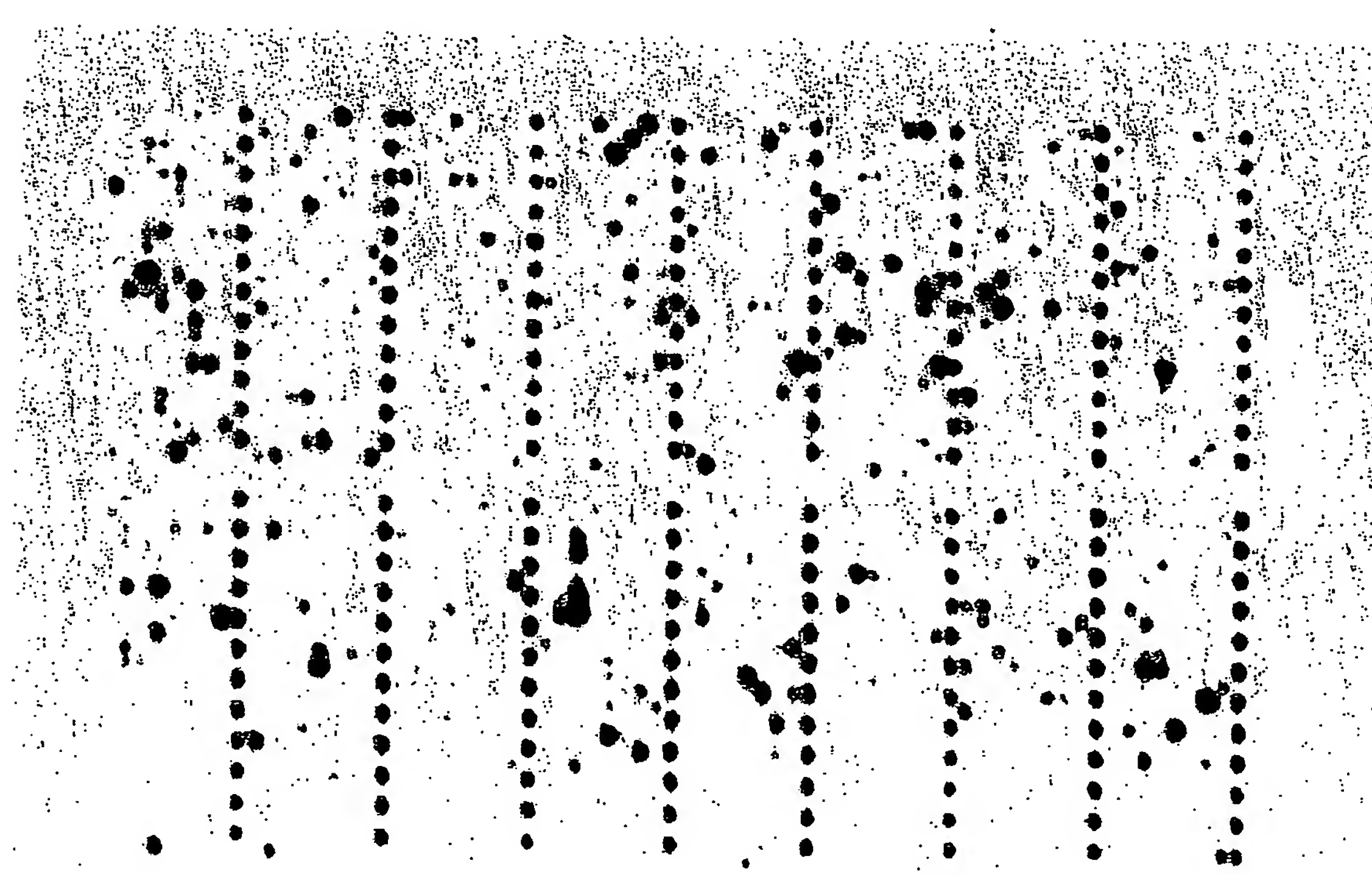
Filter II

FIG. 3B

160/161



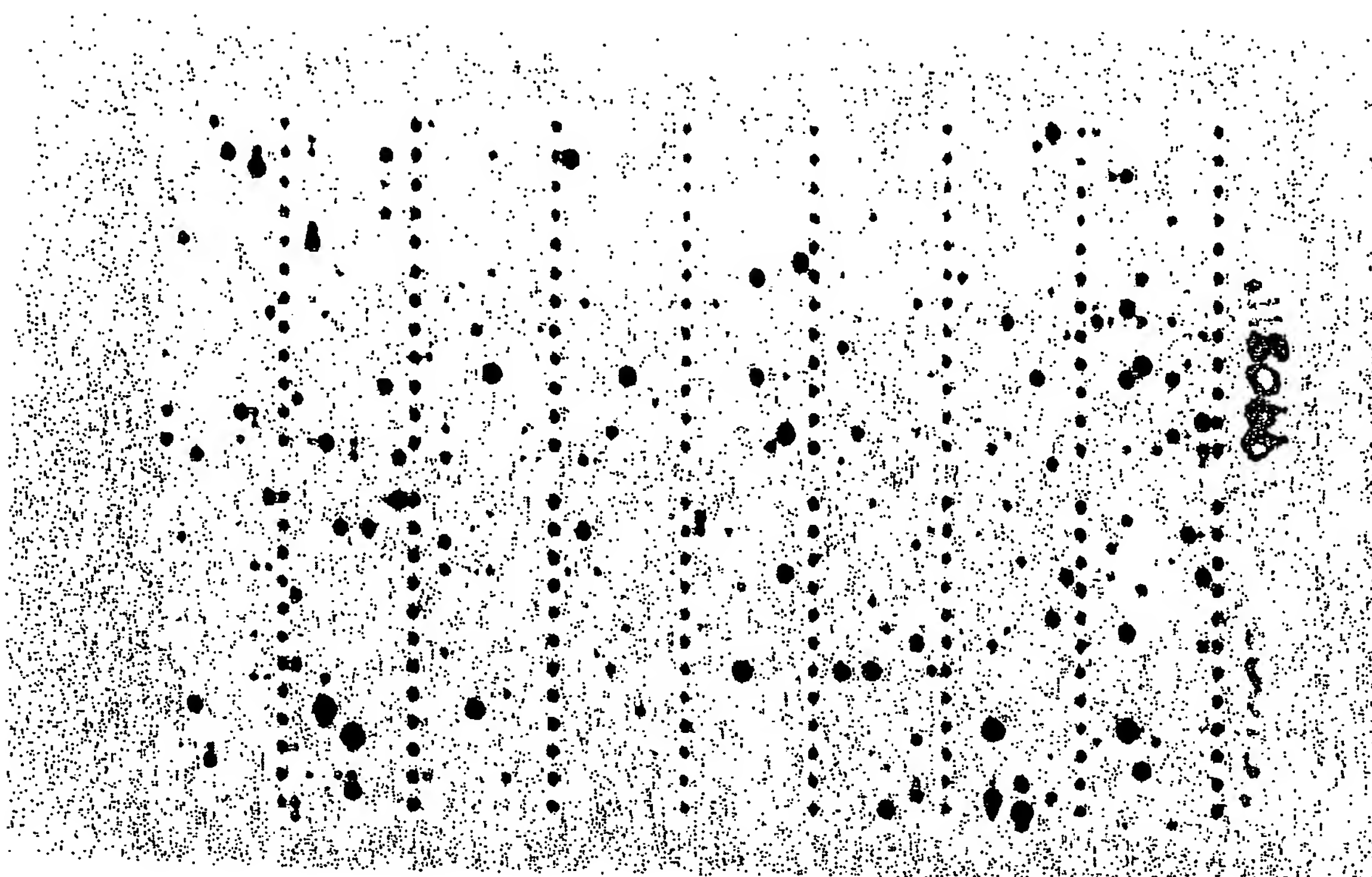
Filter I



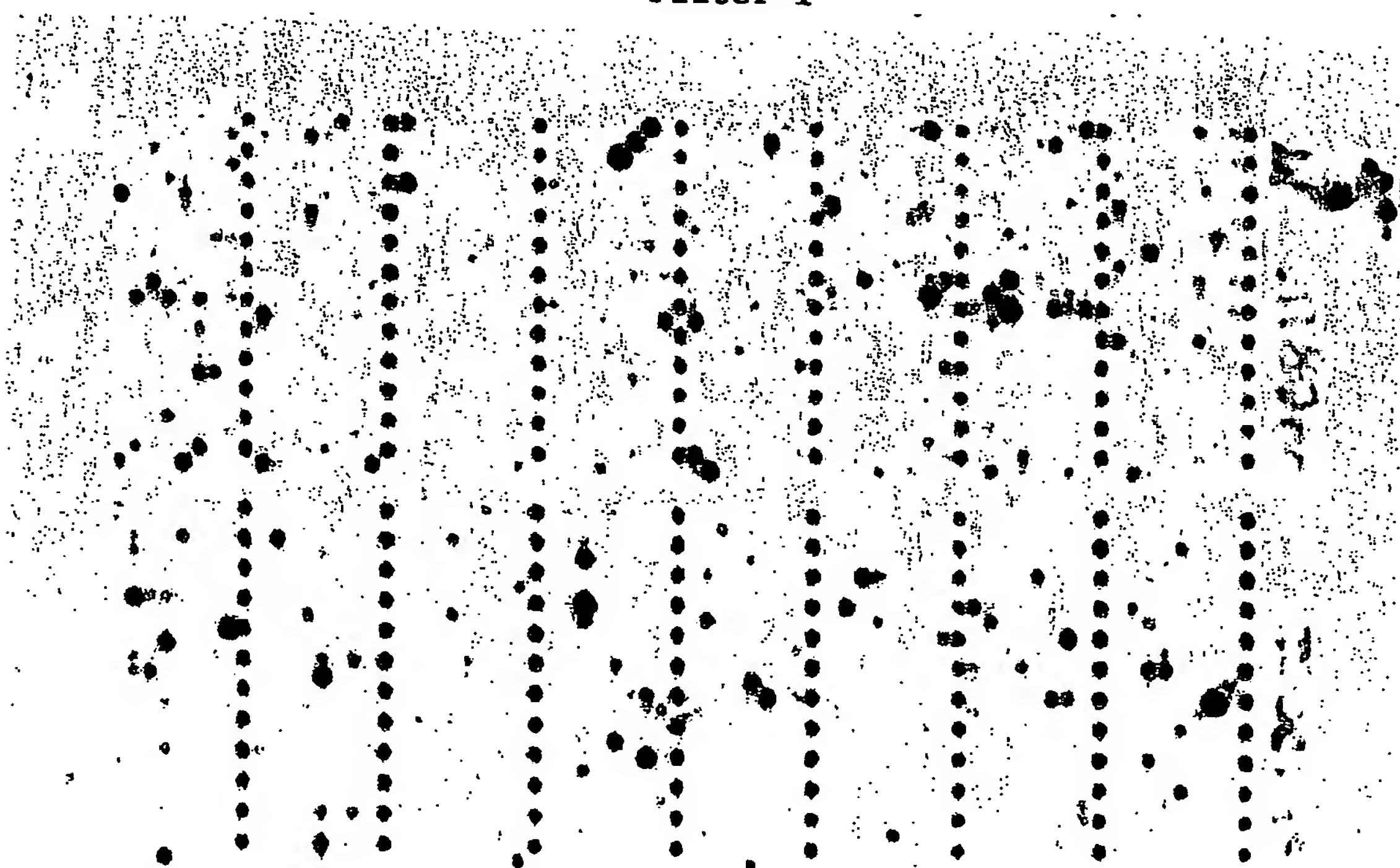
Filter II

FIG. 4A

161/161



Filter I



Filter II

FIG. 4B

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